



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115654

To: Ruixiang Li
Location: REM-4C70
Art Unit: 1646
Wednesday, March 03, 2004

Case Serial Number: 10/060765

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/449,249
FILING DATE: 24-No. 6503886-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 6503886tendburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "FGF-6"
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-449-249-15
Query Match 15.9%; Score 176.5; DB 4; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;
QY 13 LWSVVLGILLGACQAH-----IPDS---SPLLQ-----FGQV----- 44
Db 12 LNALVFLGILVGMVVPSPAGTRANNLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RQRYLYTDDAQOQTEAHLEIREDTGCGAADOQSPESLLQKALKPGVQIILGVKTSRFL 102
Db 72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYNAYESDLY 166

Search completed: March 2, 2004, 16:09:00
Job time : 38.4458 secs

12 LNALVFLGILVGMVVPSPAGTRANNLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71
45 --RQRYLYTDDAQOQTEAHLEIREDTGCGAADOQSPESLLQKALKPGVQIILGVKTSRFL 102
72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVVSLFGVRSALFV 129
103 CORPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAH 140
130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYNAYESDLY 166
RESULT 39
US-09-507-773-12
Sequence 12, Application US/09507773
Patent No. 6399386
GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kinoshita, No. 6399386iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: H095-01A2
CURRENT APPLICATION NUMBER: US/09/507,773
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: 08/776,207
PRIOR FILING DATE: 1997-06-23
PRIOR APPLICATION NUMBER: 08/441,629
PRIOR FILING DATE: 1995-05-15
PRIOR APPLICATION NUMBER: 08/279,217
PRIOR FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapien
US-09-507-773-12
Query Match 15.9%; Score 176.5; DB 4; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;
QY 13 LWSVVLGILLGACQAH-----IPDS---SPLLQ-----FGQV----- 44
Db 12 LNALVFLGILVGMVVPSPAGTRANNLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RQRYLYTDDAQOQTEAHLEIREDTGCGAADOQSPESLLQKALKPGVQIILGVKTSRFL 102
Db 72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYGLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYNAYESDLY 166

RESULT 40
US-09-449-249-15
Sequence 15, Application US/09449249
Patent No. 6503886
GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
Chandler, Lois Ann
Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERA
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "FGF-6"
US-08-718-904-15

Query Match 15.9%; Score 176.5; DB 3; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWVSVLAGLLGACQHP-----IPDS---SPLIQ-----FGQV-----44
DB 12 LWALVFLGILVGVVSPAGTRANNITLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RQRYLYTDDAQOCTEAHLEIRDTGVGGAADSPESLLQLKALPKGVITQILGVKTSRFL 102
DB 72 IKQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVWSLFGVRSALFV 129
QY 103 CQRPDGLYGLSHFDPEACSFRELLLEDGYNVQSEAH 140
DB 130 AMNSKGLYATPSFQ--BECKFRETLLPNNYNAYESDLY 166

RESULT 37
US-09-023-082A-14
Sequence 14, Application US/09023082A
Patent No. 6077692
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: COORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFPE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 198 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-023-082A-14

Query Match 15.9%; Score 176.5; DB 3; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWVSVLAGLLGACQHP-----IPDS---SPLIQ-----FGQV-----44
DB 12 LWALVFLGILVGVVSPAGTRANNITLDSRGWGTLLSRSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RQRYLYTDDAQOCTEAHLEIRDTGVGGAADSPESLLQLKALPKGVITQILGVKTSRFL 102
DB 72 IKQRRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVWSLFGVRSALFV 129
QY 103 CQRPDGLYGLSHFDPEACSFRELLLEDGYNVQSEAH 140
DB 130 AMNSKGLYATPSFQ--BECKFRETLLPNNYNAYESDLY 166

RESULT 38
US-08-776-207-12
Sequence 12, Application US/08776207A
Patent No. 6080718
GENERAL INFORMATION:
APPLICANT: Kirschner, Marc W.
APPLICANT: Kinoshita, No. 6080718iyuki
TITLE OF INVENTION: Receptor-Ligand Assay
FILE REFERENCE: H095-01A2
CURRENT APPLICATION NUMBER: US/08/776,207A
CURRENT FILING DATE: 1997-06-23
EARLIER APPLICATION NUMBER: PCT/US95/09172
EARLIER FILING DATE: 1995-07-19
EARLIER APPLICATION NUMBER: 08/441,629
EARLIER FILING DATE: 1995-05-15
EARLIER APPLICATION NUMBER: 08/279,217
EARLIER FILING DATE: 1994-07-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 198
TYPE: PRT
ORGANISM: Homo sapien
US-08-776-207-12

Query Match 15.9%; Score 176.5; DB 3; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWVSVLAGLLGACQHP-----IPDS---SPLIQ-----FGQV-----44

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; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-438-439C-10
;
; Query Match 15.9%; Score 176.5; DB 2; Length 198;
; Best Local Similarity 29.1%; Pred. No. 1.8e-09;
; Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;
;
QY 13 LNVSVLAGLLGACQAH-----IPDS---SPLLQ-----FGQV----- 44
Db 12 LWAFLVLGVLGVVPSAGTRANNLLDSRGWTLSSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RQRYLYTDDAQOTEAHLEIREDCGTGGAADQSPESLLQALKPGVLIQGVKTSRFL 102
Db 72 IKRQRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYSLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYAYESDLY 166

RESULT 35
US-08-438-439C-20
; Sequence 20, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-438-439C-20
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; Query Match 15.9%; Score 176.5; DB 2; Length 198;
; Best Local Similarity 29.1%; Pred. No. 1.8e-09;
; Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;
;
QY 13 LNVSVLAGLLGACQAH-----IPDS---SPLLQ-----FGQV----- 44
Db 12 LWAFLVLGVLGVVPSAGTRANNLLDSRGWTLSSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RQRYLYTDDAQOTEAHLEIREDCGTGGAADQSPESLLQALKPGVLIQGVKTSRFL 102
Db 72 IKRQRLYCNVG--IGFHLQVLPDGRISGTHEENPYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYSLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ-ECKFRETLLPNNYAYESDLY 166

RESULT 36
US-08-718-904-15
; Sequence 15, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6037329tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 760100.415C1
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:

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QY 13 LWSVLAGLLGACQAH-----IPDS-----SPLIQ-----FGQV-----44
Db 12 LVALVFLGILVGMVPSAGTANNTLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RORYLYTDDAQOETAHLEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFL 102
Db 72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENFYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYSLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ--BECKFRETLLPNNYNAYESDLY 166

RESULT 32
US-08-441-629-12
; Sequence 12, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 5766923iyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,629
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,217
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-629-12

Query Match 15.9%; Score 176.5; DB 1; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVLAGLLGACQAH-----IPDS-----SPLIQ-----FGQV-----44
Db 12 LVALVFLGILVGMVPSAGTANNTLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RORYLYTDDAQOETAHLEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFL 102
Db 72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENFYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYSLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ--BECKFRETLLPNNYNAYESDLY 166

RESULT 33
US-08-471-14
; Sequence 14, Application US/08867471
; Patent No. 5872226
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,471
; FILING DATE: 02-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/439,725
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 617/678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-867-471-14

Query Match 15.9%; Score 176.5; DB 2; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;

QY 13 LWSVLAGLLGACQAH-----IPDS-----SPLIQ-----FGQV-----44
Db 12 LVALVFLGILVGMVPSAGTANNTLLDSRGWGTLLSRAGLAGEIAGVNWESGYLVG 71
QY 45 --RORYLYTDDAQOETAHLEIREDTGVGGAADQSPESLLQLKALPGVITQILGVKTSRFL 102
Db 72 IKRQRRLYCNVG--IGFHLQVLPDGRISGTHEENFYSLLEISTVERGVVSLFGVRSALFV 129
QY 103 CORPDGALYSLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 130 AMNSKGRLYATPSFQ--BECKFRETLLPNNYNAYESDLY 166

RESULT 34
US-08-438-439C-10
; Sequence 10, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
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QY 41 GGQVQRVLYTDDAQOQTEAHLEIREDTGVTGGAADQSPESLLQKALPGVQILGVKTSR 100
Db 40 GGAPRRRLKLYC-----ATKYHLQHPSGRVNGSLNSAYSILLETAVEGVIAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGRLYASRHSYSAE-CEFVERIHELGYNTYASRLYRTVSTTFGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPEPPG 179
Db 152 LMWYVSVNGKGRPRRGFKTRRTQKSSFLPLRVLDHRDHVMVRQLOSLPRPPG 203

RESULT 29
US-09-248-998-21
; Sequence 21, Application US/09248998
; Patent No. 6599879
; GENERAL INFORMATION:
; APPLICANT: Jimenez, Pablo
; APPLICANT: Rampy, Mark A.
; APPLICANT: Mendrick, Donna
; APPLICANT: Russell, Deborah
; APPLICANT: Louis, Arthur
; TITLE OF INVENTION: Therapeutic Uses of Keratinocyte Growth Factor-2
; FILE REFERENCE: 1488.1060002
; CURRENT APPLICATION NUMBER: US/09/248,998
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/114,387
; EARLIER FILING DATE: 30-DEC-1998
; EARLIER APPLICATION NUMBER: US 60/074,585
; EARLIER FILING DATE: 13-FEB-1998
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-248-998-21

Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
QY 41 GGQVQRVLYTDDAQOQTEAHLEIREDTGVTGGAADQSPESLLQKALPGVQILGVKTSR 100
Db 40 GGAPRRRLKLYC-----ATKYHLQHPSGRVNGSLNSAYSILLETAVEGVIAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGRLYASRHSYSAE-CEFVERIHELGYNTYASRLYRTVSTTFGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPEPPG 179
Db 152 LMWYVSVNGKGRPRRGFKTRRTQKSSFLPLRVLDHRDHVMVRQLOSLPRPPG 203

RESULT 30
US-09-572-406B-5
; Sequence 5, Application US/09572406B
; Patent No. 6605441
; GENERAL INFORMATION:
; APPLICANT: Alderson, Ralph et al.
; TITLE OF INVENTION: Fibroblast Growth Factor 11
; FILE REFERENCE: PF184F1
; CURRENT APPLICATION NUMBER: US/09/572,406B
; CURRENT FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 60/135,524
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 09/514,587
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/093,585
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 08/464,590

; PRIOR FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-572-406B-5
Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
QY 41 GGQVQRVLYTDDAQOQTEAHLEIREDTGVTGGAADQSPESLLQKALPGVQILGVKTSR 100
Db 40 GGAPRRRLKLYC-----ATKYHLQHPSGRVNGSLNSAYSILLETAVEGVIAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGRLYASRHSYSAE-CEFVERIHELGYNTYASRLYRTVSTTFGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPEPPG 179
Db 152 LMWYVSVNGKGRPRRGFKTRRTQKSSFLPLRVLDHRDHVMVRQLOSLPRPPG 203

RESULT 31
US-08-439-725A-14
; Sequence 14, Application US/08439725A
; Patent No. 5693775
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: MacKre, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,725A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELEPHONE: 619/678-5070
; TELEFAX: 617/678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 198 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-439-725A-14

Query Match 15.9%; Score 176.5; DB 1; Length 198;
Best Local Similarity 29.1%; Pred. No. 1.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 33; Gaps 6;
QY 41 GGQVQRVLYTDDAQOQTEAHLEIREDTGVTGGAADQSPESLLQKALPGVQILGVKTSR 100
Db 40 GGAPRRRLKLYC-----ATKYHLQHPSGRVNGSLNSAYSILLETAVEGVIAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGRLYASRHSYSAE-CEFVERIHELGYNTYASRLYRTVSTTFGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPEPPG 179
Db 152 LMWYVSVNGKGRPRRGFKTRRTQKSSFLPLRVLDHRDHVMVRQLOSLPRPPG 203

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 650386tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "PGF-3"
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-449-249-12

Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVTGGADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRVNGSLNSAYSILEITAVEGVGVAIRGLFSGR 95

QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHSYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151

QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
Db 152 LMVTVSNGKGRPRRGFKTRRTQKSSLFPLRVLDHRDHVMVRQLQSGLPFRPPG 203

RESULT 26
US-09-390-207-18
Sequence 18, Application US/09390207
Patent No. 6504530
GENERAL INFORMATION:
APPLICANT: Thomason, Arlen
APPLICANT: Liu, Benxian
TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
CURRENT APPLICATION NUMBER: US/09/390,207
CURRENT FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-390-207-18

Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVTGGADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRVNGSLNSAYSILEITAVEGVGVAIRGLFSGR 95

QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHSYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151

QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
Db 152 LMVTVSNGKGRPRRGFKTRRTQKSSLFPLRVLDHRDHVMVRQLQSGLPFRPPG 203

RESULT 27
US-09-229-947-35
Sequence 35, Application US/09229947
Patent No. 6518236
GENERAL INFORMATION:
APPLICANT: Deisher, Theresa A.
APPLICANT: Conklin, Darrell C.
APPLICANT: Raymond, Fenella
APPLICANT: Bukowski, Thomas R.
APPLICANT: Holderman, Susan D.
APPLICANT: Hansen, Birgit
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: NOVEL FGF HOMOLOGS
FILE REFERENCE: 96-20C1
CURRENT APPLICATION NUMBER: US/09/229,947
CURRENT FILING DATE: 1999-01-13
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 35
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-229-947-35

Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVTGGADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRVNGSLNSAYSILEITAVEGVGVAIRGLFSGR 95

QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHSYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151

QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
Db 152 LMVTVSNGKGRPRRGFKTRRTQKSSLFPLRVLDHRDHVMVRQLQSGLPFRPPG 203

RESULT 28
US-09-564-829-5
Sequence 5, Application US/09564829
Patent No. 6593112
GENERAL INFORMATION:
APPLICANT: Alderson, Ralph et al.
TITLE OF INVENTION: Fibroblast Growth Factor 15
FILE REFERENCE: PF203PI
CURRENT APPLICATION NUMBER: US/09/564,829
CURRENT FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/132,924
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 09/425,021
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 09/103,079
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 08/462,169
PRIOR FILING DATE: 1995-06-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-09-564-829-5

Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVTGGADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRVNGSLNSAYSILEITAVEGVGVAIRGLFSGR 95

QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHSYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151

QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
Db 152 LMVTVSNGKGRPRRGFKTRRTQKSSLFPLRVLDHRDHVMVRQLQSGLPFRPPG 203

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Qy 101 FLCQPPDGAALVCSLHFDEPCASPFELLEDGYNNVYQSEAHGLPLHLPGNKSPhRDPA-- 150
Db 96 YLAMKNGKRLYASEHSAAE-CEFVERIHELGYNTYASRLYRTVSSVTFGAR--RQPSAER 151
Qy 159 -----RGPAR-----FLP-----LPGLPPALPPPPG 179
Db 152 LMWYSVNGKGRPRGFKTRTKQSSFLPRLVLDHRDHEMVRLQSLGPPPG 203

RESULT 24
US-09-425-021-11
; Sequence 11, Application US/09425021
; Patent No. 6482408
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PF203D1
; CURRENT APPLICATION NUMBER: US/09/425,021
; CURRENT FILING DATE: 1999-10-25
; EARLIER APPLICATION NUMBER: 09/103,079
; EARLIER FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-425-021-11

Query Match 15.9%; Score 177.5; DB 4; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6

Qy 41 GCGVQRVLYTDDAQCTTAHLEITREDCTVGADQSPESLLQALKPGVQILGKYSR 100
Db 40 GCAPRRRKLYC---ATKTHLQLHPSGRVNGSLNSAYSILEITAVEGVGIVAIRGLFSGR 95

```

[illegible]

NAME: No. 6037329tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: /note= "FGF-3"
US-08-718-904-12

Query Match 15.9%; Score 177.5; DB 3; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
QY 41 GGQVRQRYLYTDDAQOEAHLEIREDCGTGGAADQSPESLLQKALKPGVQILGVKTSR 100
DB 40 GGAPRRKLYC-----ATKYHLQHPGSRVNGSLNSAYSILEITAVEGVGVAIRGLPSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
DB 96 YLAMNKGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
DB 152 LWTYSVNGKGRPRRGFKTRTQKSSFLPRVLDHRDHEMVRLQSLGPRPPG 203

RESULT 21
US-09-023-082A-21
Sequence 21, Application US/09023082A
Patent No. 6077692
GENERAL INFORMATION:
APPLICANT: RUBEN, STEVEN M.
APPLICANT: JIMENEZ, PABLO
APPLICANT: DUAN, D. ROXANNE
APPLICANT: RAMPY, MARK A.
APPLICANT: MENDRICK, DONNA
APPLICANT: ZHANG, JUN
APPLICANT: NI, JIAN
APPLICANT: MOORE, PAUL A.
APPLICANT: COLEMAN, TIMOTHY A.
APPLICANT: GRUBER, JOACHIM R.
APPLICANT: DILLON, PATRICK J.
APPLICANT: GENTZ, REINER L.
TITLE OF INVENTION: KERATINOCYTE GROWTH FACTOR-2
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,082A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852
FILING DATE: 13-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,432
FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
FILING DATE: 13-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,561
FILING DATE: 13-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: STEFFKE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0360008/EKS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-023-082A-21
Query Match 15.9%; Score 177.5; DB 3; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
QY 41 GGQVRQRYLYTDDAQOEAHLEIREDCGTGGAADQSPESLLQKALKPGVQILGVKTSR 100
DB 40 GGAPRRKLYC-----ATKYHLQHPGSRVNGSLNSAYSILEITAVEGVGVAIRGLPSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
DB 96 YLAMNKGRLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
DB 152 LWTYSVNGKGRPRRGFKTRTQKSSFLPRVLDHRDHEMVRLQSLGPRPPG 203

RESULT 22
US-09-093-585-11
Sequence 11, Application US/09093585
Patent No. 6110893
GENERAL INFORMATION:
APPLICANT: HU, JING-SHAN
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICANT: Deisher, Theresa A.
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-207-412B-14

Query Match 15.9%; Score 177.5; DB 2; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVQRVYTDAAQTEAHLEIREDTGCGAADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRNGSLNSAYSILEITAVEGVIVAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSVSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPPPPG 179
Db 152 LMVYVNGKGRPRGRGFKTRRTQKSSILFLPVLDRHDEMVRQLQSGLPFRPPG 203

RESULT 18
US-08-951-822-35
; Sequence 35, Application US/08951822A
; Patent No. 5989866
; GENERAL INFORMATION:
; APPLICANT: Deisher, Theresa A.
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Raymond, Fenella
; APPLICANT: Bukowski, Thomas R.
; APPLICANT: Holderman, Susan D.
; APPLICANT: Hansen, Birgit
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL FGF HOMOLOGS
; FILE REFERENCE: 96-20
; CURRENT APPLICATION NUMBER: US/08/951,822A
; CURRENT FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-951-822-35

Query Match 15.9%; Score 177.5; DB 2; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVQRVYTDAAQTEAHLEIREDTGCGAADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRNGSLNSAYSILEITAVEGVIVAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSVSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPPPPG 179
Db 152 LMVYVNGKGRPRGRGFKTRRTQKSSILFLPVLDRHDEMVRQLQSGLPFRPPG 203

RESULT 19
US-09-103-079-11
; Sequence 11, Application US/09103079A
; Patent No. 6013477
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PF203D1
; CURRENT APPLICATION NUMBER: US/09/103,079A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/462,169
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-103-079-11

Query Match 15.9%; Score 177.5; DB 3; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVQRVYTDAAQTEAHLEIREDTGCGAADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRNGSLNSAYSILEITAVEGVIVAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSVSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPPPPG 179
Db 152 LMVYVNGKGRPRGRGFKTRRTQKSSILFLPVLDRHDEMVRQLQSGLPFRPPG 203

RESULT 20
US-08-718-904-12
; Sequence 12, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
```

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;
; 96 YLAMNKRGLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSVSTPGAR---RQPSAER 151
;
; 159 -----RGPAP-----FLP-----LPGLPALPPPPG 179
;
; 152 LMVYVNGKGRPRGRGFKTRRTQKSSILFLPVLDRHDEMVRQLQSGLPFRPPG 203
;
RESULT 19
US-09-103-079-11
; Sequence 11, Application US/09103079A
; Patent No. 6013477
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PF203D1
; CURRENT APPLICATION NUMBER: US/09/103,079A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/462,169
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-103-079-11

Query Match 15.9%; Score 177.5; DB 3; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;

QY 41 GGQVQRVYTDAAQTEAHLEIREDTGCGAADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRKLYC-----ATKYHLQHPSGRNGSLNSAYSILEITAVEGVIVAIRGLFSGR 95
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAP-- 158
Db 96 YLAMNKRGLYASEHYSAE-CEFVERIHELGYNTYASRLYRTVSVSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPALPPPPG 179
Db 152 LMVYVNGKGRPRGRGFKTRRTQKSSILFLPVLDRHDEMVRQLQSGLPFRPPG 203

RESULT 20
US-08-718-904-12
; Sequence 12, Application US/08718904
; Patent No. 6037329
; GENERAL INFORMATION:
; APPLICANT: Baird, J. Andrew
; APPLICANT: Chandler, Lois Ann
; APPLICANT: Sosnowski, Barbara A.
; TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,904
; FILING DATE: 24-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
```

Db 40 GGAPRRRLKLYC-----ATKHLQLHPSGRVNGSLNSAYSILEITAVEGVGVAIKGLFSGR 95
Qy 101 FLCORPDGALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP--HRDPAP 158
Db 96 YLAMNKGRLYADSHYNAB-CEFVERIHELGYNTYASR-----LYRTGSSGPGCAQRPQGA 149
Qy 159 RGP-----ARFLPLGLPALPEPPGILAPQPDVGVSSDPLSMVGPSCGRSPSYAS 209
Db 150 QRPWYVNVNGKGRPRGRGFKTRRTQKSSLFPLRVLGHKDHVMVRLQSSQFPAPGEGS 206

RESULT 15
US-08-464-590A-11
; Sequence 11, Application US/08464590A
; Patent No. 5763214
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-11
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NJ
; COUNTRY: US
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,590A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J. G.
; REGISTRATION NUMBER: 30,073
; REFERENCE/DOCKET NUMBER: 325800-438
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 994-1700
; TELEFAX: (201) 994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-590A-11

Query Match 15.9%; Score 177.5; DB 1; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQSPESLLQLKALPGVILGVKTSR 100
Db 40 GGAPRRRLKLYC-----ATKHLQLHPSGRVNGSLNSAYSILEITAVEGVGVAIRGLFSGR 95
Qy 101 FLCORPDGALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
Db 96 YLAMNKGRLYADSHYNAB-CEFVERIHELGYNTYASR-----LYRTGSSGPGCAQRPQGA 149
Qy 159 RGP-----ARFLPLGLPALPEPPGILAPQPDVGVSSDPLSMVGPSCGRSPSYAS 209
Db 150 QRPWYVNVNGKGRPRGRGFKTRRTQKSSLFPLRVLGHKDHVMVRLQSSQFPAPGEGS 206

; Patent No. 5773252
; GENERAL INFORMATION:
; APPLICANT: John Greene and Craig A. Rosen
; TITLE OF INVENTION: Fibroblast Growth Factor-15
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,169B
; FILING DATE: 05 JUN 95
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-441 (PF203)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-462-169B-11
Query Match 15.9%; Score 177.5; DB 1; Length 239;
Best Local Similarity 29.7%; Pred. No. 1.9e-09;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQSPESLLQLKALPGVILGVKTSR 100
Db 40 GGAPRRRLKLYC-----ATKHLQLHPSGRVNGSLNSAYSILEITAVEGVGVAIRGLFSGR 95
Qy 101 FLCORPDGALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAP-- 158
Db 96 YLAMNKGRLYADSHYNAB-CEFVERIHELGYNTYASR-----LYRTGSSGPGCAQRPQGA 149
Qy 159 RGP-----ARFLPLGLPALPEPPGILAPQPDVGVSSDPLSMVGPSCGRSPSYAS 209
Db 150 QRPWYVNVNGKGRPRGRGFKTRRTQKSSLFPLRVLGHKDHVMVRLQSSQFPAPGEGS 206

RESULT 17
US-08-207-412B-14
; Sequence 14, Application US/08207412B
; Patent No. 5817485
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; TITLE OF INVENTION: Fibroblast Growth Factor-10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```
; Sequence 11, Application US/08867471
; Patent No. 5872226
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHF-1) AND METHODS OF USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/867,471
; FILING DATE: 02-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/439,725
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-867-471-11

Query Match 16.1%; Score 179; DB 2; Length 245;
Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

QY 41 GGQVORLYTDDAQQTAEHLEIREDTGVTGGADQSPESLLQLKALPGVQILGVKTSR 100
Db 40 GGAPRRKLYC---ATKYHLQLHPSGRVNGSLNSAYSILEITAVEGVVAIKGLFSGR 95

QY 101 FLCQPDGALYSLHDFPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSP--HRDPAP 158
Db 96 YLAMNKRGLYASDHVNAE--CEFVERIHELGYNTYASR-----LYRTGSSGPGAQRPGA 149

QY 159 RGP-----ARFLPLGLPALPEPPGILAPPDPDVGSSDPLSMVGPSCQSRSPSYAS 209
Db 150 QRPWYVSVNGKGRPRGFKTRTKQSSFLPRVLGHKDHVMYRLQLSSQPRAPGEGS 206

RESULT 13
US-08-438-439C-7
; Sequence 7, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/867,471
; FILING DATE: 02-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/439,725
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-867-471-11

Query Match 16.1%; Score 179; DB 2; Length 245;
Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

QY 41 GGQVORLYTDDAQQTAEHLEIREDTGVTGGADQSPESLLQLKALPGVQILGVKTSR 100
Db 40 GGAPRRKLYC---ATKYHLQLHPSGRVNGSLNSAYSILEITAVEGVVAIKGLFSGR 95

QY 101 FLCQPDGALYSLHDFPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSP--HRDPAP 158
Db 96 YLAMNKRGLYASDHVNAE--CEFVERIHELGYNTYASR-----LYRTGSSGPGAQRPGA 149

QY 159 RGP-----ARFLPLGLPALPEPPGILAPPDPDVGSSDPLSMVGPSCQSRSPSYAS 209
Db 150 QRPWYVSVNGKGRPRGFKTRTKQSSFLPRVLGHKDHVMYRLQLSSQPRAPGEGS 206

RESULT 14
US-09-390-207-28
; Sequence 28, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-390-207-28

Query Match 16.1%; Score 179; DB 4; Length 245;
Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

QY 41 GGQVORLYTDDAQQTAEHLEIREDTGVTGGADQSPESLLQLKALPGVQILGVKTSR 100
Db 40 GGAPRRKLYC---ATKYHLQLHPSGRVNGSLNSAYSILEITAVEGVVAIKGLFSGR 95

QY 101 FLCQPDGALYSLHDFPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGKSP--HRDPAP 158
Db 96 YLAMNKRGLYASDHVNAE--CEFVERIHELGYNTYASR-----LYRTGSSGPGAQRPGA 149

QY 159 RGP-----ARFLPLGLPALPEPPGILAPPDPDVGSSDPLSMVGPSCQSRSPSYAS 209
Db 150 QRPWYVSVNGKGRPRGFKTRTKQSSFLPRVLGHKDHVMYRLQLSSQPRAPGEGS 206
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Db 40 GGAPRRRLKLC-----ATKYLHLQHPGSRVNGSLNSAYSILAITAVEGVVAIKGLFSGR 95
Qy 101 FLCQPDGALYGLSHFDPEACSFRELLLEDGVNYQSEAHGLPLHLPGNKSP--HRDPAP 158
Db 96 YLAMNKRGRLYASDHYNAB-CEFVERIHELGYNTYASR-----LYRTGSSGPGAQROPGA 149
Qy 159 RGP-----AREFLPLGLPPALPEPPGILAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 150 QRPWYVSVNGKGRPRGRGFKTRTQKSSFLPLRVLGHKHHEWVRLQLQSSQPRAPGEGS 206

RESULT 11
US-08-439-725A-11
; Sequence 11, Application US/08439725A
; Patent No. 5693775
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-1 (FHP-1) AND METHODS OF USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,725A
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/047001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 617/678-5099
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-439-725A-11
Query Match 16.1%; Score 179; DB 1; Length 245;
Best Local Similarity 28.8%; Pred. No. 1.4e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQSPESLLQKALKPGVQILGVKTSR 100
Db 40 GGAPRRRLKLC-----ATKYLHLQHPGSRVNGSLNSAYSILAITAVEGVVAIKGLFSGR 95
Qy 101 FLCQPDGALYGLSHFDPEACSFRELLLEDGVNYQSEAHGLPLHLPGNKSP--HRDPAP 158
Db 96 YLAMNKRGRLYASDHYNAB-CEFVERIHELGYNTYASR-----LYRTGSSGPGAQROPGA 149
Qy 159 RGP-----AREFLPLGLPPALPEPPGILAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 150 QRPWYVSVNGKGRPRGRGFKTRTQKSSFLPLRVLGHKHHEWVRLQLQSSQPRAPGEGS 206

RESULT 12
US-08-867-471-11

Qy 181 -----LAPQPPDVGVSSDPLSMV-GPSQGRSPSY 207
Db 183 LESDMFSSPLETDSMDPFGLVGTGLEAVRGPSPF 214

RESULT 9
US-09-621-976-4031
; Sequence 4031, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4031
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -24..-1
US-09-621-976-4031

Query Match 18.1%; Score 201.5; DB 4; Length 134;
Best Local Similarity 38.3%; Pred. No. 4e-12;
Matches 49; Conservative 27; Mismatches 43; Indels 9; Gaps 5;

Qy 13 LWSVILAGLL-LGACQAHPIPDSPLL--QFGQVRQRYLYTDDAQOQTEAHLEIREDTGV 69
Db 8 LWCALCSVCSMVLRA--PNASPLIGSSWGGLI--HLYTATARN--YHLQTHKNGHV 61

Qy 70 GGADQSPESLLQKALKPGVQILGVKTSRFLCQPDGALYGLSHFDPEACSFRELLLE 129
Db 62 DGAPHQTIYSALMIRSEDAGFVVITGVMSRYLQMDFRGNIFGSHVDFPENCROHQTLE 121

Qy 130 DGVNYQSS 137
Db 122 NGIDVYHS 129

RESULT 10
US-09-417-721-7
; Sequence 7, Application US/09417721
; Patent No. 6451303
; GENERAL INFORMATION:
; APPLICANT: Whitehouse, Martha J.
; APPLICANT: Kavanaugh, Michael W.
; TITLE OF INVENTION: Angiogenically Effective Unit Dose of FGF and Method of
; TITLE OF INVENTION: Administering
; FILE REFERENCE: 1296/12169US05
; CURRENT APPLICATION NUMBER: US/09/417,721
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/104,103
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Murine FGF-3
US-09-417-721-7

Query Match 16.1%; Score 179; DB 4; Length 240;
Best Local Similarity 28.8%; Pred. No. 1.3e-09;
Matches 51; Conservative 30; Mismatches 78; Indels 18; Gaps 5;

Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQSPESLLQKALKPGVQILGVKTSR 100

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1998-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1998-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 59
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-59

Query Match 23.8%; Score 265; DB 4; Length 216;
Best Local Similarity 36.3%; Pred. No. 5.2e-18;
Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;
QY 11 SGLVSVLAGLLGACQAHPIPDSSPLLQF--GGVQRORYLYTDDAQ-QTEAHLEIREDG 67
DB 14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWDPIRLRLHLYTSGPHGLSSCFLIRADG 66
QY 68 TVGGADQSPESLLOLKALPGVIOILGVKTSRFLCORPDGALYGLSHDFDPACSFRELL 127
DB 67 VVDCARGQSAHSLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEESI 126
QY 128 LEDGVNVYQSEAHGLPHLPNGKSPHRDPAPRGPARFLPLGLPPALP-----EPPGI--- 180
DB 127 RPDGVNVYSEKHLFVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPMVPEPEDLRGH 182
QY 181 ----LAPQPDVGVSSDPLSMV-GPSQGRSPSY 207
DB 183 LESDMFSSPLETSDMPDFGLVTGLEAVRSPSF 214

RESULT 8
US-09-902-775A-59
Sequence 59, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1998-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1998-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1998-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 59
LENGTH: 216
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-59
Query Match 23.8%; Score 265; DB 4; Length 216;
Best Local Similarity 36.3%; Pred. No. 5.2e-18;
Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;
QY 11 SGLVSVLAGLLGACQAHPIPDSSPLLQF--GGVQRORYLYTDDAQ-QTEAHLEIREDG 67
DB 14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWDPIRLRLHLYTSGPHGLSSCFLIRADG 66
QY 68 TVGGADQSPESLLOLKALPGVIOILGVKTSRFLCORPDGALYGLSHDFDPACSFRELL 127
DB 67 VVDCARGQSAHSLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEESI 126
QY 128 LEDGVNVYQSEAHGLPHLPNGKSPHRDPAPRGPARFLPLGLPPALP-----EPPGI--- 180
DB 127 RPDGVNVYSEKHLFVSLSSAKQ-RQLYKNRG---FLPLSHFLPMLPMVPEPEDLRGH 182

QY 61 LEIREDTVGGAADQSPESLQIK 84
Db 61 LEIREDTVGGAADQSPESLQIK 84

RESULT 6

US-09-907-794A-59

; Sequence 59, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: PCT/US00/00219

; PRIOR FILING DATE: 2000-01-05

; NUMBER OF SEQ ID NOS: 423

; SEQ ID NO 59

; LENGTH: 216

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-907-794A-59

Query Match

23.8%; Score 265; DB 4; Length 216;

Best Local Similarity 36.3%; Pred. No. 5.2e-18;

Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;

QY 11 SGLWVSVLAGLLGACQAHPIPDSSPLQF--GGQVRQRYLYTDDAQ-QTEAHLEIREDS 67
Db 14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWDPIRLRLHLYTSGPHGLSSCFRLIRADG 66
QY 68 TVGGAADQSPESLQIKALKPGVQILGWKTSRFLCQRPDGLYSLHFDPEACSPRELL 127
Db 67 VVDCARGQSAHSLLEIKAVALTVAIKGVHSVRYLCMGADGKMQGLLOYSEEDCAFEET 126
QY 128 LEDGVNVYQSEAHGLPLHLPGNKSPhRDPAPRGPAFLPLGLPPALP---EPPGI--- 180
Db 127 RPDGVNVYRSEKRLPVLSUAKQ-RQLYNKG---FLFLSHFLPMLPWPVPEPDELRGH 182
QY 181 ---LAPQPPDVGVSSDPLSMV-GPSQGRSPSY 207
Db 183 LBSDMESSPLETDSMDPFGLVGTGLEAVRSPSF 214

RESULT 7

US-09-905-125A-59

; Sequence 59, Application US/09905125A

; Patent No. 6664376

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/905,125A

; CURRENT FILING DATE: 2001-07-12

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

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; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match      86.2%; Score 959; DB 4; Length 181;
Best Local Similarity 99.4%; Pred. No. 1.8e-85;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 HPIPDSSPLLOFGGQVRQRYLYTDDAQTEAHLEIREDDGTGGAADQSPESLLQLKALKP 88
DB 1 HPIPDSSPLLOFGGQVRQRYLYTDDAQTEAHLEIREDDGTGGAADQSPESLLQLKALKP 60
QY 89 GVIQILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLP 148
DB 61 GVIQILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLP 120
QY 149 NKSPHRDPAPRGPARFLPLGLPPALPEPPGIIAPQPPDVGGSDPLSMVGPQGRSPSYA 208
DB 121 NKSPHRDPAPRGPARFLPLGLPPALPEPPGIIAPQPPDVGGSDPLSMVGPQGRSPSYA 180
QY 209 S 209
DB 181 S 181

RESULT 3
US-09-390-207-4
; Sequence 4, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-4

Query Match      71.3%; Score 793.5; DB 4; Length 210;
Best Local Similarity 78.9%; Pred. No. 2.5e-69;
Matches 157; Conservative 10; Mismatches 31; Indels 1; Gaps 1;

QY 12 GLWVS-VLAGLLGACQAHPIPDSSPLLOFGGQVRQRYLYTDDAQTEAHLEIREDDGTG 70
DB 12 GLWVRLLAFLGLGVYQAVPIPDSSPLLOFGGQVRQRYLYTDDAQTEAHLEIREDDGTV 71
QY 71 GAADQSPESLLQLKALKPQVITLGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLED 130
DB 72 GAARSPESLLELALKPGVITLGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLED 131
QY 131 GYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPPALPEPPGIIAPQPPDVGS 190
DB 132 GYNVYQSEAHGLPLRPLPKQDSPNQDATSWGCVFRLPMPGLLHPEPQQAGFLPPEPDVGS 191
QY 191 SDPLSMVGPQGRSPSYAS 209
DB 192 SDPLSMVGPQGRSPSYAS 210

RESULT 4
US-09-390-207-6
; Sequence 6, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-6

Query Match      67.7%; Score 753; DB 4; Length 181;
Best Local Similarity 80.7%; Pred. No. 1.8e-65;
Matches 146; Conservative 9; Mismatches 26; Indels 0; Gaps 0;

QY 29 HPIPDSSPLLOFGGQVRQRYLYTDDAQTEAHLEIREDDGTGGAADQSPESLLQLKALKP 88
DB 1 YFIIPDSSPLLOFGGQVRQRYLYTDDAQTEAHLEIREDDGTGGAARSPESLLELALKALP 60
QY 89 GVIQILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLP 148
DB 61 GVIQILGVKTSRFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLRPLQ 120
QY 149 NKSPHRDPAPRGPARFLPLGLPPALPEPPGIIAPQPPDVGGSDPLSMVGPQGRSPSYA 208
DB 121 KDSNQDATSWGCVFRLPMPGLLHPEPQQAGFLPPEPDDVGGSDPLSMVPELQGRSPSYA 180
QY 209 S 209
DB 181 S 181

RESULT 5
US-09-621-976-5213
; Sequence 5213, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTe and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5213
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28..-1
; NAME/KEY: UNSURE
; LOCATION: 57
; OTHER INFORMATION: Xaa = Ala,Pro
; NAME/KEY: UNSURE
; LOCATION: 52
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-5213

Query Match      38.8%; Score 432; DB 4; Length 85;
Best Local Similarity 98.8%; Pred. No. 9.2e-35;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLOFGGQVRQRYLYTDDAQTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLOFGGQVRQRYLYTDDAQTEAH 60
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 16:02:23 ; Search time 37.4458 Seconds
(without alignments)
288.145 Million cell updates/sec

Title: US-10-060-765-4
Perfect score: 1113
Sequence: 1 MDSDETFEHSGLWVSLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1106	99.4	209	4	US-09-390-207-2
2	959	86.2	181	4	US-09-390-207-5
3	793.5	71.3	210	4	US-09-390-207-4
4	753	67.7	181	4	US-09-390-207-6
5	432	38.8	85	4	US-09-621-976-5213
6	265	23.8	216	4	US-09-907-794A-59
7	265	23.8	216	4	US-09-905-125A-59
8	265	23.8	216	4	US-09-902-775A-59
9	201.5	18.1	134	4	US-09-621-976-4031
10	179	16.1	240	4	US-09-417-721-7
11	179	16.1	245	1	US-08-439-725A-11
12	179	16.1	245	2	US-08-867-471-11
13	179	16.1	245	2	US-08-438-439C-7
14	179	16.1	245	4	US-09-390-207-28
15	177.5	15.9	239	1	US-08-464-590A-11
16	177.5	15.9	239	1	US-08-462-169B-11
17	177.5	15.9	239	2	US-08-207-412B-14
18	177.5	15.9	239	2	US-08-951-822-35
19	177.5	15.9	239	3	US-09-103-079-11
20	177.5	15.9	239	3	US-08-718-904-12
21	177.5	15.9	239	3	US-09-023-082A-21
22	177.5	15.9	239	3	US-09-093-585-11
23	177.5	15.9	239	4	US-09-368-951-35
24	177.5	15.9	239	4	US-09-449-249-12
25	177.5	15.9	239	4	US-09-390-207-18
26	177.5	15.9	239	4	US-09-229-947-35
27	177.5	15.9	239	4	US-09-229-947-35

28 177.5 15.9 239 4 US-09-564-829-5 Sequence 5, Appli
29 177.5 15.9 239 4 US-09-248-998-21 Sequence 21, Appli
30 177.5 15.9 239 4 US-09-572-406B-5 Sequence 5, Appli
31 176.5 15.9 198 1 US-08-439-725A-14 Sequence 14, Appli
32 176.5 15.9 198 1 US-08-441-629-12 Sequence 12, Appli
33 176.5 15.9 198 2 US-08-867-471-14 Sequence 14, Appli
34 176.5 15.9 198 2 US-08-438-439C-10 Sequence 20, Appli
35 176.5 15.9 198 2 US-08-438-439C-20 Sequence 10, Appli
36 176.5 15.9 198 3 US-08-718-904-15 Sequence 15, Appli
37 176.5 15.9 198 3 US-09-023-082A-14 Sequence 14, Appli
38 176.5 15.9 198 3 US-08-776-207-12 Sequence 12, Appli
39 176.5 15.9 198 4 US-09-507-773-12 Sequence 12, Appli
40 176.5 15.9 198 4 US-09-449-249-15 Sequence 15, Appli
41 176.5 15.9 198 4 US-09-248-998-14 Sequence 14, Appli
42 176.5 15.9 198 5 PCT-US95-09172-12 Sequence 12, Appli
43 176.5 15.9 207 1 US-08-551-171-5 Sequence 5, Appli
44 176.5 15.9 207 3 US-08-902-233-5 Sequence 10, Appli
45 176.5 15.9 207 4 US-09-417-721-10 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-390-207-2
; Sequence 2, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arien
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2

Query Match 99.4%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 1.2e-99;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 MDSDETFEHSGLWVSLAGLLGACQAHIPDSSPLLQFGGQVRQRYLYTDDAQTEAH 60
Db 1 MDSDETFEHSGLWVSLAGLLGACQAHIPDSSPLLQFGGQVRQRYLYTDDAQTEAH 60
Qy 61 LEIREDCIVGGAADQSPESLLQLKALPGVIQILGVKTSRFLCORPDGALYGLHFDPEA 120
Db 61 LEIREDCIVGGAADQSPESLLQLKALPGVIQILGVKTSRFLCORPDGALYGLHFDPEA 120
Qy 121 CSFRELLELDGYNVYQSEAHGLPHLFGNKSPHRDPAHPGPARFLPLGPPALPEPPGI 180
Db 121 CSFRELLELDGYNVYQSEAHGLPHLFGNKSPHRDPAHPGPARFLPLGPPALPEPPGI 180
Qy 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 2
US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arien
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207

inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. NO. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETGFEHSGIWNVSLAGLLIGACQAHPIPDSSPLQFGGQVORXYLYTDDAQQTEAH 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MDSDETGFEHSGIWNVSLAG-LIGACQAHPIPDSSPLQFGGQVORXYLYTDDAQQTEAH 59
QY 61 LEIREDTGVGGADQSPESLLQKALKPGVQIQLGVKTSRFLCQRPDGLYSLHFDPEA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
60 LEIREDTGVGGADQSPESLLQKALKPGVQIQLGVKTSRFLCQRPDGLYSLHFDPEA 119
QY 121 CSFREILLEGGYNNVQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
120 CSFREILLEGGYNNVQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 179
QY 181 LAPQPDVGSDDPLSMVGPQGRSPSYAS 209
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
180 LAPQPDVGSDDPLSMVGPQGRSPSYAS 208

Search completed: March 2, 2004, 16:04:50
Job time : 128.4 secs

US2003073816-A1.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)- α from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO1080, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322, PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1415 polypeptides are useful for stimulating the release of tumour necrosis factor (TNF) - α from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO836, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322, PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO3408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA:

CC	tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC	liver tumour. (I) is useful as molecular weight markers, for tissue
CC	typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC	useful for chromosome and gene mapping or gene therapy. (II) is useful
CC	for generating transgenic animals or knock-out animals which are useful
CC	screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC	is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC	sport injuries). This is the amino acid sequence of a human secreted and
CC	transmembrane PRO polypeptide.
XX	
SQ	Sequence 208 AA;
	Query Match 98.7%; Score 1098.5; DB 7; Length 208;
	Best Local Similarity 99.5%; Pred. No. 8.6e-91;
	Matches 208. Conservative 0; Mismatches 0; Indels 11; Gaps 1

XX DE Novel human secreted and transmembrane protein PRO10196.
XX KW human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
XX KW antiarthritic; pericyte cell proliferation;
XX KW pericyte cell differentiation; chondrocyte cell proliferation;
XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;
XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
XX KW liver tumour; tissue typing; chromosome mapping; gene mapping;
XX KW gene therapy.
XX KW Homo sapiens.
XX OS
XX PN US2003088071-A1.
XX PD
XX PD 08-MAY-2003.
XX PF 29-AUG-2002; 2002US-00232231.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX PI WPI; 2003-801156/75.
XX DR N-PSDB; ADC49543.
XX DR
XX XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX PT in gene therapy, chromosome identification, tissue typing, or as
XX PT hybridization probes in chromosome and gene mapping.
XX XX
XX PS Claim 11; SEQ ID NO 78; 315pp; English.
XX CC The invention describes an isolated PRO (secreted and transmembrane)
XX CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX CC useful for stimulating the proliferation of or gene expression in
XX CC pericyte cells. PRO357, PRO229, PRO1272 or PRO405 polypeptide are useful
XX CC for stimulating the proliferation or differentiation of chondrocyte
XX CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
XX CC are useful for stimulating the release of tumour necrosis factor (TNF)-
XX CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
XX CC PRO247, PRO337, PRO526, PRO363, PRO331, PRO1083, PRO840, PRO1080,
XX CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
XX CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
XX CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
XX CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
XX CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322,
XX CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
XX CC stimulating the proliferation of normal human dermal fibroblasts cells.
XX CC PRO181, PRO229, PRO7154, or PRO7425 polypeptide are useful for
XX CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
XX CC polypeptides such as PRO6004, PRO4981, PRO1174, PRO5778, PRO4332, etc.,
XX CC are useful for detecting the presence of tumour in a mammal which
XX CC involves comparing the level of expression of the above PRO polypeptides
XX CC in a test sample of cells taken from the mammal, and a control sample of
XX CC normal cells of the same cell type, where a higher level of expression of
XX CC the PRO polypeptides in the test sample as compared to the control sample
XX CC is indicative of the presence of tumour in the mammal. The tumour is lung
XX CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
XX CC liver tumour. (I) is useful as molecular weight markers, for tissue
XX CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
XX CC useful for chromosome and gene mapping or gene therapy. (II) is useful
XX CC for generating transgenic animals or knock-out animals which are useful
XX CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO405 polypeptide
XX CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
XX CC sport injuries). This is the amino acid sequence of a human secreted and

CC transmembrane PRO polypeptide.
XX Sequence 208 AA;
SQ
Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91; Indels 1; Gaps 1;
Matches 208; Conservative 0; Mismatches 0;
QY 1 MDSDETGFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOQTEAH 60
Db 1 MDSDETGFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOQTEAH 59
QY 61 LEIREDTGVGAADQSPESLLQLKALKEGVTOILGVKTSRFLCORPDGALYGLHFDPEA 120
Db 60 LEIREDTGVGAADQSPESLLQLKALKEGVTOILGVKTSRFLCORPDGALYGLHFDPEA 119
QY 121 CSFRELLEDGYNVYOSEAHGLPLHGNKSHRDPAPRGPARFLPLGLPALPEPPI 180
Db 120 CSFRELLEDGYNVYOSEAHGLPLHGNKSHRDPAPRGPARFLPLGLPALPEPPI 179
QY 181 LAPQPPDVGSSDPLSNWGPSCGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSNWGPSCGRSPSYAS 208
RESULT 36
ADC47405
ID ADC47405 standard; protein; 208 AA.
XX AC
XX AC ADC47405;
XX DT 18-DEC-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.
XX KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
XX KW antiarthritic; pericyte cell proliferation;
XX KW pericyte cell differentiation; chondrocyte cell proliferation;
XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;
XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
XX KW liver tumour; tissue typing; chromosome mapping; gene mapping;
XX KW gene therapy.
XX OS Homo sapiens.
XX PN US2003088072-A1.
XX PD 08-MAY-2003.
XX PF 29-AUG-2002; 2002US-00232233.
XX PR 25-JUL-2000; 2000US-0220605P.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX PI WPI; 2003-801157/75.
XX DR N-PSDB; ADC47404.
XX XX New PRO polypeptide for use as molecular weight markers for protein
XX PT electrophoresis purposes and for detecting the presence of tumor in a
XX PT mammal.
XX PS Claim 11; Fig 78; 314pp; English.
XX XX The invention describes an isolated PRO (secreted and transmembrane)

is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (III) is useful for generating transgenic animals or knock-out animals which are useful for screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

XX Sequence 208 AA;
Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFGHSGLWVSLAGLLGACQAHPIPDSSPLQFGGQVQRVLYTDDAQTEAH 60
DB 1 MDSDETFGHSGLWVSLAG-LLGACQAHPIPDSSPLQFGGQVQRVLYTDDAQTEAH 59
QY 61 LEIREDTGVTGGAADQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYSLHFDPEA 120
DB 60 LEIREDTGVTGGAADQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYSLHFDPEA 119
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGPPALPEPGI 180
DB 120 CSFRELLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGPPALPEPGI 179
QY 181 LAPQPDVGSSDPLSMVGPQGRSPSYAS 209
DB 180 LAPQPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 34
ADC49027
ID ADC49027 standard; protein; 208 AA.
AC ADC49027;
XX 18-DEC-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO10196.
XX human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX Homo sapiens.
XX US2003088070-A1.
XX 08-MAY-2003.
XX 28-AUG-2002; 2002US-00230260.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen MB, Goddard A, Godowski PU;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX WPI; 2003-801155/75.
XX N-PSDB; ADC49026.

New PRO polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.

Claim 11; SEQ ID NO 78; 315pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4444, PRO4322, PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful for screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFGHSGLWVSLAGLLGACQAHPIPDSSPLQFGGQVQRVLYTDDAQTEAH 60
DB 1 MDSDETFGHSGLWVSLAG-LLGACQAHPIPDSSPLQFGGQVQRVLYTDDAQTEAH 59
QY 61 LEIREDTGVTGGAADQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYSLHFDPEA 120
DB 60 LEIREDTGVTGGAADQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYSLHFDPEA 119
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGPPALPEPGI 180
DB 120 CSFRELLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGPPALPEPGI 179
QY 181 LAPQPDVGSSDPLSMVGPQGRSPSYAS 209
DB 180 LAPQPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 35
ADC49544
ID ADC49544 standard; protein; 208 AA.
XX AC ADC49544;
XX DT 18-DEC-2003 (first entry)

PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253466P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2000WO-US034956.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX N-PSDB; ADC21796.
DR WPI; 2003-765526/72.
XX Novel isolated PRO polypeptide useful for tissue typing, as molecular
PT weight markers in protein electrophoresis, for treating arthritis, tumor.
XX Claim 11; Fig 78; 308pp; English.
XX The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. They are particularly useful for
CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
CC blood, for stimulating the proliferation or differentiation of
CC chondrocyte cells, for stimulating the proliferation of or gene
CC expression in pericyte cells or for stimulating the proliferation of
CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
CC technology, in generating transgenic animals or knock-out animals which
CC may be used in the development and screening of therapeutically useful
CC reagents, in gene therapy, in chromosome identification, as chromosome
CC markers and in generating probes. The PRO polypeptides, or anti-PRO
CC antibodies, are useful for preparing a medicament for treating a
CC condition which is responsive to the PRO polypeptides or anti-PRO
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polypeptide of the invention.
XX Sequence 208 AA;
Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPTPDSPLQFGQVQRQYLYTDDAQQTAEH 60
DB 1 MDSDETFEHSGLWVSVLAG-LLGACQAHPTPDSPLQFGQVQRQYLYTDDAQQTAEH 59
QY 61 LEITREDTGVGAADQSPESLQLKALPGVITQILGVKTSRPLCORPDGALYLSLHFDPEA 120
DB 60 LEITREDTGVGAADQSPESLQLKALPGVITQILGVKTSRPLCORPDGALYLSLHFDPEA 119
QY 121 CSFRELLEGVNYYQSEAHGLPLHLPGNKSPPHDPAPRGPARFLPLGPPALPEPPGI 180
DB 120 CSFRELLEGVNYYQSEAHGLPLHLPGNKSPPHDPAPRGPARFLPLGPPALPEPPGI 179
QY 181 LAPQPPDVGSDPLSMWGPSQGRSPSVAS 209
DB 180 LAPQPPDVGSDPLSMWGPSQGRSPSVAS 208

RESULT 33
ADC49828
ID ADC49828 standard; protein; 208 AA.
XX AC ADC49828;
XX DT 18-DEC-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.
XX KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
KW antiarthritic; pericyte cell proliferation;
KW chondrocyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX OS Homo sapiens.
XX PN US2003088064-A1.
XX PD 08-MAY-2003.
XX PF 14-AUG-2002; 2002US-00219075.
XX PR 25-JUL-2000; 2000US-0220605P.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-801154/75.
XX DR N-PSDB; ADC49827.
XX PT New secreted and transmembrane PRO polypeptide useful for preparing a
PT medicament for treating a condition that is responsive to the PRO
PT polypeptide or anti-PRO antibody, e.g. cancer.
XX Claim 11; SEQ ID NO 78; 314pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4332,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4381, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample

chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.

Homo sapiens.

US2003092887-A1.

15-MAY-2003.

12-AUG-2002; 2002US-00218956.

29-JUN-2001; 2001WO-US021066.

09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI; N-PSDB; ADB72968.

WPI; 2003-777258/73.

Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis, tumor.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322, PRO9340, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322, PRO9340, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 MDSDETFEHSGLVSVLGLGACOAHPIDSSPLLQGGVGRVRYLYTDDAQTEAH 60
 |||||
 1 MDSDETFEHSGLVSVLGLGACOAHPIDSSPLLQGGVGRVRYLYTDDAQTEAH 59
 |||||

61 LEIREDTGVCAGADQSPESLQLKALPGVYIQLGVKTSFLCORPDGALYGSILHFDPEA 120
 |||||
 60 LEIREDTGVCAGADQSPESLQLKALPGVYIQLGVKTSFLCORPDGALYGSILHFDPEA 119
 |||||

121 CSFRELLEGGYNNVQSEAHGLPLHLPGNKSHPHDPAPRGAPFLPLGLPPALPEPGI 180
 |||||
 120 CSFRELLEGGYNNVQSEAHGLPLHLPGNKSHPHDPAPRGAPFLPLGLPPALPEPGI 179
 |||||

181 LAPQPPDVGSSDPLSMVSGQGRSPSYAS 209
 |||||
 180 LAPQPPDVGSSDPLSMVSGQGRSPSYAS 208
 |||||

RESULT 30
 ADB72969
 ID ADB72969 standard; protein; 208 AA.
 XX AC ADB72969;
 XX DT 04-DEC-2003 (first entry)
 XX DE Novel human secreted and transmembrane protein PRO10196.
 XX KW human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;

DB 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPPALPEPPI 179

QY 181 LAPQPPDVGSSDPLSMVGFSGRSPSYAS 209

DB 180 LAPQPPDVGSSDPLSMVGFSGRSPSYAS 208

RESULT 28

ADB84699

ID ADB84699 standard; protein; 208 AA.

AC ADB84699;

XX

XX

XX 04-DEC-2003 (first entry)

XX Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;

KW cancer; lung; colon; breast; prostate; rectum; liver;

KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;

KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;

KW arthritis; sports injury; cytostatic; antiarthritic.

XX

XX Homo sapiens.

OS

XX US200302890-A1.

XX

XX 15-MAY-2003.

XX

XX 14-AUG-2002; 2002US-00219536.

XX

XX 28-JUL-1999; 99US-0146222P.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US005841.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-777259/73.

DR N-PSDB; ADB84698.

XX

XX New isolated PRO polypeptides, useful for tissue typing, gene therapy, as

PT molecular weight markers in protein electrophoresis, and for treating

PT arthritis and tumors.

XX

XX Claim 11; Fig 78; 308pp; English.

XX

XX The invention relates to human PRO polypeptides (secreted and

XX transmembrane polypeptides) and the PRO polynucleotides encoding them.

XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,

XX diagnostics, biosensors or bioreactors. They are particularly useful for

XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,

XX prostate tumour, rectal tumour or liver tumour) in a mammal, for

XX stimulating the release of tumour necrosis factor (TNF)-alpha from human

XX blood, for stimulating the proliferation or differentiation of

XX chondrocyte cells, for stimulating the proliferation of or gene

XX expression in pericyte cells or for stimulating the proliferation of

XX normal human dermal fibroblasts. The PRO nucleic acids are useful as

XX hybridisation probes, in chromosome and gene mapping, in generating

XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant

XX technology, in generating transgenic animals or knock-out animals which

XX may be used in the development and screening of therapeutically useful

XX reagents, in gene therapy, in chromosome identification, as chromosome

XX markers and in generating probes. The PRO polypeptides, or anti-PRO

XX antibodies, are useful for preparing a medicament for treating a

XX condition which is responsive to the PRO polypeptides or anti-PRO

XX antibodies, such as pericyte-associated tumours and bone and/or cartilage

XX disorders (e.g. arthritis, sports injuries), involving inducing the re-

CC differentiation of chondrocytes. The PRO polypeptides are useful as

CC molecular markers for protein electrophoresis, and in tissue typing. This

CC sequence represents a human PRO polypeptide of the invention.

XX

SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;

Best Local Similarity 99.5%; Pred. No. 8.6e-91;

Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDSDETFEHSGLWYVLAGLLGACQAHPIPDSSPLLFQGGVQRVRYLYTDDAQOQTEAH 60

DB 1 MDSDETFEHSGLWYVLAG-LLGACQAHPIPDSSPLLFQGGVQRVRYLYTDDAQOQTEAH 59

QY 61 LEIRDGTVGGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYGLSLHFDPEA 120

DB 60 LEIRDGTVGGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYGLSLHFDPEA 119

QY 121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPPALPEPPI 180

DB 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPPALPEPPI 179

QY 181 LAPQPPDVGSSDPLSMVGFSGRSPSYAS 209

DB 180 LAPQPPDVGSSDPLSMVGFSGRSPSYAS 208

RESULT 29

ADB83814

ID ADB83814 standard; protein; 208 AA.

XX

AC ADB83814;

XX

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;

KW antiarthritic; pericyte cell proliferation;

KW pericyte cell differentiation; chondrocyte cell proliferation;

KW chondrocyte cell differentiation; tumour necrosis factor alpha release;

KW (TNF)-alpha release; dermal fibroblast cell proliferation;

KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW liver tumour; tissue typing; chromosome mapping; gene mapping;

KW gene therapy.

XX

XX Homo sapiens.

OS

XX US2003069397-A1.

XX

XX 10-APR-2003.

XX

XX 09-AUG-2002; 2002US-00216159.

XX

XX 25-JUL-2000; 2000US-0220607P.

PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-657584/62.

DR N-PSDB; ADB83813.

XX

XX New isolated polypeptides designated PRO polypeptides including

PT polypeptides useful for stimulating the proliferation or differentiation

PT of specific cell types, and for diagnosing cancer.

XX

XX Claim 11; Fig 78; 314pp; English.

	Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour; cancer; lung; colon; breast; prostate; rectum; liver; tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; pericyte cell; dermal fibroblast; bone disorder; cartilage disorder; arthritis; sports injury; cytostatic; antiarthritic.
XX	Homo sapiens.
OS	US2003088067-A1.
PN	08-MAY-2003.
XX	13-AUG-2002; 2002US-00219479.
PF	01-JUN-2001; 2001WO-US017800.
XX	29-JUN-2001; 2001WO-US021066.
PR	09-APR-2002; 2002US-00119480.
XX	(GETH) GENENTECH INC.
PA	Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI	Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
FPI	WPI; 2003-657981/62.
DR	N-PSDB; ADB87116.
XX	One hundred and twenty two nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, or as hybridization probes in chromosome and gene mapping.
PT	Claim 11; Fig 78; 314pp; English.
XX	The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynucleotides encoding them. The PRO polypeptides and polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. They are particularly useful for detecting tumours (e.g. lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour) in a mammal, for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferating of or gene expression in pericyte cells or for stimulating the proliferation of normal human dermal fibroblasts. The PRO nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant technology, in generating transgenic animals or knock-out animals which may be used in the development and screening of therapeutically useful reagents, in gene therapy, in chromosome identification, as chromosome markers and in generating probes. The PRO polypeptides, or anti-PRO antibodies, are useful for preparing a medicament for treating a condition which is responsive to the PRO polypeptides or anti-PRO antibodies, such as pericyte-associated tumours and bone and/or cartilage disorders (e.g. arthritis, sports injuries), involving inducing the re- differentiation of chondrocytes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and in tissue typing. This sequence represents a human PRO polypeptide of the invention.
XX	Sequence 208 AA;
SQ	Query Match 98.7%; Score 1098.5; DB 7; Length 208; Best Local Similarity 99.5%; Pred. No. 8.6e-91; Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1 MSDDTGFHSGLWYSVLAGLLGCACAHPLPDSPLLQFGGVRORYLYTDDAQOTEAH 60
Db	1 MSDDTGFHSGLWYSVLAG-LLGACCAHP LPDSSLQFGGVRORYLYTDDAQOTEAH 59
QY	61 LEIREDTGVGGADOSPESLLQLKALPGVTQILGVKTSRFLCORPDGALYSLHFDPDEA 120
Db	60 LEIREDTGVGGADOSPESLLQLKALPGVTQILGVKTSRFLCORPDGALYSLHFDPDEA 119
QY	121 CSFREILLEDDGVNYQSFAHLGLFIHLPNKNSPHRDDPAPRGPARFLPLFGLPPALPEPGI 130

CC condition which is responsive to the PRO polypeptides or anti-PRO
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polypeptide of the invention.
XX
SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDSDETFEHSGLVWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOQTEAH 60
DB 1 MDSDETFEHSGLVWVSLAG-LLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOQTEAH 59
QY 61 LEIREDDGTGGAAQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYGLHFDPEA 120
DB 60 LEIREDDGTGGAAQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYGLHFDPEA 119
QY 121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRFLPLGLPALPEPPGI 180
DB 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRFLPLGLPALPEPPGI 179
QY 181 LAPQPDVGVSSDPLSMVGPQGRSPSYAS 209
DB 180 LAPQPDVGVSSDPLSMVGPQGRSPSYAS 208

RESULT 26
ADB84945
ID ADB84945 standard; protein; 208 AA.
XX
AC ADB84945;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PRO polypeptide #39.
XX
KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
KW cancer; lung; colon; breast; prostate; rectum; liver;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
KW arthritis; sports injury; cytostatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN US2003073817-A1.
XX
PD 17-APR-2003.
XX
PF 26-AUG-2002; 2002US-00227883.
XX
PR 01-AUG-2000; 2000US-0222425P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX
XX WPI; 2003-730024/69.
DR N-PSDB; ADB84944.
XX
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX e.g. in gene therapy, disease diagnosis, chromosome identification and
XX tissue typing.
XX
PS Claim 11; Fig 78; 314pp; English.
XX
XX The invention relates to human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the PRO polynucleotides encoding them.
XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioreactors. They are particularly useful for
XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
XX prostate tumour, rectal tumour or liver tumour) in a mammal, for
XX stimulating the release of tumour necrosis factor (TNF)-alpha from human
XX blood, for stimulating the proliferation or differentiation of
XX chondrocyte cells, for stimulating the proliferation of or gene
XX expression in pericyte cells or for stimulating the proliferation of
XX normal human dermal fibroblasts. The PRO nucleic acids are useful as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant
XX technology, in generating transgenic animals or knock-out animals which
XX may be used in the development and screening of therapeutically useful
XX reagents, in gene therapy, in chromosome identification, as chromosome
XX markers and in generating probes. The PRO polypeptides, or anti-PRO
XX antibodies, are useful for preparing a medicament for treating a

CC condition which is responsive to the PRO polypeptides or anti-PRO
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polypeptide of the invention.
XX
SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDSDETFEHSGLVWVSLAGLLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOQTEAH 60
DB 1 MDSDETFEHSGLVWVSLAG-LLGACQAHPIPDSSPLLQFGQVQRVLYTDDAQOQTEAH 59
QY 61 LEIREDDGTGGAAQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYGLHFDPEA 120
DB 60 LEIREDDGTGGAAQSPESLLQKALKPGVQILGVKTSRFLCORPDGALYGLHFDPEA 119
QY 121 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRFLPLGLPALPEPPGI 180
DB 120 CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRFLPLGLPALPEPPGI 179
QY 181 LAPQPDVGVSSDPLSMVGPQGRSPSYAS 209
DB 180 LAPQPDVGVSSDPLSMVGPQGRSPSYAS 208

RESULT 26
ADB78051
ID ADB78051 standard; protein; 208 AA.
XX
AC ADB78051;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
KW antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
XX
XX gene therapy.
XX
OS Homo sapiens.
XX
PN US2003092886-A1.
XX
PD 15-MAY-2003.
XX
PF 09-AUG-2002; 2002US-00216165.
XX
PR 25-JUL-2000; 2000US-0220607P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX
XX WPI; 2003-765494/72.
DR N-PSDB; ADB78050.
XX
XX Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as
XX molecular weight markers in protein electrophoresis, for treating

are useful for stimulating the release of tumour necrosis factor (TNF)-
alpha from human blood. PRO982, PRO1306, PRO1419, PRO214,
PRO247, PRO337, PRO526, PRO531, PRO1083, PRO840, PRO1080,
PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
stimulating the proliferation of normal human dermal fibroblast cells.
PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
inhibiting the proliferation of normal human dermal fibroblast cells. PRO
polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
are useful for detecting the presence of expression of the above PRO polypeptides
in a test sample of cells taken from the mammal, and a control sample of
normal cells of the same cell type, where a higher level of expression of
the PRO polypeptides in the test sample as compared to the control sample
is indicative of the presence of tumour in the mammal. The tumour is lung
tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
liver tumour. (I) is useful as molecular weight markers, for tissue
typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
useful for chromosome and gene mapping or gene therapy. (II) is useful
for generating transgenic animals or knock-out animals which are useful
for screening useful reagents. PRO357, PRO1272 or PRO4405 polypeptide
is useful for treating bone and/or cartilage disorders (e.g., arthritis,
sport injuries). This is the amino acid sequence of a human secreted and
transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAH 60
Db 1 MDSDETFEHSGLWVSVLAG-LLGACQAHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAH 59
QY 61 LEIREDTGVGGAADQSPESLLQLKALPGVITQLGVKTSFLCQPDGALYGLSHFDPEA 120
Db 60 LEIREDTGVGGAADQSPESLLQLKALPGVITQLGVKTSFLCQPDGALYGLSHFDPEA 119
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSFHRDPAFPGFARFLPLFGLPPALPEPFGI 180
Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSFHRDPAFPGFARFLPLFGLPPALPEPFGI 179
QY 181 LAPQPPDVGSSDPLSMVGPQSGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSMVGPQSGRSPSYAS 208

RESULT 24

ADB78297
ADB78297 standard; protein; 208 AA.

XX ADB78297;

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cytotstatic; vulneryary;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.

OS Homo sapiens.
XX US2003092889-A1.
XX 15-MAY-2003.
XX 13-AUG-2002; 2002US-00219478.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-765495/72.
XX N-PSDB; ADB78296.
XX New isolated PRO polypeptide useful for tissue typing, gene therapy, as
XX molecular weight markers in protein electrophoresis, and for treating
XX arthritis and tumors.
XX Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane)
polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
useful for stimulating the proliferation of or gene expression in
pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
for stimulating the proliferation or differentiation of chondrocyte
cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
are useful for stimulating the release of tumour necrosis factor (TNF)-
alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
stimulating the proliferation of normal human dermal fibroblast cells.
PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
inhibiting the proliferation of normal human dermal fibroblast cells. PRO
polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
are useful for detecting the presence of expression of the above PRO polypeptides
in a test sample of cells taken from the mammal, and a control sample of
normal cells of the same cell type, where a higher level of expression of
the PRO polypeptides in the test sample as compared to the control sample
is indicative of the presence of tumour in the mammal. The tumour is lung
tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
liver tumour. (I) is useful as molecular weight markers, for tissue
typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
useful for chromosome and gene mapping or gene therapy. (II) is useful
for generating transgenic animals or knock-out animals which are useful
for screening useful reagents. PRO357, PRO1272 or PRO4405 polypeptide
is useful for treating bone and/or cartilage disorders (e.g., arthritis,
sport injuries). This is the amino acid sequence of a human secreted and
transmembrane PRO polypeptide.

Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAH 60
Db 1 MDSDETFEHSGLWVSVLAG-LLGACQAHPIPDSSPLQFGGVRQRYLYTDDAQOQTEAH 59
QY 61 LEIREDTGVGGAADQSPESLLQLKALPGVITQLGVKTSFLCQPDGALYGLSHFDPEA 120

KW antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX Homo sapiens.
XX US2003088069-A1.
XX 08-MAY-2003.
XX 13-AUG-2002; 2002US-00219481.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX N-PSDB; ADB80673.
XX WPI; 2003-657982/62.
XX N-PSDB; ADB80673.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful in gene therapy, chromosome identification, tissue typing, or as
XX hybridization probes in chromosome and gene mapping.
XX Claim 11; Fig 78; 305pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX useful for stimulating the proliferation of or gene expression in
XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
XX are useful for stimulating the release of tumour necrosis factor (TNF)-
XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
XX PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
XX PRO1286, PRO1130, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
XX PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
XX PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
XX stimulating the proliferation of normal human dermal fibroblasts cells.
XX PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
XX PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
XX polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
XX are useful for detecting the presence of tumour in a mammal which
XX involves comparing the level of expression of the above PRO polypeptides
XX in a test sample of cells taken from the mammal, and a control sample of
XX normal cells of the same cell type, where a higher level of expression of
XX the PRO polypeptides in the test sample as compared to the control sample
XX is indicative of the presence of tumour in the mammal. The tumour is lung
XX tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. (I) is useful as molecular weight markers, for tissue
XX typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
XX useful for chromosome and gene mapping or gene therapy. (II) is useful
XX for generating transgenic animals or knock-out animals which are useful
XX screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
XX is useful for treating bone and/or cartilage disorders (e.g., arthritis,
XX sport injuries). This is the amino acid sequence of a human secreted and
XX transmembrane PRO polypeptide.
XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFEHSGLVSWVLGALLGACQAHPIPDSSPLQLQFGQVQRVLYTDDAQOQTEAH 60
Db 1 MDSDETFEHSGLVSWVLG-LLGACQAHPIPDSSPLQLQFGQVQRVLYTDDAQOQTEAH 59
QY 61 LEIREDTVGGAADQSPESLLQLKALPGVIOILGVKTSRFLCORPDGALYGLSHFDPEA 120
Db 60 LEIREDTVGGAADQSPESLLQLKALPGVIOILGVKTSRFLCORPDGALYGLSHFDPEA 119
QY 121 CSFRELLLEDGNNVYQSEAHGLPLHLPNGKSHRPPAPRGPARFLPLGLPALPEPPGI 180
Db 120 CSFRELLLEDGNNVYQSEAHGLPLHLPNGKSHRPPAPRGPARFLPLGLPALPEPPGI 179
QY 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 208
RESULT 23
ADB73215
ID ADB73215 standard; protein; 208 AA.
XX AC ADB73215;
XX DT 04-DEC-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.
XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX Homo sapiens.
XX OS US2003096968-A1.
XX PN 22-MAY-2003.
XX PD 29-AUG-2002; 2002US-00232223.
XX PF 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-765525/72.
XX N-PSDB; ADB73214.
XX New isolated PRO polypeptides useful as molecular weight markers in
XX protein electrophoresis, useful for tissue typing, and for treating
XX arthritis and tumors.
XX Claim 11; Fig 78; 308pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX useful for stimulating the proliferation of or gene expression in
XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide

CC invention may have cytostatic activities through the stimulation of
CC chondrocytes. The nucleic acids of the invention may be useful for the
CC manufacture of a medicament for diagnosing or treating a tumour in a
CC mammal. In addition, they may be useful for measuring or detecting the
CC expression of a tumour associated gene. The present sequence is the amino
CC acid sequence of a human PRO protein of the invention
XX
XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFEHSGLMVSVLAGLLGACQAHPTPDSPLLQFGQVQRVLYTDDAQQTAEH 60
Db 1 MDSDETFEHSGLMVSVLAG-LLGACQAHPTPDSPLLQFGQVQRVLYTDDAQQTAEH 59
QY 61 LEIREDTGVGAADQSPESLILQKALXPGVLIQLGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 60 LEIREDTGVGAADQSPESLILQKALXPGVLIQLGVKTSRFLCQRPDGLYSLHFDPEA 119
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPALPEPPGI 180
Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPALPEPPGI 179
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 21
ADB83568
ID ADB83568 standard; protein; 208 AA.
XX AC ADB83568;
XX DT 04-DEC-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.

XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
KW antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX Homo sapiens.
XX US2003073914-A1.
XX 17-APR-2003.
XX 12-AUG-2002; 2002US-00218849.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-644806/61.
XX N-FSDS; ADB83567.
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.

XX PS Claim 11; Fig 78; 315pp; English.
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1083, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO363, PRO531, PRO1083, PRO840, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
CC PRO9940, PRO6079, or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
XX transmembrane PRO polypeptide.
XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 7; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MDSDETFEHSGLMVSVLAGLLGACQAHPTPDSPLLQFGQVQRVLYTDDAQQTAEH 60
Db 1 MDSDETFEHSGLMVSVLAG-LLGACQAHPTPDSPLLQFGQVQRVLYTDDAQQTAEH 59
QY 61 LEIREDTGVGAADQSPESLILQKALXPGVLIQLGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 60 LEIREDTGVGAADQSPESLILQKALXPGVLIQLGVKTSRFLCQRPDGLYSLHFDPEA 119
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPALPEPPGI 180
Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPALPEPPGI 179
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 22
ADB80674
ID ADB80674 standard; protein; 208 AA.
XX AC ADB80674;
XX DT 04-DEC-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.
XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;

KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.

OS Homo sapiens.

XX US2003027988-A1.

XX 06-FEB-2003.

XX 26-AUG-2002; 2002US-00227884.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-503301/47.

XX N-PSDB; ABT44547.

XX New PRO protein encoding nucleic acid, useful for preparing PRO

XX polypeptides and anti-PRO antibodies for detecting the presence of a

XX tumor in a mammal.

XX Claim 11; Fig 78; 324pp; English.

XX The invention relates to a novel isolated PRO protein encoding nucleic

XX acid. The nucleic acid of the invention may be useful for preparing PRO

XX polypeptides and anti-PRO antibodies for detecting the presence of a

XX tumor in a mammal. Furthermore, the molecules of the invention may be

XX useful for stimulating proliferation or gene expression in pericyte

XX cells, the release of tumour necrosis factor (TNF)-alpha from human

XX blood, the proliferation or differentiation of chondrocyte cells and for

XX inhibiting the proliferation of normal human dermal fibroblast cells.

XX Finally, the molecules may be utilised during gene therapy. The current

XX sequence is that of the human PRO protein of the invention

XX SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 6; Length 208;

Best Local Similarity 99.5%; Pred. No. 8.6e-91;

Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MDSDETGFEHSGLVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 60

Db 1 MDSDETGFEHSGLVSVLAG--LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 59

Qy 61 LEIRDGTGGAADQSPESLLQKALKEGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 120

Db 60 LEIRDGTGGAADQSPESLLQKALKEGVIQILGVKTSRFLCQRPDGLYSLHFDPEA 119

Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPALPEPGI 180

Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPNGKSPHRDPAPRGPARFLPLGLPALPEPGI 179

Qy 181 LAPQPPDVGSSDPLSMVGFSGRSFSYAS 209

Db 180 LAPQPPDVGSSDPLSMVGFSGRSFSYAS 208

XX Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.

XX Homo sapiens.

XX US2003044934-A1.

XX 06-MAR-2003.

XX 28-AUG-2002; 2002US-00230338.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-492274/46.

XX N-PSDB; ACD82214.

XX New transmembrane polypeptides and nucleic acids encoding the

XX polypeptides, useful in gene therapy, in chromosome identification, as

XX chromosome markers, or in generating probes.

XX Claim 19; Fig 78; 315pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO

XX polypeptide. Nucleic acids that encode PRO can be used to generate either

XX transgenic animals or knock-out animals useful in developing and

XX screening of therapeutically useful reagents. The nucleic acids may also

XX be used in gene therapy for replacing defective gene, in chromosome

XX identification, as chromosome markers, or in generating probes to isolate

XX full length PRO cDNA. The PRO polypeptides are useful for chondrocyte

XX stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation

XX and for detecting the presence of tumour in an animal. The PRO

XX polypeptides are useful as molecular markers for protein electrophoresis

XX and the isolated nucleic acids may be used for recombinantly expressing

XX those markers. The PRO polypeptides and nucleic acids may also be used in

XX tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

XX PRO and in affinity purification of PRO from recombinant cell culture or

XX natural sources. The present sequence represents the amino acid sequence

XX of a human secreted/transmembrane PRO polypeptide

XX SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 6; Length 208;

Best Local Similarity 99.5%; Pred. No. 8.6e-91;

Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MDSDETGFEHSGLVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 60

Db 1 MDSDETGFEHSGLVSVLAG--LLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 59

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XX 13-FEB-2003.
 XX 22-JUL-2002; 2002WO-US021290.
 XX 30-JUL-2001; 2001US-0308702P.
 XX 10-JAN-2002; 2002US-0347991P.
 XX (ELIL) LILLY & CO ELI.
 XX Glasebrook AL, Hammond LJ, Kharitonov A, Shiyanova TL;
 XX WPI; 2003-248106/24.
 XX N-PSDB; ABZ79797.
 XX Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or
 XX obesity, by administering composition comprising fibroblast growth factor
 XX -21.
 XX Claim 3; Fig 1; 32pp; English.
 XX The present sequence represents human fibroblast growth factor 21 (FGF-
 XX 21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-
 XX 21. The present invention describes a method for treating a mammal
 XX exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for
 XX obesity which comprises administering to the mammal a composition
 XX comprising FGF-21 which has at least 95% amino acid sequence identity to
 XX the 208 amino acid sequence given in ABP96156. Also described: (1)
 XX inducing an increase in glucose uptake in adipocyte cells by
 XX administering FGF-21 to induce an increase in glucose uptake; and (2)
 XX manufacturing a medicament for treating type 1 diabetes, type 2 diabetes
 XX or obesity in a mammal using FGF-21 having 95% amino acid sequence
 XX identity to ABP96156. FGF-21 has antidiabetic and anorectic activities.
 XX The method is useful for treating a mammal exhibiting type 2 or 1
 XX diabetes or for treating a mammal for obesity. The method is preferably
 XX useful for treating humans exhibiting type 1 or type 2 diabetes, and for
 XX treating domestic animals for obesity
 XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 6; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
 Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 59
 Qy 61 LEIREDTGVGAADQSPESLLQLKALKEGVIQILGVKTSRFLCQRPDQALYGSLSHFDEA 120
 Db 60 LEIREDTGVGAADQSPESLLQLKALKEGVIQILGVKTSRFLCQRPDQALYGSLSHFDEA 119
 Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
 Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 179
 Qy 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 Db 180 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 16
 ABJ72266
 ID ABJ72266 standard; protein; 208 AA.
 XX AC ABJ72266;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human PRO10196 protein.
 XX KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
 KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.

XX Homo sapiens.
 XX US2003050448-A1.
 XX 13-MAR-2003.
 XX 28-AUG-2002; 2002US-00230414.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (SETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-521818/49.
 XX N-PSDB; ABT44264.
 XX New nucleic acid encoding for a PRO protein, useful for the manufacture
 XX of a medicament for diagnosing or treating tumors or for measuring or
 XX detecting expression of an associated gene.
 XX Claim 11; Fig 78; 315pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding a fully
 XX defined PRO polypeptide. The molecules of the invention may be useful for
 XX stimulating proliferation or gene expression in pericyte cells or the
 XX release of TNF-alpha from human blood. Other possible uses include the
 XX stimulation or inhibition of chondrocyte proliferation or
 XX differentiation, the stimulation of human dermal fibroblast cell
 XX proliferation and the detection of the presence of a tumour within a
 XX mammal. Furthermore, the nucleic acid may be useful for the manufacture
 XX of a medicament for diagnosing or treating a tumour within a mammal or
 XX as during gene therapy. The current sequence is that of the human PRO
 XX protein of the invention
 XX Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 6; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
 Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 59
 Qy 61 LEIREDTGVGAADQSPESLLQLKALKEGVIQILGVKTSRFLCQRPDQALYGSLSHFDEA 120
 Db 60 LEIREDTGVGAADQSPESLLQLKALKEGVIQILGVKTSRFLCQRPDQALYGSLSHFDEA 119
 Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
 Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 179
 Qy 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 Db 180 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 17
 ABJ72394
 ID ABJ72394 standard; protein; 208 AA.
 XX AC ABJ72394;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human PRO10196 protein.

CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any these 122
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 CC in a mammal, for stimulating the release of TNF-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating proliferation of pericyte cells, or for modulating
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX
 CC Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 6; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MDSDETFEHSGLVWSVLGALLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTAAH 60
 Db 1 MDSDETFEHSGLVWSVLGALLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTAAH 59
 QY 61 LEIREDTGCGAADOQPESLILQKALKEGVITQILGVKTSRFLCORPDGALYGSLLHFDPEA 120
 Db 60 LEIREDTGCGAADOQPESLILQKALKEGVITQILGVKTSRFLCORPDGALYGSLLHFDPEA 119
 QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPKNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
 Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPKNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 179
 QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 Db 180 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 14
 ABU82086
 ID ABU82086 standard; protein; 208 AA.
 AC ABU82086;
 XX
 DT 25-JUN-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 XX
 KW Human; secreted and transmembrane protein; PRO; cardiac; cytostatic;
 KW antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 FN US200308063-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 12-AUG-2002; 2002US-00219003.

XX 25-JUL-2000; 2000US-0220664P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PI;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 PI WPI; 2003-393229/37.
 DR N-PSDB; ACA68535.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 11; Fig 78; 314pp; English.

XX The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX
 CC Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 6; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 MDSDETFEHSGLVWSVLGALLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTAAH 60
 Db 1 MDSDETFEHSGLVWSVLGALLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTAAH 59
 QY 61 LEIREDTGCGAADOQPESLILQKALKEGVITQILGVKTSRFLCORPDGALYGSLLHFDPEA 120
 Db 60 LEIREDTGCGAADOQPESLILQKALKEGVITQILGVKTSRFLCORPDGALYGSLLHFDPEA 119
 QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPKNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
 Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPKNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 179
 QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 Db 180 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 208

RESULT 15
 ABP96156
 ID ABP96156 standard; protein; 208 AA.
 AC ABP96156;
 XX
 DT 12-MAY-2003 (first entry)
 XX
 DE Human fibroblast growth factor 21 protein SEQ ID NO:2.
 XX
 KW Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter;
 KW diabetes; obesity; antidiabetic; anorectic; type 2 diabetes;
 KW type 1 diabetes.
 XX
 OS Homo sapiens.
 XX
 FN WO2003011213-A2.

XX SQ Sequence 208 AA;
Query Match 98.7%; Score 1098.5; DB 5; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91; Indels 1; Gaps 1;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 59
Qy 61 LEIREDTGVCGRADQSPESLLQKALKEGVIIQILGVKTSRFLCORPDGALYGSILHFDPEA 120
Db 60 LEIREDTGVCGRADQSPESLLQKALKEGVIIQILGVKTSRFLCORPDGALYGSILHFDPEA 119
Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLFGLPPALPEPPGI 180
Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLFGLPPALPEPPGI 179
Qy 181 LAPQPPDVGSSDPLSMVGPSSQGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSMVGPSSQGRSPSYAS 208

RESULT 12
ABU80777
ID ABU80777 standard; protein; 208 AA.
XX AC ABU80777;
XX AC ABU80777;
XX DT 23-JUN-2003 (first entry)
XX DE Human PRO polypeptide #39.
XX DE Human; PRO polypeptide; secreted and transmembrane protein;
XX KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX KW Homo sapiens.
XX OS US2003036635-A1.
XX FN 20-FEB-2003.
XX PD 28-AUG-2002; 2002US-00230163.
XX PF 25-JUN-2000; 2000US-0220638P.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH) GENENTECH INC.
XX PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX XX WPI; 2003-342045/32.
XX DR N-PSDB; ACA66879.
XX XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX PT useful for the manufacture of a medicament for diagnosing or treating
XX PT tumor.
XX PT Claim 11; Fig 78; 314pp; English.
XX PS

XX CC The present invention relates to the isolation of novel human PRO
XX CC polypeptides, and the polynucleotide sequences encoding them. The PRO
XX CC polypeptides are secreted and transmembrane proteins. The PRO
XX CC polypeptides and polynucleotides are useful for preparing a medicament
XX CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
XX CC useful in diagnostic assays for PRO, by detecting its expression in
XX CC specific cells, tissues or serum, and for affinity purification of PRO
XX CC from recombinant cell culture or natural sources. ABU80739-ABU80860
XX CC represent the human PRO polypeptides of the invention. Note: The sequence

CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsIDEntry.html
XX SQ Sequence 208 AA;
Query Match 98.7%; Score 1098.5; DB 6; Length 208;
Best Local Similarity 99.5%; Pred. No. 8.6e-91; Indels 1; Gaps 1;
Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 60
Db 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQOTEAH 59
Qy 61 LEIREDTGVCGRADQSPESLLQKALKEGVIIQILGVKTSRFLCORPDGALYGSILHFDPEA 120
Db 60 LEIREDTGVCGRADQSPESLLQKALKEGVIIQILGVKTSRFLCORPDGALYGSILHFDPEA 119
Qy 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLFGLPPALPEPPGI 180
Db 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAPRGPARFLPLFGLPPALPEPPGI 179
Qy 181 LAPQPPDVGSSDPLSMVGPSSQGRSPSYAS 209
Db 180 LAPQPPDVGSSDPLSMVGPSSQGRSPSYAS 208

RESULT 13
ABO33743
ID ABO33743 standard; protein; 208 AA.
XX AC ABO33743;
XX AC ABO33743;
XX DT 17-SEP-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.
XX DE Human; secreted and transmembrane protein; PRO; cytostatic;
XX KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
XX KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
XX KW pharmaceutical; diagnostic; biosensor; bioindicator; tumour; lung tumour;
XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
XX KW liver tumour; bone disorder; cartilage disorder; sports injury;
XX KW arthritis; wound.
XX OS Homo sapiens.
XX XX US2003045687-A1.
XX FN 06-MAR-2003.
XX PD 12-AUG-2002; 2002US-00218631.
XX PF 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX XX (GETH) GENENTECH INC.
XX XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX XX WPI; 2003-512315/48.
XX DR N-PSDB; ACD68631.
XX DR

XX PT New genes, and its encoded secreted and transmembrane polypeptides,
XX PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
XX PT pericyte proliferation, especially for treating lung tumors, arthritis or
XX PT wounds in a mammal.
XX XX Claim 11; Fig 78; 314pp; English.
XX XX The invention describes an isolated nucleic acid molecule comprising a
XX CC sequence with at least 80% identity to: (a) a nucleotide encoding any of

XX 05-NOV-2002 (first entry)
XX Human fibroblast growth factor (FGF) homologue, zFGF11.
XX Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFR11c;
XX osteoblastic lineage cell; diabetes mellitus; neuropathy;
XX neural cell development; amyotrophic lateral sclerosis;
XX cerebrovascular stroke; neuronal differentiation; congenital disorder;
XX nervous system disorder; cardiac function; wound healing.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..27
XX /label= Signal_sequence
XX Protein 28..208
XX /note= "Mature fibroblast growth factor homologue, zFGF11. This sequence is specifically claimed in claim 4"
XX US2002081663-A1.
XX 27-JUN-2002.
XX 05-JAN-2001; 2001US-00755695.
XX 05-JAN-2000; 2000US-0174526P.
XX (CONK/) CONKLIN D C.
XX (CHEN/) CHEN Z.
XX Conklin DC, Chen Z;
XX WPI; 2002-626540/67.
XX N-PSDB; ABK91310.
XX Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in
XX treatment of disorders associated with diabetes mellitus, neural cell
XX development or degeneration, amyotrophic lateral sclerosis,
XX cerebrovascular stroke.
XX Claim 4; Fig 1; 35pp; English.
XX The invention relates to an isolated human polypeptide (I) for zFGF11 (a
XX fibroblast growth factor), and the encoding polynucleotide (II). (I) and
XX (II) are used in methods of the invention stimulating proliferation of
XX mesenchymal cells, detecting the presence of zFGF11 in a biological
XX sample, detecting the presence of FGFR11c in a biological sample and
XX stimulating proliferation of osteoblastic lineage cells. The
XX polypeptides, nucleic acid and/or antibodies of the invention may be used
XX in treatment of disorders associated with diabetes mellitus, neural cell
XX development or degeneration, amyotrophic lateral sclerosis,
XX cerebrovascular stroke, neuropathy associated with lack of maintenance of
XX neuronal differentiation, and congenital disorders of the nervous system
XX or lack of neuronal development. Molecules of the invention may also be
XX useful for improving cardiac function and for promoting wound healing of
XX the epidermis. The present sequence represents the amino acid sequence of
XX human zFGF11
XX Sequence 208 AA;
XX Query Match 98.7%; Score 1098.5; DB 5; Length 208;
XX Best Local Similarity 99.5%; Pred. No. 8.6e-91;
XX Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
XX 1 MDSDTGTFHSLWVSLAGLLGACQAHPIPDSSPLLFQGGQVRVLYTDDAQQTAAH 60
XX 1 MDSDTGTFHSLWVSLAG-LLGACQAHPIPDSSPLLFQGGQVRVLYTDDAQQTAAH 59
XX 61 LEIRDGTGVGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYGLSLHFDPEA 120
XX 60 LEIRDGTGVGAADQSPESLLQKALKPGVILGVKTSRFLCQRPDGLYGLSLHFDPEA 119

QY 121 CSFRELLEDGNYVYQSEAHGLPLHLFQNKSPHRDPAPRGPARFLPLGLPALPEPPI 180
DB |||||
120 CSFRELLEDGNYVYQSEAHGLPLHLFQNKSPHRDPAPRGPARFLPLGLPALPEPPI 179
QY 181 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB |||||
180 LAPOPPDVGSSDPLSMVGPSQGRSPSYAS 208
RESULT 11
AAE17601
ID AAE17601 standard; protein; 208 AA.
XX
AC AAE17601;
XX
DT 22-APR-2002 (first entry)
XX
DR Human extracellular messenger (XMES)-3 protein.
XX
KW Human; extracellular messenger; neurological disorder; epilepsy; XMES-3;
KW Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke;
KW acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic;
KW developmental disorder; anaemia; Cushing's syndrome; endocrine disorder;
KW vascular malformation; cell proliferative disorder; gene therapy; cancer;
KW neuroprotective; trauma; hypopituitarism; hypothyroidism; antihelminthic;
KW hyperthyroidism; gonadal steroid hormone; pancreatic disorder; neotropic;
KW diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial;
KW antiviral; antifungal; parasitic; protozoal; allergy.
XX
OS Homo sapiens.
XX
PN WO200194587-A2.
XX
PD 13-DEC-2001.
XX
PF 06-JUN-2001; 2001WO-US018476.
XX
PR 06-JUN-2000; 2000US-0210233P.
PR 23-JUN-2000; 2000US-0213465P.
PR 14-NOV-2000; 2000US-0249019P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, He A, Nguyen DB, Walia N, Gandhi AR, Azimzai Y;
PI Bandman O, Tang YT, Lu Y, Baughn MR, Duggan BW, Lee S, Hafalia A;
PI Policy JI;
XX
DR WPI; 2002-154573/20.
DR N-PSDB; AAD28493.
XX
PT New extracellular messenger polypeptides and polynucleotides encoding
PT them, useful for diagnosing, treating or preventing e.g. neurological,
PT autoimmune, inflammatory, developmental and endocrine disorders.
XX
PS Claim 1; Page 111; 123pp; English.
XX
CC The present invention relates to new extracellular messenger polypeptides
CC and polynucleotides encoding them. XMES is useful in the diagnosis,
CC treatment and prevention of neurological disorders (e.g. epilepsy,
CC stroke or Alzheimer's disease), autoimmune/inflammatory disorders (e.g.
CC acquired immune deficiency syndrome, AIDS, Addison's disease, or
CC allergies), developmental disorders (e.g. renal tubular acidosis, anaemia
CC or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy,
CC aneurysm or vascular malformation), and cell proliferative disorders
CC (e.g. cancer), and in the assessment of the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC extracellular messengers. XMES may also be used in the treatment of
CC viral, bacterial, fungal, parasitic, protozoal and helminthic
CC infections, trauma, disorders associated with hypopituitarism,
CC hypothyroidism, hyperthyroidism or gonadal steroid hormones, and
CC pancreatic disorders such as type I or type II diabetes mellitus. The
CC XMES may be used for somatic or germline gene therapy. The present
CC sequence is human XMES-3 protein

CC mellitus, neural cell development or degeneration, amyotrophic lateral
 CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of
 CC maintenance of neuronal differentiation and congenital disorders of the
 CC nervous system or lack of neuronal development, promoting angiogenesis
 CC and wound healing, for revascularisation in eye, complications related to
 CC poor circulation such as diabetic foot ulcers, improving cardiac
 CC function, modulating surfactant production in the lung epithelium, to
 CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
 CC events, particularly in the heart or brain and for inducing skeletal
 CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
 CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
 CC are useful for inhibiting disorders associated with kidney epithelium
 CC such as glomerulonephritis
 XX
 SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 4; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
 DB 1 MDSDETFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 59
 QY 61 LEIREDTGVGAADQSPESLLQLKALPGVVIQILGVKTSRFLCORPDGALYGSILHFDPEA 120
 DB 60 LEIREDTGVGAADQSPESLLQLKALPGVVIQILGVKTSRFLCORPDGALYGSILHFDPEA 119
 QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAHPARFLPLPGLPPALPEPPGI 180
 DB 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAHPARFLPLPGLPPALPEPPGI 179
 QY 181 LAPQPPDVGSSDPLSMVGPQSGRSPSYAS 209
 DB 180 LAPQPPDVGSSDPLSMVGPQSGRSPSYAS 208

RESULT 9
 AAU83630
 ID AAU83630 standard; protein; 208 AA.
 AC AAU83630;
 XX
 XX 08-MAY-2002 (first entry)
 XX Human PRO protein, Seq ID No 78.
 XX
 XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 XX breast cancer; prostate tumour; rectal tumour; liver tumour;
 XX pericyte cell proliferation; chondrocyte cell proliferation;
 XX tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 XX WO200208298-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 29-JUN-2001; 2001WO-US021066.
 XX
 XX 20-JUL-2000; 2000US-0219556P.
 XX 25-JUL-2000; 2000US-0220585P.
 XX 25-JUL-2000; 2000US-0220605P.
 XX 25-JUL-2000; 2000US-0220607P.
 XX 25-JUL-2000; 2000US-0220624P.
 XX 25-JUL-2000; 2000US-0220638P.
 XX 25-JUL-2000; 2000US-0220664P.
 XX 25-JUL-2000; 2000US-0220666P.
 XX 26-JUL-2000; 2000US-0220893P.
 XX 28-JUL-2000; 2000WO-US020710.
 XX 01-AUG-2000; 2000US-0222425P.
 XX 22-AUG-2000; 2000US-0227133P.
 XX 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABK33574.
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX
 PS Claim 11; Fig 78; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX
 SQ Sequence 208 AA;

Query Match 98.7%; Score 1098.5; DB 5; Length 208;
 Best Local Similarity 99.5%; Pred. No. 8.6e-91;
 Matches 208; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 60
 DB 1 MDSDETFEHSGLWVSVLAG-LLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQOTEAH 59
 QY 61 LEIREDTGVGAADQSPESLLQLKALPGVVIQILGVKTSRFLCORPDGALYGSILHFDPEA 120
 DB 60 LEIREDTGVGAADQSPESLLQLKALPGVVIQILGVKTSRFLCORPDGALYGSILHFDPEA 119
 QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAHPARFLPLPGLPPALPEPPGI 180
 DB 120 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhRDPAHPARFLPLPGLPPALPEPPGI 179
 QY 181 LAPQPPDVGSSDPLSMVGPQSGRSPSYAS 209
 DB 180 LAPQPPDVGSSDPLSMVGPQSGRSPSYAS 208

RESULT 10
 ABG32358
 ID ABG32358 standard; protein; 208 AA.
 XX
 AC ABG32358;

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QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 8
AAE05078
ID AAE05078 standard; protein; 208 AA.
XX
AC AAE05078;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
XX
KW Human; fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;
KW proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis;
KW chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture;
KW bone formation; diabetes mellitus; neural cell development; angiogenesis;
KW amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer;
KW congenital disorder; wound healing; cardiac function; glomerulonephritis;
KW surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
KW hypertension; cytostatic; vasotropic; therapy.
XX
OS Homo sapiens.
XX
EH Key
FT Peptide 1..27
FT Protein /label= Signal_peptide
FT /label= Human_mature_zFGF11_protein
FT Binding-site 28..208
FT /note= "Heparin binding domain"
XX
XX WO200149849-A1.
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US000324.
XX
XX 05-JAN-2000; 2000US-00477886.
XX
XX (ZYMO ) ZYMOGENETICS INC.
XX
XX Conklin DC, Chen Z;
XX
XX WPI; 2001-441880/47.
XX N-PSDB; AAD09151.
XX
XX Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast
XX growth factor family, for stimulating proliferation of mesenchymal,
XX osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
XX cancer.
XX
XX Claim 1; Page 63; 69pp; English.
XX
XX The present sequence is human fibroblast growth factor (FGF) homologue,
XX zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
XX for stimulating proliferation of mesenchymal cells, osteoblastic lineage
XX cells. zFGF11 is useful for identifying chromosomal disorders associated
XX with abnormal expression of zFGF11 protein. zFGF11 is also useful for
XX stimulation, inhibition or proliferation of myocytes, smooth muscle
XX cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
XX crest stem cells and neuronal progenitors, pancreatic cells, prostate-
XX derived cells and endothelial cells and inhibiting chondrosarcomas,
XX atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
XX results in bone formation useful for treating bone defects, fractures,
XX osteoporosis and other deficiencies in bone structure and formation.
XX zFGF11 is useful for treating disorders associated with diabetes

```

```

QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLGLPPALPEPPGI 180
QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 7
AAB83951
ID AAB83951 standard; protein; 209 AA.
XX
AC AAB83951;
XX
DT 06-AUG-2001 (first entry)
XX
DE Amino acid sequence of a human sbgFGF-19a polypeptide.
XX
KW Human; sbgFGF-19a; fibroblast growth factor; stroke; cancer; psoriasis;
KW traumatic brain injury; cerebral ischemia; atherosclerosis;
KW rheumatoid arthritis; cirrhosis; sarcoidosis; wound repair;
KW idiopathic pulmonary fibrosis; tumour development;
KW vaccine developmental disorder; skeletal disorder; acrocephaly.
XX
OS Homo sapiens.
XX
XX WO200132678-A1.
XX
XX 10-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-US030478.
XX
XX 05-NOV-1999; 99US-00434358.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Agarwal P, Barone F, Feild JA, Kabnick KS, Mcquaney MS;
XX
XX WPI; 2001-316413/33.
XX N-PSDB; AAF89921.
XX
XX Novel sbgFGF-19a polypeptide, a member of fibroblast growth factor family
XX PT and polynucleotides encoding them useful for diagnosing, treating stroke,
XX PT psoriasis, cancer, atherosclerosis, rheumatoid arthritis and cirrhosis.
XX
XX Claim 1; Page 23; 31pp; English.
XX
XX The present sequence represents a human sbgFGF-19a polypeptide. The
XX polypeptide is a member of fibroblast growth factor family of
XX polypeptides. The polynucleotides and polypeptides are useful in the
XX treatment of diseases such as stroke, traumatic brain injury, cerebral
XX ischemia, cancer, atherosclerosis, rheumatoid arthritis, cirrhosis,
XX psoriasis, sarcoidosis, idiopathic pulmonary fibrosis, tumour
XX development, developmental disorders, skeletal disorders, wound repair,
XX and acrocephaly. They are also useful as vaccines for inducing an
XX immunological response in a mammal
XX
XX Sequence 209 AA;
XX
XX Query Match 99.4%; Score 1106; DB 4; Length 209;
XX Best Local Similarity 99.5%; Pred. No. 1.8e-91;
XX Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 MDSDETGFHSLGWSVLGALLGACQAHPIPDSSPLQFGQVQRVLYTDDAQTEAH 60
XX
XX 1 MDSDETGFHSLGWSVLGALLGACQAHPIPDSSPLQFGQVQRVLYTDDAQTEAH 60
XX
XX 61 LEIRDGTGVGAADQSPESLLQKALPGVILGVKTSRFLCORPDGALYSLHFDPEA 120
XX
XX 61 LEIRDGTGVGAADQSPESLLQKALPGVILGVKTSRFLCORPDGALYSLHFDPEA 120

```

PR 22-NOV-1999; 99US-00444165.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 PI Khodadoust MM;
 XX
 DR WPI; 2001-355881/37.
 XX
 DR N-PSDB; AAF90326, AAF90327.
 XX
 XX Isolated JAFFA nucleic acid molecules which encode novel fibroblast
 PT growth factor family members (JAFFA) are useful for developing novel
 PT diagnostic and therapeutic agents for JAFFA-associated disorders such as
 PT cancers.
 XX
 XX Claim 2; Fig 1; 137pp; English.
 PS
 XX
 XX The present sequence is that of human JAFFA, a novel member of the
 CC fibroblast growth factor family. Analysis of rare sequences in the
 CC Millennium database led to the identification of an expressed sequence
 CC tag from a human prostate tumour library which coded for a novel
 CC hypothetical signal peptide. Further analysis led to the identification
 CC of JAFFA. The invention provides JAFFA polypeptides, polynucleotides and
 CC anti-JAFFA antibodies. It also provides antisense nucleic acid molecules,
 CC recombinant expression vectors, host cells and transgenic animals. JAFFA
 CC proteins may be useful for developing novel diagnostic and therapeutic
 CC agents for JAFFA-associated disorders such as cancers and other disorders
 CC which demonstrate ABO(H) blood group disorders and for controlling
 CC cellular proliferative and/or differentiative disorders. The JAFFA
 CC nucleic acid and protein may be used to treat and/or diagnose a variety
 CC of immune disorders such as autoimmune disease and multiple sclerosis.
 CC The proteins may also be used to screen for naturally occurring JAFFA
 CC substrates, to screen for drugs or compounds which modulate JAFFA
 CC activity, and to raise anti-JAFFA antibodies, which can be used to detect
 CC and isolate JAFFA proteins, regulate the bioavailability of JAFFA
 CC proteins and modulate JAFFA activity
 XX
 XX Sequence 209 AA;

Query Match 99.4%; Score 1106; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.8e-91;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MDSDETFEHSGLWVSVIAGLLGACQAHPIPDSSPLLOFGGVQRVRYLYTDDAQQTAAH 60
 DB 1 MDSDETFEHSGLWVSVIAGLLGACQAHPIPDSSPLLOFGGVQRVRYLYTDDAQQTAAH 60
 QY 61 LEIREDTGVGAADQSPESLLQKALKPQVILGVKTSRFLCORPDGALYXSLHFDEPA 120
 DB 61 LEIREDTGVGAADQSPESLLQKALKPQVILGVKTSRFLCORPDGALYXSLHFDEPA 120
 QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKGPHRDPAPRGPARFLPLGLPPALPEPPGI 180
 DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKGPHRDPAPRGPARFLPLGLPPALPEPPGI 180
 QY 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209
 DB 181 LAPQPPDVGSSDPLSMVGPQGRSPSYAS 209

RESULT 6
 AAU00957
 ID AAU00957 standard; protein; 209 AA.
 XX
 XX AAU00957;
 AC
 DT 24-MAY-2001 (first entry)
 XX
 DE Human Fibroblast Growth Factor-like (FGF-like) polypeptide.
 XX
 XX Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
 KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
 KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
 KW neurodegenerative disease; haematopoietic cell reconstruction; cachexia;

chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
 multiple sclerosis; short stature; delayed maturation; excessive growth;
 acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
 androgen target organ abnormality; respiratory distress syndrome; stroke;
 cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness;
 osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
 decreased stamina; decreased cardiac function; immune system dysfunction;
 Parkinson's disease; Alzheimer's disease; decreased cognitive function;
 senile dementia; human.

Homo sapiens.

Key Location/Qualifiers
 Peptide 1..28
 Protein /note= "Signal peptide"
 /note= "Mature human FGF-like protein"

WO2000118172-A2.

15-MAR-2001.

05-SEP-2000; 2000WO-US024373.

07-SEP-1999; 39US-00391861.

23-AUG-2000; 2000US-00644052.

(AMGE-) AMGEN INC.

Thomason AR, Liu B;

WPI; 2001-226743/23.

N-PSDB; RAS00779.

Novel isolated fibroblast growth factor-like polypeptide useful for
 treating, preventing or ameliorating cirrhosis, inflammatory bowel
 disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
 osteoporosis.

Claim 13; Fig 2; 138pp; English.

The sequence represents a fibroblast growth factor-like (FGF-like)
 polypeptide. FGF-like protein and its associated nucleic acid play a role
 in modulating body growth, maturation or life-span. They are also useful
 for treating, preventing or ameliorating disorders such as cirrhosis,
 inflammatory bowel disease, mucositis, Crohn's disease, diabetes,
 obesity, gastrointestinal abnormalities, neurodegenerative diseases,
 damage to renal tubules as a result of acute tubular necrosis,
 haematopoietic cell reconstruction following chemotherapy, wasting
 syndromes (e.g., cancer associated cachexia), damage to the corneal
 epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
 stature, delayed maturation, excessive growth (e.g. acromegaly),
 premature maturation, alopecia, abnormalities of androgen target organs,
 bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
 of the eye or other tissues, atherosclerosis, hypercholesterolemia,
 stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
 baldness, wrinkles, increased fatigue, decreased stamina, decreased
 cardiac function, immune system dysfunction, cancer, Parkinson's disease,
 senile dementia, Alzheimer's disease, and decreased cognitive function

Sequence 209 AA;

Query Match 99.4%; Score 1106; DB 4; Length 209;
 Best Local Similarity 99.5%; Pred. No. 1.8e-91;
 Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVIAGLLGACQAHPIPDSSPLLOFGGVQRVRYLYTDDAQQTAAH 60

DB 1 MDSDETFEHSGLWVSVIAGLLGACQAHPIPDSSPLLOFGGVQRVRYLYTDDAQQTAAH 60

QY 61 LEIREDTGVGAADQSPESLLQKALKPQVILGVKTSRFLCORPDGALYXSLHFDEPA 120

DB 61 LEIREDTGVGAADQSPESLLQKALKPQVILGVKTSRFLCORPDGALYXSLHFDEPA 120

Db 61 LEIREDTVGGAADQSPESLLQLKALKEGVIQLGVKTSRFLCQRPDGLYSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPALPEPPGI 180
QY 181 LAPOPPDVGGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPOPPDVGGSSDPLSMVGPQGRSPSYAS 209

RESULT 4
AAE18826
ID AAE18826 standard; protein; 209 AA.
AC AAE18826;
XX
XX
DT 17-MAY-2002 (first entry)
XX
XX Human FGF-21 protein.
XX
XX Fibroblast growth factor; FGF-like protein; wound healing; bullosa;
KW epidermolysis; erosive gastritis; inflammatory bowel disease; ulcer;
KW oesophagitis; Crohn's disease; hyaline membrane disease; emphysema;
KW pulmonary fibrosis; hepatic cirrhosis; liver failure; angiogenesis;
KW multiple sclerosis; neurodegenerative disease; lung abnormality;
KW viral hepatitis; respiratory distress syndrome; tumour; skin aging;
KW gene therapy; vaccine; human.
XX
XX Homo sapiens.
XX
XX US2002001825-A1.
PN
XX
XX 03-JAN-2002.
PD
XX
XX 02-APR-2001; 2001US-00822485.
PF
XX
XX 31-MAR-2000; 2000US-00540118.
PR
XX
XX (ITOH//) ITOH N.
FA
XX
XX Itoh N;
PI
XX
XX WPI; 2002-187704/24.
DR
XX
XX Novel fibroblast growth factor-like polypeptide useful for treating,
FT ameliorating and/or preventing dermal wounds, gastric ulcer, Crohn's
FT disease and pulmonary inflammation.
FT
XX
XX Disclosure; Fig 3; 63pp; English.
PS
XX
XX The invention relates to fibroblast growth factor (FGF)-like polypeptides
CC and nucleic acid molecules encoding such polypeptides. Sequences of the
CC invention are useful for treating, preventing or ameliorating a medical
CC condition. They are useful for treating dermal wounds, epidermolysis,
CC bullosa, male pattern alopecia, gastric ulcer, duodenal ulcer, erosive
CC gastritis, oesophagitis, oesophageal reflux disease, inflammatory bowel
CC disease, Crohn's disease, radiation- or chemotherapy-induced gut
CC toxicity, hyaline membrane disease, necrosis of the respiratory
CC epithelium, emphysema, pulmonary inflammation, pulmonary fibrosis,
CC hepatic cirrhosis, toxic insults to the liver, fulminant liver failure,
CC viral hepatitis, mucositis, infantile sclerosis and other
CC neurodegenerative diseases, multiple sclerosis and other
CC bronchopulmonary dysplasia, acute respiratory distress syndrome, or other
CC lung abnormalities, tumours of the eye or the other tissues and organs.
CC FGF-like polypeptides are useful stimulating angiogenesis, promoting
CC wound healing, modulating differentiation of neuronal cells, adipocytes
CC and skeletal muscle cells, preventing or ameliorate skin aging,
CC preventing hair loss, stimulating the growth and differentiation of
CC haematopoietic cells and bone marrow cells and maintaining organs before
CC transplantation and for supporting cultures of primary cells and tissues.
CC Sequences of the invention are also used in gene therapy and as vaccines.
CC

CC The present sequence is human FGF-21 protein which is a member of the FGF
CC family
XX
SQ Sequence 209 AA;
Query Match 100.0%; Score 1113; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVIAGLLGACQAHPTPDSSPLQLQFGGVQRVLYLTDDAQQTEAH 60
Db 1 MDSDETFEHSGLWVSVIAGLLGACQAHPTPDSSPLQLQFGGVQRVLYLTDDAQQTEAH 60
QY 61 LEIREDTVGGAADQSPESLLQLKALKEGVIQLGVKTSRFLCQRPDGLYSLHFDPEA 120
Db 61 LEIREDTVGGAADQSPESLLQLKALKEGVIQLGVKTSRFLCQRPDGLYSLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPALPEPPGI 180
Db 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPHRDPAPRGPARFLPLPGLPALPEPPGI 180
QY 181 LAPOPPDVGGSSDPLSMVGPQGRSPSYAS 209
Db 181 LAPOPPDVGGSSDPLSMVGPQGRSPSYAS 209

RESULT 5
AAB82351
ID AAB82351 standard; protein; 209 AA.
XX
XX AAB82351;
XX
XX 23-JUL-2001 (first entry)
DT
XX
XX Human JAFFA protein.
DE
XX
XX JAFFA; human; fibroblast growth factor; diagnosis; therapy; cancer;
KW autoimmune disease; cytostatic; immunosuppressive; neuroprotective.
KW
XX
XX Homo sapiens.
OS
XX
XX
FH
XX
XX Key Location/Qualifiers
FT Peptide 1..28 /label= Signal_peptide
FT Modified-site 6..9 /note= "predicted casein kinase II phosphorylation site"
FT Modified-site 12..17 /note= "N-myristoylation"
FT Modified-site 20..25 /note= "N-myristoylation"
FT Protein 29..209 /label= Mature_protein
FT Domain 60..140 /note= "fibroblast growth factor domain"
FT Modified-site 67..72 /note= "N-myristoylation"
FT Modified-site 95..100 /note= "N-myristoylation"
FT Modified-site 98..100 /note= "protein kinase C predicted phosphorylation site"
FT Modified-site 108..113 /note= "N-myristoylation"
FT Modified-site 122..125 /note= "predicted casein kinase II phosphorylation site"
FT Modified-site 122..124 /note= "protein kinase C predicted phosphorylation site"
XX WO200138357-A2.
PD 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US032181.
PF
XX
XX

CC represent amino acid sequences of some members of the FGF family

XX Sequence 209 AA;
SQ
Query Match 100.0%; Score 1113; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGQVRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGQVRQRYLYTDDAQOTEAH 60
QY 61 LEIREDTGVGAADQSPESLLQKALKPGVIOILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
DB 61 LEIREDTGVGAADQSPESLLQKALKPGVIOILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhrdPAPRGPARFLPLFGLPPALPEPFGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhrdPAPRGPARFLPLFGLPPALPEPFGI 180
QY 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 2

AAU79289 standard; protein; 209 AA.
AC AAB68417;
XX

DT 23-JUL-2001 (first entry)

DE Amino acid sequence of human fibroblast growth factor-21 (FGF-21).

XX Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation;
KW hepatic cell; cirrhosis; infertility; impotence; testicular cancer;
KW leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.

XX Homo sapiens.

XX WO200136640-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031745.

XX 18-NOV-1999; 99US-0166540P.

PR 11-MAY-2000; 2000US-0203633P.

XX (CHIR) CHIRON CORP.

PA (KYOU) UNIV KYOTO.

XX Itoh N, Kavanaugh WM;

XX WPI; 2001-343823/36.

DR N-PSDB; AAF85329.

XX New nucleic acid molecule useful for treating disease, e.g. infertility,
PT impotence, or testicular cancer.

XX Claim 14; Fig 5A-B; 61pp; English.

XX The present sequence represents a human fibroblast growth factor-21 (FGF-
CC 21). FGF proteins regulate growth and differentiation of a variety of
CC cell types. FGF-21 nucleic acids and polypeptides are useful for treating
CC diseases and disorders characterised by inadequate numbers of hepatic
CC cells, preferably cirrhosis of the liver. They may also be used in the
CC treatment of infertility, impotence, and testicular cancer, as well as
CC leukemia, lymphoma, autoimmune disease, or proliferative disorders of the
CC thymus

XX Sequence 209 AA;

Query Match 100.0%; Score 1113; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGQVRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGQVRQRYLYTDDAQOTEAH 60
QY 61 LEIREDTGVGAADQSPESLLQKALKPGVIOILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
DB 61 LEIREDTGVGAADQSPESLLQKALKPGVIOILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120
QY 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhrdPAPRGPARFLPLFGLPPALPEPFGI 180
DB 121 CSFRELLEDGYNVYQSEAHGLPLHLPGNKSPhrdPAPRGPARFLPLFGLPPALPEPFGI 180
QY 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209
DB 181 LAPQPPDVGSSDPLSMVGPSQGRSPSYAS 209

RESULT 3

AAU79289 standard; protein; 209 AA.
ID AAU79289 standard; protein; 209 AA.

XX AC AAU79289;

XX DT 13-AUG-2002 (first entry)

XX DE Human FGF-related protein.

XX Human; injury; burn; thrombosis; arteriosclerosis; pancreopathy;
KW hepatopathy; FGF-related protein.

XX Homo sapiens.

XX JP2002112772-A.

XX 16-APR-2002.

XX 04-SEP-2000; 2000JP-00271516.

XX 10-JUL-2000; 2000JP-00213385.

PR 03-AUG-2000; 2000JP-00240398.

XX (TAKE) TAKEDA CHEM IND LTD.

XX WPI; 2002-448752/48.

DR N-PSDB; ABK52425.

XX A protein and a partial peptide of the protein useful for treating
PT injuries, burns, thrombosis, arteriosclerosis, hepatopathy, pancreopathy,
PT and diabetes.

XX Claim 8; Fig 2; 44pp; Japanese.

XX The invention relates to a protein and the polynucleotide encoding it,
CC useful as drugs for injuries, burns, thrombosis, arteriosclerosis,
CC hepatopathy, pancreopathy and diabetes. This sequence represents a human
CC FGF-related protein of the invention

XX Sequence 209 AA;

Query Match 100.0%; Score 1113; DB 5; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.3e-92;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGQVRQRYLYTDDAQOTEAH 60
DB 1 MDSDETFEHSGLWVSVLAGLLGACQAHPIPDSSPLLFQGGQVRQRYLYTDDAQOTEAH 60
QY 61 LEIREDTGVGAADQSPESLLQKALKPGVIOILGVKTSRFLCQRPDGCALYGSLLHFDPEA 120

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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:50:07 ; Search time 125.4 Seconds

(without alignments)
470.913 Million cell updates/sec

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Perfect score: 1113
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	209	4	AAG65667 Human fib
2	1113	100.0	209	4	AAB68417 Amino aci
3	1113	100.0	209	5	Aau79289 Human FGF
4	1113	100.0	209	5	Aae18826 Human FGF
5	1106	99.4	209	4	AAB82351 Human JAF
6	1106	99.4	209	4	Aau00957 Human Fib
7	1106	99.4	209	4	AAB83951 Amino aci
8	1098.5	98.7	208	4	Aae05078 Human fib
9	1098.5	98.7	208	5	AAB83630 Human PRO
10	1098.5	98.7	208	5	ABG32358 Human fib
11	1098.5	98.7	208	5	Aae17601 Human ext
12	1098.5	98.7	208	6	Abu80777 Human PRO
13	1098.5	98.7	208	6	ABO33743 Novel hum
14	1098.5	98.7	208	6	Abu82086 Novel hum
15	1098.5	98.7	208	6	ABP96156 Human fib
16	1098.5	98.7	208	6	ABJ72266 Human PRO
17	1098.5	98.7	208	6	ABJ72394 Human PRO
18	1098.5	98.7	208	6	ABO34289 Human sec
19	1098.5	98.7	208	7	AD327038 Human fib
20	1098.5	98.7	208	7	ABJ72096 Human mem
21	1098.5	98.7	208	7	ADB83568 Novel hum
22	1098.5	98.7	208	7	ADB80674 Novel hum
23	1098.5	98.7	208	7	ADB73215 Novel hum
24	1098.5	98.7	208	7	ADB78297 Novel hum
25	1098.5	98.7	208	7	ADB84945 Human PRO

ALIGNMENTS

RESULT 1

AAG65667
ID AAG65667 standard; protein; 209 AA.

XX AAG65667;

XX 07-JAN-2002 (first entry)

XX Human fibroblast growth factor (FGF)-21.

XX Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
KW fat deposition; vulnery; antiulcer; dermatological; anorectic;
KW antidiabetic; antiinflammatory; cytostatic; hepatic; virucide;
KW neuroprotectant; pulmonary; gene therapy; vaccine; human.

XX Homo sapiens.

XX WO200172957-A2.

XX 04-OCT-2001.

XX 02-APR-2001; 2001WO-IB000664.

XX 31-MAR-2000; 2000US-00540118.

XX (ITOH/) ITOH N.

XX Itoh N;

XX WPI; 2001-611623/70.

XX New human nucleic acid encoding fibroblast growth factor-like peptide,
PT useful for treatment and diagnosis of e.g. wounds and inflammatory bowel
PT disease.

XX Disclosure; Fig 3; 172pp; English.

XX The invention provides human nucleic acids encoding fibroblast growth
CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
CC standard recombinant methodology and are mitogenic for a wide range of
CC cells, inducing differentiation and proliferation, and inhibiting
CC deposition of fat. The FGF-like polypeptides, polynucleotides and
CC specific antibodies and modulators are useful for treating a very wide
CC range of diseases and conditions, e.g. wounds, ulcers, skin aging,
CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
CC the eye, etc., also for maintaining organs before transplant and
CC supporting culture of primary cells and tissues. Sequences AAG65647-67

Adb78051 Novel hum
Adb78117 Human PRO
Adb84699 Human PRO
Adb83814 Novel hum
Adb72969 Novel hum
Adb36807 Human PRO
Adb21797 Human PRO
Adb49828 Novel hum
Adb49027 Novel hum
Adb49544 Novel hum
Adb47405 Novel hum
Adb47150 Novel hum
Adb78025 Novel hum
Adb06260 Novel hum
Adb77779 Novel hum
Add50742 Novel hum
Add50988 Novel hum
Add50469 Human PRO
Add50223 Human PRO
Add51234 Novel hum

26 1098.5 98.7 208 7 ADB78051
27 1098.5 98.7 208 7 ADB78117
28 1098.5 98.7 208 7 ADB84699
29 1098.5 98.7 208 7 ADB83814
30 1098.5 98.7 208 7 ADB72969
31 1098.5 98.7 208 7 ADB36807
32 1098.5 98.7 208 7 ADB21797
33 1098.5 98.7 208 7 ADB49828
34 1098.5 98.7 208 7 ADB49027
35 1098.5 98.7 208 7 ADB49544
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41 1098.5 98.7 208 7 ADD50742
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44 1098.5 98.7 208 7 ADD50223
45 1098.5 98.7 208 7 ADD51234

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
OM protein - protein search, using sw model
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(without alignments)
288.145 Million cell updates/sec
Title: US-10-060-765-7
Perfect score: 86
Sequence: 1 RQRYLYTDDAQTEAH 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 389414 seqs, 51625971 residues
Total number of hits satisfying chosen parameters: 389414
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /cgn2_6/prodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/2/iaa/6C COMB.pep:*
6: /cgn2_6/prodata/2/iaa/6D COMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	85	4	US-09-621-976-5213
2	86	100.0	181	4	US-09-390-207-5
3	86	100.0	209	4	US-09-390-207-2
4	75	87.2	181	4	US-09-390-207-6
5	75	87.2	210	4	US-09-390-207-4
6	48	55.8	479	4	US-09-489-039A-14225
7	42	48.8	137	4	US-09-107-532A-4355
8	41	47.7	1121	4	US-09-171-461-28
9	40	46.5	152	4	US-09-252-991A-28391
10	40	46.5	366	4	US-09-489-039A-10181
11	39	45.3	735	4	US-09-147-236-7
12	39	45.3	735	4	US-09-522-474-7
13	38	44.2	136	4	US-09-621-976-4224
14	38	44.2	164	4	US-09-634-238-396
15	38	44.2	285	4	US-09-489-039A-14221
16	38	44.2	526	4	US-09-489-039A-10731
17	38	44.2	557	4	US-09-134-001C-5569
18	38	44.2	747	3	US-08-089-397A-16
19	38	44.2	776	1	US-07-603-133B-17
20	38	44.2	776	1	US-07-603-133B-20
21	38	44.2	776	3	US-08-089-397A-15
22	38	44.2	2396	1	US-08-157-005-2
23	38	44.2	2396	3	US-08-747-863-2
24	38	44.2	2396	4	US-09-565-864-2
25	37	43.0	310	4	US-09-252-991A-31483
26	37	43.0	317	4	US-09-134-001C-3993
27	37	43.0	318	4	US-09-540-236-2086

Sequence 5213, Ap
Sequence 5, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 14225, A
Sequence 4355, Ap
Sequence 28, Appl
Sequence 28391, A
Sequence 10181, A
Sequence 7, Appli
Sequence 4224, Ap
Sequence 396, App
Sequence 14221, A
Sequence 10731, A
Sequence 5569, Ap
Sequence 16, Appl
Sequence 17, Appl
Sequence 20, Appl
Sequence 15, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 31483, A
Sequence 3993, Ap
Sequence 2086, Ap

Sequence 5499, Ap
Sequence 28, Appl
Sequence 29728, A
Sequence 6926, Ap
Sequence 3, Appli
Sequence 2, Appli
Sequence 12, Appl
Sequence 21514, A
Sequence 3716, Ap
Sequence 288, App
Sequence 4500, Ap
Sequence 4626, Ap
Sequence 8159, Ap
Sequence 3429, Ap
Sequence 13575, A

37 43.0 338 4 US-09-543-681A-5499
37 43.0 377 3 US-09-352-990-28
37 43.0 400 4 US-09-252-991A-29728
37 43.0 497 4 US-09-543-681A-5926
37 43.0 547 1 US-08-785-048-3
37 43.0 547 2 US-08-996-799-3
37 43.0 553 1 US-08-785-048-2
37 43.0 553 2 US-08-996-799-2
37 43.0 635 4 US-09-252-991A-21514
37 43.0 775 1 US-07-603-133B-12
37 43.0 775 4 US-09-134-001C-3716
36.5 42.4 789 4 US-09-198-452A-288
40 36 41.9 82 4 US-09-134-001C-4500
41 36 41.9 249 4 US-09-328-352-4626
42 36 41.9 308 4 US-09-134-000C-4652
43 36 41.9 347 4 US-09-543-681A-8159
44 36 41.9 383 4 US-09-134-001C-3429
45 36 41.9 508 4 US-09-489-039A-13575

ALIGNMENTS

RESULT 1
US-09-621-976-5213
; Sequence 5213, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5213
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -28...-1
; NAME/KEY: UNSURE
; LOCATION: 57
; OTHER INFORMATION: Xaa = Ala,Pro
; NAME/KEY: UNSURE
; LOCATION: 52
; OTHER INFORMATION: Xaa = Leu,Val
US-09-621-976-5213

Query Match 100.0%; Score 86; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEAH 16
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Db 45 RQRYLYTDDAQTEAH 60

RESULT 2
US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match      100.0%; Score 86; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 17 RQRYLYTDDAQOQTEAH 32
   |||||

RESULT 3
US-09-390-207-2
; Sequence 6, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2

Query Match      100.0%; Score 86; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 45 RQRYLYTDDAQOQTEAH 60
   |||||

RESULT 4
US-09-390-207-6
; Sequence 6, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-6

Query Match      87.2%; Score 75; DB 4; Length 181;
Best Local Similarity 87.5%; Pred. No. 2.3e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 17 RQRYLYTDDAQOQTEAH 32
   |||||

RESULT 5
US-09-390-207-4
; Sequence 4, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-390-207-4

Query Match      87.2%; Score 75; DB 4; Length 210;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 46 RQRYLYTDDAQOQTEAH 61
   |||||

RESULT 6
US-09-489-039A-14225
; Sequence 14225, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14225
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14225

Query Match      55.8%; Score 48; DB 4; Length 479;
Best Local Similarity 62.5%; Pred. No. 2.5;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
   |||||
Db 460 RQRYHPGDROQPQAH 475
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RESULT 7
US-09-107-532A-4355
; Sequence 4355, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
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MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4355:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...137
SEQUENCE DESCRIPTION: SEQ ID NO: 4355:
US-09-107-532A-4355

Query Match 48.8%; Score 42; DB 4; Length 137;
Best Local Similarity 54.5%; Pred. No. 6.9;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 0;

QY 4 YLYTDDAQOTE 14
DB 108 YIYTDSEDETE 118

RESULT 8
US-09-171-461-28
; Sequence 28, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chiocca, Susanna
; APPLICANT: Kurzbauer, Robert
; APPLICANT: Schaffner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171,461
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; EARLIER FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 1121
; TYPE: PRT
; ORGANISM: CELO VIRUS
; FEATURE:
; OTHER INFORMATION: Position: 6501...9866/Product: E2b pol
US-09-171-461-28

Query Match 47.7%; Score 41; DB 4; Length 1121;
Best Local Similarity 50.0%; Pred. No. 99;
Matches 7; Conservative 3; Mismatches 4; Indels 4; Gaps 0;

QY 1 RQRYLYTDDAQOTE 14
DB 731 RQQFRYADDPQEE 744

RESULT 9
US-09-252-991A-28391
; Sequence 28391, Application US/09252991A
; Patent No. 6851795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28391
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28391

Query Match 46.5%; Score 40; DB 4; Length 152;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 YTDDAQOTEAH 16
DB 129 WEDDAPQTESH 139

RESULT 10
US-09-489-039A-10181
; Sequence 10181, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10181
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10181

Query Match 46.5%; Score 40; DB 4; Length 366;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOTEAH 16
DB 83 RYIYTDNQKKNWH 96

RESULT 11
US-09-147-236-7
; Sequence 7, Application US/09147236A
; Patent No. 6316251
; GENERAL INFORMATION:
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: YOSHINAGA, Fumihiko

; APPLICANT: TAHARA, Naoki
; APPLICANT: HAYASHI, Takahisa
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-OPCT
; CURRENT APPLICATION NUMBER: US/09/147,236A
; CURRENT FILING DATE: 1999-04-08
; EARLIER APPLICATION NUMBER: PCT/JP97/03633
; EARLIER FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; OTHER INFORMATION: c
US-09-147-236-7

Query Match 45.3%; Score 39; DB 4; Length 735;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TDDAQOTEAH 16
|||:|||||
Db 718 TDDSQQTWH 727

RESULT 12
US-09-522-474-7
; Sequence 7, Application US/09522474
; Patent No. 6573076
; GENERAL INFORMATION:
; APPLICANT: TONOUCHI, Naoto
; APPLICANT: TSUCHIDA, Takayasu
; APPLICANT: YOSHINAGA, Fumihiko
; APPLICANT: TAHARA, Naoki
; APPLICANT: HAYASHI, Takahisa
; TITLE OF INVENTION: NOVEL GENE, GROUP OF GENES, AND NOVEL BETA-GLUCOSIDASE
; FILE REFERENCE: 6537-011-OPCT
; CURRENT APPLICATION NUMBER: US/09/522,474
; CURRENT FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US/09/147,236
; PRIOR FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/JP97/03633
; PRIOR FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Acetobacter xylinum
; FEATURE:
; OTHER INFORMATION: n at positions 15741 and 15767 may be a, g, t, or
; OTHER INFORMATION: c
US-09-522-474-7

Query Match 45.3%; Score 39; DB 4; Length 735;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TDDAQOTEAH 16
|||:|||||
Db 718 TDDSQQTWH 727

RESULT 13
US-09-621-976-4224
; Sequence 4224, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4224
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -41...-1
US-09-621-976-4224

Query Match 44.2%; Score 38; DB 4; Length 136;
Best Local Similarity 53.8%; Pred. No. 33;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQOTE 14
:|||||:|||||
Db 11 BEVLYLDFSHQTE 23

RESULT 14
US-09-634-238-396
; Sequence 396, Application US/09634238
; Patent No. 6544772
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Havukkala, Ilkka J.
; APPLICANT: Blosberg, Leonard, N.
; APPLICANT: Lubbers, Mark W.
; APPLICANT: Dekker, James
; APPLICANT: Christensson, Anna C.
; APPLICANT: Holland, Ross
; APPLICANT: O'Toole, Paul W.
; APPLICANT: Reid, Julian R.
; APPLICANT: Coolbear, Timothy
; TITLE OF INVENTION: Polynucleotides, materials incorporating
; TITLE OF INVENTION: them and methods for using them.
; FILE REFERENCE: 11000.1043U1
; CURRENT APPLICATION NUMBER: US/09/634,238
; CURRENT FILING DATE: 2000-08-08
; NUMBER OF SEQ ID NOS: 422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(164)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-634-238-396

Query Match 44.2%; Score 38; DB 4; Length 164;
Best Local Similarity 46.2%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 XLYTDDAQOTEAH 16
:|||||:|
Db 23 FLYTDEANVRFFH 35

RESULT 15
US-09-489-039A-14221
; Sequence 14221, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

```

/ / TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ /
/ / FILE REFERENCE: 2709.2004001
/ /
/ / CURRENT APPLICATION NUMBER: US/09/489,039A
/ /
/ / PRIORITY FILING DATE: 2000-01-27
/ /
/ / PRIOR APPLICATION NUMBER: US 60/117,747
/ /
/ / PRIOR FILING DATE: 1999-01-29
/ /
/ / NUMBER OF SEQ ID NOS: 14342
/ /
/ / SEQ ID NO 14221
/ /
/ / LENGTH: 285
/ /
/ / TYPE: PRT
/ /
/ / ORGANISM: Klebsiella pneumoniae
/ /
/ / US-09-489-039A-14221

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Query Match	44.2%	Score 38;	DB 4;	Length 285;
Best Local Similarity	46.2%	Pred. NO. 73;		
Matches 6;	Conservative	3;	Mismatches 4;	Indels 0;
				Gaps 0;

Qy 4 YLYTDDAQQTEAH 16
|:|:|:|:|
Db 204 YVYSDNAOHVAMH 216

RESULT 16
US-09-489-039A-10731
; Sequence 10731, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:

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/ GENERED INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27
/ PRIOR APPLICATION NUMBER: US 60/117,747
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 14342
/ SEQ ID NO 10731
/ LENGTH: 526
/ TYPE: PRT
/ ORGANISM: Klebsiella pneumoniae
/ US-09-489-039A-10731

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Query Match	44.2%	Score 38;	DB 4;	Length 526;
Best Local Similarity	54.5%	Pred. No. 1.4e+02;		
Matches	6:	Conservative	2:	Mismatches 3;
				Indels 0;
				Gaps 0;

QY 6 YTDDAQQTEAH 16
330 YAEFGGCCCCAH 340

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RESULT 17
US-09-134-001C-5569
, Sequence 5569, Application US/09134001C
, Patent No. 6380370
, GENERAL INFORMATION:
, APPLICANT: Lynn Doucette-Stamm et al
, TITLE OF INVENTION: NUCLEIC ACID AND AMINO
, TITLE OF INVENTION: EPIDERMIDIS FOR DIAGN
, FILE REFERENCE: GTC-007
, CURRENT APPLICATION NUMBER: US/09/134,001C
, PRIOR FILING DATE: 1998-08-13
, PRIOR APPLICATION NUMBER: US 60/064,964
, PRIOR FILING DATE: 1997-11-08
, PRIOR APPLICATION NUMBER: US 60/055,779
, PRIOR FILING DATE: 1997-08-14
, NUMBER OF SEQ ID NOS: 5674
, SEQ ID NO 5569
, LENGTH: 557
, TYPE: PRT
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5569

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Query Match 44.2%; Score 38; DB 4; Length 557;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 3; Mismatches 1; Indels

Qy	7	TDDAQQTEAH	16
		: : :	
D _b	522	TDDTEKTKAH	531

RESULT 18
US-08-089-397A-16
? Sequence 16, Application US/08089397A
? Patent No. 608680
? GENERAL INFORMATION:
? APPLICANT: SABARA, MARTA I.J.
? APPLICANT: FRENCHICK, PATRICK J.
? APPLICANT: POTTER, ANDREW A.
? APPLICANT: IJAZ, MOHAMMAD K.
? APPLICANT: GILCHRIST, JAMES E.
? APPLICANT: REDMOND, MARK J.
? TITLE OF INVENTION: ROTAVIRUS VACCINES
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: MORRISON & FOERSTER
? STREET: 2000 Pennsylvania Avenue, NW
? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20006-1888
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Ver
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/089.397A
? FILING DATE: 07-JUL-1993
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: ADLER, REID G.
? REGISTRATION NUMBER: 30,988
? REFERENCE/DOCKET NUMBER: 29311-20003
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 887-1500
? TELEFAX: (202) 887-0763
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 747 amino acids
? TYPE: amino acid
? STRANDEDNESS: unknown
? TOPOLOGY: unknown
? MOLECULE TYPE: protein
? US-08-089-397A-16

Query Match 44.2%; Score 38; DB 3; Length 747;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6: Conservative 3; Mismatches 5; Indels

QY 3 RYLYTDDAQQTEAH 16
: | | | : : | |
Db 299 OYTYTRDGEFEVTAH 312

RESULT 19
US-07-603-133B-17
; Sequence 17, Application US/07603133B
; Patent No. 5298244
; GENERAL INFORMATION:
; APPLICANT: Redmond, Mark J.
; APPLICANT: Ijaz, Mohammed K.
; APPLICANT: Parker, Michael D.
; TITLE OF INVENTION: ASSEMBLED VIR.
; TITLE OF INVENTION: USE IN A VACC

```
;
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/603,133B
; FILING DATE: 19901025
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9313-0004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-7250
; TELEFAX: (415) 327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-07-603-133B-17

Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RYLTYDDAQTEAH 16
Db 302 QYTYRDGEVTAH 315

RESULT 20
US-07-603-133B-20
; Sequence 20, Application US/07603133B
; Patent No. 5296244
; GENERAL INFORMATION:
; APPLICANT: Redmond, Mark J.
; APPLICANT: Ijaz, Mohammed K.
; APPLICANT: Parker, Michael D.
; TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
; TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/603,133B
; FILING DATE: 19901025
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
```

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;
; REFERENCE/DOCKET NUMBER: 9313-0004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-7250
; TELEFAX: (415) 327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-603-133B-20

Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RYLTYDDAQTEAH 16
Db 302 QYTYRDGEVTAH 315

RESULT 21
US-08-089-397A-15
; Sequence 15, Application US/08089397A
; Patent No. 6086880
; GENERAL INFORMATION:
; APPLICANT: SABARA, MARTA I.J.
; APPLICANT: FRENCHICK, PATRICK J.
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: IJAZ, MOHAMMAD K.
; APPLICANT: GILCHRIST, JAMES B.
; APPLICANT: REDMOND, MARK J.
; TITLE OF INVENTION: ROTAVIRUS VACCINES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089,397A
; FILING DATE: 07-JUL-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: ADLER, REID G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 29311-20003.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-089-397A-15

Query Match 44.2%; Score 38; DB 3; Length 776;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 3 RYLTYDDAQTEAH 16
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us-10-060-765-7.rai

Wed Mar 3 08:19:48 2004

Db 302 QYTYRDGEVTAH 315

RESULT 22
US-08-157-005-2
; Sequence 2, Application US/08157005
; Patent No. 5620691
; GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
; APPLICANT: Terpstra, Catharinus
; APPLICANT: Pol, Johannes M
; APPLICANT: Moorman, Robertus J
; APPLICANT: Meulenbergh, Johanna J
; TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,005
; FILING DATE: 26-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91201398.4
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92200781.0
; FILING DATE: 18-MAR-1992
; APPLICATION DATA:
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, Thomas F
; REGISTRATION NUMBER: 16,579
; REFERENCE/DOCKET NUMBER: 44819
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 315-1931
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-157-005-2

Query Match 44.2%; Score 38; DB 1; Length 2396;
Best Local Similarity 54.5%; Pred. No. 7.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 YTDDAQOQTEAH 16
|||||:|:
Db 2278 YTDSRYTQDH 2288

RESULT 23
US-08-747-863-2
; Sequence 2, Application US/08747863
; Patent No. 6197310
; GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
; APPLICANT: Terpstra, Catharinus

APPLICANT: Pol, Johannes M
APPLICANT: Moorman, Robertus J
APPLICANT: Meulenbergh, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Trask, Britt & Rossea
STREET: 525 South 300 East
CITY: Salt Lake City
STATE: Utah
COUNTRY: USA
ZIP: 84111

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: WINDOWS95
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,863
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/157,005
; FILING DATE: 26-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 91201398.4
; FILING DATE: 06-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92200781.0
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NL92/00096
; FILING DATE: 05-JUN-1992

ATTORNEY/AGENT INFORMATION:
; NAME: Turner, Allen C.
; REGISTRATION NUMBER: 33041
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 532-1922
; TELEFAX: (801) 531-9168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2396 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-747-863-2

Query Match 44.2%; Score 38; DB 3; Length 2396;
Best Local Similarity 54.5%; Pred. No. 7.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 YTDDAQOQTEAH 16
|||||:|:
Db 2278 YTDSRYTQDH 2288

RESULT 24
US-09-565-864-2
; Sequence 2, Application US/09565864
; Patent No. 6455245

GENERAL INFORMATION:
; APPLICANT: Wensvoort, Gert
; APPLICANT: Terpstra, Catharinus
; APPLICANT: Pol, Johannes M
; APPLICANT: Moorman, Robertus J
; APPLICANT: Meulenbergh, Johanna J
; TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/565,864
FILING DATE: 05-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157,005
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Moran, Thomas F
REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 44819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 315-1931
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2396 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-565-864-2

Query Match 44.2%; Score 38; DB 4; Length 2396;
Best Local Similarity 54.5%; Pred. No. 7.2e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 YTDDAQOQTEAH 16
DB 2278 YTDSDRYTQDH 2288

RESULT 25
US-09-252-991A-31483
; Sequence 31483, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31483
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31483

Query Match 43.0%; Score 37; DB 4; Length 310;
Best Local Similarity 43.8%; Pred. No. 1.2e+02;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQTEAH 16
DB 294 RQNIYTGDTQNTNSN 309

RESULT 26
US-09-134-001C-3993
; Sequence 3993, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3993
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3993

Query Match 43.0%; Score 37; DB 4; Length 317;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTE 14
DB 273 RQRYLYHEDATLNE 286

RESULT 27
US-09-540-236-2086
; Sequence 2086, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2086
; LENGTH: 318
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2086

Query Match 43.0%; Score 37; DB 4; Length 318;
Best Local Similarity 53.3%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEA 15
DB 236 RERALTQTSQOTES 250

RESULT 28
US-09-543-681A-5499
; Sequence 5499, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRAB1
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2086
; LENGTH: 318
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2086

FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5499
LENGTH: 338
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-5499

Query Match 43.0%; Score 37; DB 4; Length 338;
Best Local Similarity 43.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQQTAEH 16
Db 268 REVLYTDSRKDKPYH 283

RESULT 29

US-09-352-990-28
Sequence 28, Application US/09352990
Patent No. 6255090

GENERAL INFORMATION:
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-tRNA Synthetase
FILE REFERENCE: BB-1191
CURRENT APPLICATION NUMBER: US/09/352,990
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,866
EARLIER FILING DATE: July 15, 1998
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Microsoft Office 97
SEQ ID NO 28
LENGTH: 377
TYPE: PRT
ORGANISM: Synechocystis sp.

US-09-352-990-28

Query Match 43.0%; Score 37; DB 3; Length 377;
Best Local Similarity 46.7%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQQTAEH 16
Db 272 QRLWFDDPERPECH 286

RESULT 30

US-09-252-991A-29728
Sequence 29728, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 29728
LENGTH: 400
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29728

Query Match 43.0%; Score 37; DB 4; Length 400;
Best Local Similarity 43.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 2; Indels 8; Gaps 2;

Qy 2 QRYLY---TDDAQ-----QTEAH 16
Db 295 EQLYRRAADDGQHACQPRTEAH 317

RESULT 31

US-09-543-681A-6926
Sequence 6926, Application US/09543681A
Patent No. 6605709

GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543.681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6926
LENGTH: 497
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-6926

Query Match 43.0%; Score 37; DB 4; Length 497;
Best Local Similarity 46.2%; Pred. No. 2e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQQTE 14
Db 260 QRYIVTDSIKETK 272

RESULT 32

US-08-785-048-3
Sequence 3, Application US/08785048
Patent No. 5763246

GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 5763246el tRNA Synthetase
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,048
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31355-3

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 547 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-785-048-3
;
; Query Match 43.0%; Score 37; DB 1; Length 547;
; Best Local Similarity 60.0%; Pred. No. 2.2e+02;
; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 7 TDDAQOTEAH 16
; Db 512 TDDIEKTKAH 521
;
; RESULT 33
; US-08-996-799-3
; Sequence 3, Application US/08996799
; Patent No. 5965416
; GENERAL INFORMATION:
; APPLICANT: Hodgson, John
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5965416el tRNA Synthetase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,799
; FILING DATE:
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/785,048
; FILING DATE: 17-JAN-1997
; APPLICATION NUMBER: 9601099.6
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: 9615845.6
; FILING DATE: 27-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmli, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31355-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 547 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-996-799-3
;
; Query Match 43.0%; Score 37; DB 2; Length 547;
; Best Local Similarity 60.0%; Pred. No. 2.2e+02;
; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 7 TDDAQOTEAH 16
; Db 512 TDDIEKTKAH 521
;
; RESULT 34
; US-08-785-048-2
; Sequence 2, Application US/08785048
; Patent No. 5763246
; GENERAL INFORMATION:
; APPLICANT: Hodgson, John
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5763246el tRNA Synthetase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/785,048
; FILING DATE: 17-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601099.6
; FILING DATE: 19-JAN-1996
; APPLICATION NUMBER: 9615845.6
; FILING DATE: 27-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmli, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31355-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-785-048-2
;
; Query Match 43.0%; Score 37; DB 1; Length 553;
; Best Local Similarity 60.0%; Pred. No. 2.2e+02;
; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
;
; QY 7 TDDAQOTEAH 16
; Db 518 TDDIEKTKAH 527
;
; RESULT 35
; US-08-996-799-2
; Sequence 2, Application US/08996799
; Patent No. 5965416
; GENERAL INFORMATION:
; APPLICANT: Hodgson, John
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5965416el tRNA Synthetase
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
```

ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/785,048
FILING DATE: 17-JAN-1997
APPLICATION NUMBER: 9601099.6
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: 9615845.6
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31355-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-799-2

Query Match 43.0%; Score 37; DB 2; Length 553;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TDDAQOQTEAH 16
|||:|:|
Db 518 TDDIETKAH 527

RESULT 36
US-09-252-991A-21514
; Sequence 21514, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21514
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21514

Query Match 43.0%; Score 37; DB 4; Length 635;
Best Local Similarity 43.8%; Pred. No. 2.6e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 RORVLYTDDAQOQTEAH 16
|||:|:|
Db 254 RHHHLHADDEADRPAAH 269

RESULT 37
US-07-603-133B-12
; Sequence 12, Application US/07603133B
; Patent No. 5298244
; GENERAL INFORMATION:
; APPLICANT: Redmond, Mark J.
; APPLICANT: Ijaz, Mohammed K.
; APPLICANT: Parker, Michael D.
; TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
; TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/603,133B
; FILING DATE: 19901025
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Robins, Roberta L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9313-0004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 327-7250
; TELEFAX: (415) 327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 775 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-603-133B-12

Query Match 43.0%; Score 37; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 3.2e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOQTEAH 16
|||:|:|
Db 302 QVYTRDEEVTAAH 315

RESULT 38
US-09-134-001C-3716
; Sequence 3716, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779

62 QQQYDYTDKEQQ 73

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; PRIOR FILING DATE: 1997-08-14
;
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3716
; LENGTH: 1335
; TYPE: PRF
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3716

```

Query Match 43.0%; Score 37; DB 4; Length 1335;
Best Local Similarity 43.8%; Pred. No. 5.7e+02;
Matches 7: Conservative 4; Mismatches 5; Indels

Qy 1 RQRYLYTDDAQQTEAH 16
: : : : : : :
Db 107 KQQSLSTDDANQNTN 122

```

RESULT 39
US-09-198-452A-288
; Sequence 288, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION
; APPLICANT: Grifvals, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 288
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-288

```

Query Match 42.4%; Score 36.5; DB 4; Length 789;
Best Local Similarity 42.1%; Pred. No. 3.9e+02;
Matches 8: Conservative 3; Mismatches 3; Indels

QY 3 RYLTTDAQ-----QTEAH 16
 ||||:|:
 Db 629 RYLSDEEKEEALAEETH 647

RESULT 40
US-09-134-001C-4500
; Sequence 4500, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4500
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4500

Query Match 41.9%; Score 36; DB 4; Length 82;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7: Conservative 2: Mismatches 3: Indels

QY 1 RQRYLYTDDAQQ 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:51:42 ; Search time 87.0833 Seconds
(without alignments)
757.244 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 1113
Sequence: 1 MDSDETFEHSGLWVSLAG.....SSDPLSMVGPSQGRSPSYAS 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rhodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	1106	99.4	209	4	Q8N683	Q8N683	Q8N683 homo sapien
2	803.5	72.2	208	11	Q8V180	Q8V180	Q8V180 rattus norv
3	216.5	19.5	227	13	Q8V180	Q8V180	Q8V180 rattus norv
4	206.5	18.6	218	11	Q8V181	Q8V181	Q8V181 rattus norv
5	176.5	15.9	205	13	Q8AXAL	Q8AXAL	Q8AXAL brachydanio
6	171.5	15.4	208	11	Q8R5L5	Q8R5L5	Q8R5L5 rattus norv
7	171.5	15.4	206	13	Q8VGD8	Q8VGD8	Q8VGD8 oncorhynch
8	171	15.4	245	11	Q8R5L9	Q8R5L9	Q8R5L9 rattus norv
9	170.5	15.3	195	11	Q8C399	Q8C399	Q8C399 mus musculu
10	168	15.1	196	13	Q8VH31	Q8VH31	Q8VH31 notophthalm
11	168	15.1	212	11	Q8R5L9	Q8R5L9	Q8R5L9 mus musculu
12	167.5	15.0	124	13	Q8VH31	Q8VH31	Q8VH31 ambystoma m
13	165	14.8	211	11	Q8C7A8	Q8C7A8	Q8C7A8 mus musculu
14	161	14.5	247	11	Q8R5L7	Q8R5L7	Q8R5L7 rattus norv
15	161	14.5	247	11	Q8BST0	Q8BST0	Q8BST0 mus musculu
16	160	14.4	111	13	Q90XQ1	Q90XQ1	Q90XQ1 ambystoma m

17	160	14.4	212	11	Q9EST9	Q9EST9	Q9EST9 rattus norv
18	159.5	14.3	191	13	Q9DFC9	Q9DFC9	Q9DFC9 brachydanio
19	159	14.3	237	13	Q9IAI6	Q9IAI6	Q9IAI6 gallus gall
20	157.5	14.2	208	13	Q7ZZN4	Q7ZZN4	Q7ZZN4 gallus gall
21	157.5	14.2	268	4	Q8NF90	Q8NF90	Q8NF90 homo sapien
22	155.5	14.0	245	13	Q9W6A2	Q9W6A2	Q9W6A2 gallus gall
23	155	13.9	208	6	Q95112	Q95112	Q95112 sus scrofa
24	153	13.7	208	13	Q8R4X0	Q8R4X0	Q8R4X0 xenopus lae
25	153	13.7	211	11	Q8R4X0	Q8R4X0	Q8R4X0 rattus norv
26	153	13.7	252	11	Q89096	Q89096	Q89096 mus musculu
27	152.5	13.7	245	11	Q8VCY9	Q8VCY9	Q8VCY9 mus musculu
28	151.5	13.6	207	11	Q8ERQ5	Q8ERQ5	Q8ERQ5 mus musculu
29	151	13.6	252	4	Q86YN7	Q86YN7	Q86YN7 homo sapien
30	151	13.6	253	13	Q9IAI5	Q9IAI5	Q9IAI5 gallus gall
31	150	13.5	170	4	Q8NFT9	Q8NFT9	Q8NFT9 homo sapien
32	150	13.5	208	6	Q95K97	Q95K97	Q95K97 macaca fasc
33	148.5	13.3	192	11	Q9ERW3	Q9ERW3	Q9ERW3 rattus norv
34	147.5	13.3	199	13	Q9IAI3	Q9IAI3	Q9IAI3 gallus gall
35	147.5	13.3	207	11	Q9ESL8	Q9ESL8	Q9ESL8 mus musculu
36	147	13.2	208	4	Q96P59	Q96P59	Q96P59 homo sapien
37	144.5	13.0	236	13	Q804S4	Q804S4	Q804S4 meleagris g
38	144	12.9	212	13	Q42407	Q42407	Q42407 gallus gall
39	143.5	12.9	213	6	Q9N1B9	Q9N1B9	Q9N1B9 ovis aries
40	141.5	12.7	268	5	Q816J7	Q816J7	Q816J7 clona inces
41	138	12.4	162	11	Q8VI79	Q8VI79	Q8VI79 rattus norv
42	137	12.3	186	6	Q95L47	Q95L47	Q95L47 mustela vis
43	136	12.2	154	13	Q7ZZK5	Q7ZZK5	Q7ZZK5 brachydanio
44	135	12.1	185	11	Q9ERN5	Q9ERN5	Q9ERN5 rattus norv
45	132	11.9	111	13	Q90Y71	Q90Y71	Q90Y71 xenopus lae

ALIGNMENTS

RESULT 1

Q8N683	PRELIMINARY;	PRT;	209 AA.
ID	Q8N683		
AC	Q8N683		
DT	01-OCT-2002 (TRENBLrel. 22, Created)		
DT	01-OCT-2002 (TRENBLrel. 22, Last sequence update)		
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)		
DE	Fibroblast growth factor 21.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RA	Strausberg R.;		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC018404; AAH18404.1; -		
DR	GO; GO:0008083; F: growth factor activity; IEA.		
DR	InterPro; IPR008996; Cytok_III__like.		
DR	InterPro; IPR002348; IL1_HBGF.		
DR	Pfam; PF00167; FGF; 1.		
DR	PRINTS; PR00262; IL1HBGF.		
DR	ProDom; PD000831; IL1_HBGF; 1.		
DR	SMART; SM00442; FGF; 1.		
SQ	SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;		

Query Match	99.4%;	Score 1106;	DB 4;	Length 209;
Best Local Similarity	99.5%;	Pred. No. 8.2e-94;		
Matches	208;	Conservative	1;	Indels 0; Gaps 0;
QY	1	MDSDETFEHSGLWVSLAGLLGACQAHPTDSSPLAQFGGVQRVLYTTDAQTEAH	60	
DB	1	MDSDETFEHSGLWVSLAGLLGACQAHPTDSSPLAQFGGVQRVLYTTDAQTEAH	60	
QY	61	LEIREDTGVGGADQSPESLLQKALKPGVIGILGVKTSRFLCQRPDGCALYSLHFDPEA	120	
DB	61	LEIREDTGVGGADQSPESLLQKALKPGVIGILGVKTSRFLCQRPDGCALYSLHFDPEA	120	

QY	121	CSFRELLEDGNYVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI	180
Db	121	CSFRELLEDGNYVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGI	180
QY	181	LAPQPPDVGSDDPLSMVGPQGRSPSYAS	209
Db	181	LAPQPPDVGSDDPLSMVGPQGRSPSYAS	209
RESULT 2			
QY	Q8VI80	PRELIMINARY;	PRT; 208 AA.
AC	Q8VI80;		
DT	01-MAR-2002	(TREMELrel. 20, Created)	
DT	01-MAR-2002	(TREMELrel. 20, Last sequence update)	
DT	01-OCT-2003	(TREMELrel. 25, Last annotation update)	
DE	Fibroblast growth factor 21.		
GN	FGF21.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	"Rattus norvegicus FGF21.";		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AB078901; BAB84299.1; -.		
DR	GO; GO:0008083; F: growth factor activity; IEA.		
DR	InterPro; IPR008996; Cytok IL1_like.		
DR	InterPro; IPR002348; IL1_HBGF.		
DR	Pfam; PF00167; FGF; 1.		
DR	PRINTS; PR00262; IL1HBGF.		
DR	ProDom; PD000831; IL1_HBGF; 1.		
DR	SMART; SM00442; FGF; 1.		
DR	PROSITE; PS00247; HBGF_FGF; 1.		
SQ	SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;		
Query Match 72.2%; Score 803.5; DB 11; Length 208;			
Best Local Similarity 78.9%; Pred. No. 5.6e-66;			
Matches 157; Conservative 12; Mismatches 27; Indels 3; Gaps 2;			
QY	12	GLWVSVLACL-LLGACQAHPIPDSPFLQFGQVQRVLYTDDAQTEAHLEIREDTVG	70
Db	12	GLWVCLLPVLLGVCEAYPISDSPFLQFGQVQRVLYTDQQTEAHLEIREDTGV	71
QY	71	GAADQSPESLLOLKALPGVIOILGVKTSRFLCORPDGALYGLSHFDPEACSFRELLLED	130
Db	72	GTAFHSPESLLELKALPGVIOILGVKASRFLCQQPDGTLGSPHFDPEACSFRELLLED	131
QY	131	GYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGIAPQPPDVGS	190
Db	132	GYNVYQSEAHGLPLHLPGNKSHPDRDPAPRGPARFLPLGLPALPEPPGIAPQPPDVGS	189
QY	191	SDPLSMVGPQGRSPSYAS	209
Db	190	SDPLSMVGPQGRSPSYAS	208
RESULT 3			
QY	Q9DDN0	PRELIMINARY;	PRT; 227 AA.
AC	Q9DDN0;		
DT	01-MAR-2001	(TREMELrel. 16, Created)	
DT	01-MAR-2001	(TREMELrel. 16, Last sequence update)	
DT	01-OCT-2003	(TREMELrel. 25, Last annotation update)	
DE	Fibroblast growth factor 19.		
GN	FGF-19.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
RN	[1]		
Query Match 18.6%; Score 206.5; DB 11; Length 218;			
Best Local Similarity 30.7%; Pred. No. 5.2e-11;			
Matches 62; Conservative 37; Mismatches 92; Indels 11; Gaps 7;			
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20564778; PubMed=11110663;		
RA	Ladher R.K., Anakwe K.U., Gurney A.L., Schoenwolf G.C.,		
RA	Francis-West P.H.;		
RT	"Identification of Synergistic Signals Initiating Inner Ear		
RT	Development.";		
RL	Science 290:1965-1968(2000).		
DR	EMBL; AF315355; AAG39478.1; -.		
DR	HSSP; P09038; 1BFG.		
DR	GO; GO:0008083; F: growth factor activity; IEA.		
DR	InterPro; IPR008996; Cytok IL1_like.		
DR	InterPro; IPR002348; IL1_HBGF.		
DR	Pfam; PF00167; FGF; 1.		
DR	PRINTS; PR00262; IL1HBGF.		
DR	ProDom; PD000831; IL1_HBGF; 1.		
DR	SMART; SM00442; FGF; 1.		
DR	PROSITE; PS00247; HBGF_FGF; 1.		
SQ	SEQUENCE 227 AA; 24568 MW; 875D76FBFD09F8E2 CRC64;		
Query Match 19.5%; Score 216.5; DB 13; Length 227;			
Best Local Similarity 30.9%; Pred. No. 6.6e-12;			
Matches 67; Conservative 33; Mismatches 84; Indels 33; Gaps 10;			
QY	18	LAGLLGACQAH--PIPD--SPFLQFG--GQ--VRORYLYTDDAQ--TEAHLEIREDTVG	70
Db	15	LLGIATAAAAAARSLEPLPDVGGFHVNYGWGEPIRLHLHLRFGKGLFSCFLRIGDGRVD	74
QY	71	GAADQSPESLLOLKALPGVIOILGVKTSRFLCORPDGALYGLSHFDPEACSFRELLLED	130
Db	75	AVGQSQSPQSLLLEIRAVAVRTVAIKGVQSSRYLCLWDEAGRLHGLSYSDCSFEEIRPD	134
QY	131	GYNVYQSEAHGLPLHLPGNKSHP---RDPAPRGPARFLPLGLPPA-----	173
Db	135	GYNVYKSKYGISVSLSSAKQOQFGKDKFLPL--SHELPMINTVPVEVTFDGEYDYSQ	192
QY	174	--LPEPPGILAPQPPDVGSDDPLSMVGP--SQGRSPSY	207
Db	193	AFEPE---VYSSPLETSDMDPFGITSKLSPVKSPSF	225
RESULT 4			
QY	Q8VI81	PRELIMINARY;	PRT; 218 AA.
AC	Q8VI81;		
DT	01-MAR-2002	(TREMELrel. 20, Created)	
DT	01-MAR-2002	(TREMELrel. 20, Last sequence update)	
DT	01-OCT-2003	(TREMELrel. 25, Last annotation update)	
DE	Fibroblast growth factor 15.		
GN	FGF15.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Itoh N.;		
RT	"Rattus norvegicus FGF15.";		
RL	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; AB078900; BAB84298.1; -.		
DR	GO; GO:0008083; F: growth factor activity; IEA.		
DR	InterPro; IPR008996; Cytok IL1_like.		
DR	InterPro; IPR002348; IL1_HBGF.		
DR	Pfam; PF00167; FGF; 1.		
DR	PRINTS; PR00262; IL1HBGF.		
DR	ProDom; PD000831; IL1_HBGF; 1.		
DR	SMART; SM00442; FGF; 1.		
DR	PROSITE; PS00247; HBGF_FGF; 1.		
SQ	SEQUENCE 218 AA; 25207 MW; ED989684B5307C58 CRC64;		
Query Match 18.6%; Score 206.5; DB 11; Length 218;			
Best Local Similarity 30.7%; Pred. No. 5.2e-11;			
Matches 62; Conservative 37; Mismatches 92; Indels 11; Gaps 7;			

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13 LWVSVLAGLLIGACQAHPIDSSPLQFG--GVV-RORYLYTDDAQOQTEAHLBIREDGVVG 70
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
19 LWLAVSGRPLVQ--QSQSVSDGFLYLGWKGKTRLLQYLSAGPYVSNCFIRISDGSVD 76
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
71 GAADQSPESLLQLKALKPGVITLIIGVYTSRFLCORPDGALYGLSLHFDPEACSFRELLLED 130
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
77 CEEDQNERNLLEFRAVALKTKTATKQDSSVRYLCMSADGKIYGLIRYSESDCTFREEMDCL 136
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
131 GYNYVQSEAHGLHLHPGNKS--PHRDPAPRGPARFLPL--PGLPPALPPPPGILAPQPPD 187
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
137 GYNQYRSWKH--HLHIIIFIKAKEREQLQGKPFNFPIPHRSFFSTDQLRSKMFLSPLPE 194
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
188 VGSDDPLSMVGPQSQ--RSPSY 207
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
195 SDSMDPFRMVEDVDHLVKSPSF 216
   ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 5
ID Q8AXA1 PRELIMINARY; PRT; 205 AA.
DB Q8AXA1;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Fibroblast growth factor 6.
GN FGF6.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1] RN
RN SEQUENCE FROM N.A.
RA Ralliere C., Rescan P.-Y.;
RT "Identification of a fgf6 gene in zebrafish.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AF516334; AAC15997.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD00831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR SEQUENCE 205 AA; 23244 MW; 2BBD1D93D6533696 CRC64;

Query Match 15.9%; Score 176.5; DB 13; Length 205;
Best Local Similarity 28.4%; Pred. No. 2.8e-08;
Matches 56; Conservative 26; Mismatches 70; Indels 45; Gaps 7

QY 9 EHSGLW---VSVLAGLLIGACQAHPIDP----- 33
DB 13 ESSGRWTTAVVLLGLFLIGISYPTSDRTNATSLKRWKLFKRSVLGIVSEKSLDANW 72
QY 34 SSFLQFGQVRQRYLYTDDAQOQTEAHLBIREDGVGGAADQSPESLLQLKALKPGVIOI 93
DB 73 SDYLL---GIKVRRLYCNVG--IGFHLQVLPDGRINGVHNEQYLSLIEISAVERGVSIL 127
QY 94 LGVKTSRFLCORPDGALYGLSLHFDPEACSFRELLLEDGYNYVQSEAH-GIPLHLPGN--- 149
DB 128 YGVKSLGLFVAMSSRGRLYGTRAFRDE-CKFKETLLPNNTYAYESSIYKGFYMAKLSKHGRL 166
QY 150 K3PHRDPAPRGPARFLP 166
DB 187 KRGHRSAPMTVTTHFLP 203

RESULT 6
Q8R5L5 PRELIMINARY; PRT; 208 AA.
ID Q8R5L5

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AC	Q9R5L5;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Fibroblast growth factor.
DE	FGF6.
GN	Rattus norvegicus (Rat).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=101116;
RP	[1]
RN	SEQUENCE FROM N.A.
RA	Itoh N.;
RT	"Rattus norvegicus FGF6 mRNA.";
RL	Submitted (FEb-2002) to the EMBL/GenBank/DBDJ databases.
DR	EMBL; AB079674; BAB84704.1; -.
DR	GO; GO:0008083; F:growth factor activity; IEA.
DR	InterPro; IPR001064; Crystallin.
DR	InterPro; IPR008996; Cytok IL1_like.
DR	InterPro; IPR002348; IL1_HBGF.
DR	Pfam; PF00167; FGF; 1.
DR	PRINTS; PR00262; IL1HBGF.
DR	PRODom; PD000831; IL1_HBGF; 1.
DR	SMART; SMO0442; FGF; 1.
DR	PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR	PROSITE; PS00247; HBGF_FGF; 1.
SQ	SEQUENCE 208 AA; 22789 MW; 4BEAA0301BB78986 CRC64;
Query Match 15.4%; Score 171.5; DB 11; Length 208;	
Best Local Similarity 36.4%; Pred.No.8.2e-08;	
Matches 36; Conservative 21; Mismatches 39; Indels 3; Gaps 2	
QY	42 GQVRQRXYLTDDAQTEAHLEIREDGTVGGAADSPESLLQLKALKPGVIOILGVKTSRF 101
DB	81 GIKRRELNYCNG--IGFHLOVPDGRISGTHEENPYSLLEISTVERGWSLFGVKSAIF 138
QY	102 LCRPDGALYGSHFDPEACSFRLELLEDGNNVQSEAH 140
DB	139 IAMNSKRLYTTPSFQDE-CKFRETLPLPNYNAYESDIY 176
RESULT 7	
Q9YGD8	PRELIMINARY; PRT; 206 AA.
ID	Q9YGD8
AC	Q9YGD8;
DT	01-MAY-1999 (TrEMBLrel. 10, Created)
DT	01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Fibroblast growth factor 6-related protein.
DE	FGF6.
GN	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX	NCBI_TaxID=8022;
RP	[1]
RN	SEQUENCE FROM N.A.
RX	MDLINE=99096461; PubMed=9878802;
RA	Rescan P.Y.;
RT	"Identification of a fibroblast growth factor 6 (FGF6) in a non-
RT	mammalian vertebrate: Continuous expression of FGF6 accompanies muscle
RT	fiber hyperplasia.";
RL	Biochim. Biophys. Acta 1443:305-314 (1998).
DR	EMBL; Y16850; CAA76422.1; -.
DR	HSP; P31371; 1G82.
DR	GO; GO:0008083; F:growth factor activity; IEA.
DR	InterPro; IPR001064; Crystallin.
DR	InterPro; IPR008996; Cytok IL1_like.
DR	InterPro; IPR002348; IL1_HBGF.
DR	Pfam; PF00167; FGF; 1.
DR	PRINTS; PR00262; IL1HBGF.
DR	PRODom; PD000831; IL1_HBGF; 1.
DR	SMART; SMO0442; FGF; 1.

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DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 206 AA; 23375 MW; B3883328F17BB6E4 CRC64;

Query Match 15.4%; Score 171; DB 13; Length 206;
Best Local Similarity 26.9%; Pred. No. 9e-08;
Matches 43; Conservative 28; Mismatches 57; Indels 32; Gaps 4;

QY 10 HSGLMVSVLACLLGACAAHPD-----SSPLQFGGQ----- 43
Db 18 HWTJTAIVLLGFIIVGVSYPPIRSTNATLEKWEITLFRSILGISGEKSDIWNESDYL 77
QY 44 ---VRQRYLYTDDAQOQTAHLEIRDEGTVGGAADQSPESLLQKALKEGVQIILGVKTSR 100
Db 78 LGIKRVRELYCNAG--IGFHLQVLPDGRINGVHNEQVSLTEISTVERGVVSLYGVRSSEL 135
QY 101 FLCQRPDGLYGSLLHFDPEACSFRELLLEDGNNVYQSEAH 140
Db 136 FVAMNSRGLYGTIVFHDE-CKFRESMLPNNYNAYESSVY 174

RESULT 8
Q8R5L9 PRELIMINARY; PRT; 245 AA.
AC Q8R5L9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1] : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RP SEQUENCE FROM N.A.
RA "Rattus norvegicus FGF3 mRNA.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB079262; BAB84564.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1-like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 245 AA; 27150 MW; C9305D307E7D0648 CRC64;

Query Match 15.4%; Score 171; DB 11; Length 245;
Best Local Similarity 35.0%; Pred. No. 1.1e-07;
Matches 43; Conservative 20; Mismatches 48; Indels 12; Gaps 4;

QY 41 GQVQRVLYTDDAQOQTAHLEIRDEGTVGGAADQSPESLLQKALKEGVQIILGVKTSR 100
Db 40 GQAPRRKLYC----ATKYLQLHPSGRVNSAYSILEITAVEGVWAIGLFGSR 95
QY 101 FLCQRPDGLYGSLLHFDPEACSFRELLLEDGNNVYQSEAHGLPLHGKSP--HRDPAP 158
Db 96 YLAMNKRGLYASEHYNAB-CEFVERIHELGYNTASR-----LYRTGSGPGARRQPGA 149
QY 159 RGP 161
Db 150 QRP 152

RESULT 9
Q8C399 PRELIMINARY; PRT; 195 AA.
AC Q8C399;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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DE Fibroblast growth factor 6 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK086530; BAC39686.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR008996; Cytok IL1-like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
FT NON TER 1
SQ SEQUENCE 195 AA; 21318 MW; BABA90EF368994FC CRC64;

Query Match 15.3%; Score 170.5; DB 11; Length 195;
Best Local Similarity 36.4%; Pred. No. 9.3e-08;
Matches 36; Conservative 21; Mismatches 39; Indels 3; Gaps 2;

QY 42 GQVQRVLYTDDAQOQTAHLEIRDEGTVGGAADQSPESLLQKALKEGVQIILGVKTSR 101
Db 68 GIKRRLYCNVG--IGFHLQVPPDGRISGTHEENPYSLLLEISTVERGVVSLFGVKSALF 125

QY 102 LCQRPDGLYGSLLHFDPEACSFRELLLEDGNNVYQSEAH 140
Db 126 IAMNSKRLYTPPSFHDE-CKFRETLPLNNYNAYESDLY 163

RESULT 10
Q9YH31 PRELIMINARY; PRT; 196 AA.
AC Q9YH31;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative fibroblast growth factor-4.
OS Notoptthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Notoptthalmus.
OX NCBI_TaxID=8316;
RN [1] : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RP SEQUENCE FROM N.A.
RA Wei Y.;
RT "Putative Newt Fibroblast Growth Factor-4.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U76998; AAC98812.1; -.
DR HSSP; P09038; 1BFP.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR008996; Cytok IL1-like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 196 AA; 22033 MW; AC4688CD989C6EAF CRC64;
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Query Match      15.1%; Score 168; DB 13; Length 196;
Best Local Similarity 28.9%; Pred. No. 1.6e-07;
Matches 44; Conservative 27; Mismatches 45; Indels 36; Gaps 5;

QY 17 VLGLLACQAHPIPD-SSPLLQFGGQVRQRYLYTDD-----AQQTEA----- 59
DB 15 VLLGLSLGLARCLPSPGNGTLEWSWT-----LYSQSLIARLAGGORTDAHRYGYLLGI 70

QY 60 -----HLEIREDTGCGAADQSPESLILQALKALPGVITQILGVKTSRFLQCR 105
DB 71 XELRLYCNVGVGFHLQVLDPGRHGHMSESYSLLEISPVVERGVVCGVQSGLFLAWN 130

QY 106 PDGALYGSLLHFDPEACSFRELLLEDGYNVYQS 137
DB 131 SKGRLFSGKYFSD-CKFKEMLLPNYINAYES 161

RESULT 11
Q9ESL9 PRELIMINARY; PRT; 212 AA.
AC Q9ESL9;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Fibroblast growth factor 20.
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-20 (FGF20).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049218; BAB16406.1; -.
DR HSSP; P31371; IG82.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR MGD; MGI:1891346; Fgf20.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 212 AA; 23659 MW; 174DBC8915B69EF CRC64;

Query Match      15.1%; Score 168; DB 11; Length 212;
Best Local Similarity 33.5%; Pred. No. 1.8e-07;
Matches 54; Conservative 19; Mismatches 62; Indels 26; Gaps 6;

QY 32 PDSSPLLQFGGQVRQRYLYTDDAQTEAHLEIREDTGCGA-ADQSPESLILQALKPGV 90
DB 52 PGSVELAHHLGILRRRLQYC-----RTGFHLQILPDGVTVQTRDHSILFGILEISVAVGL 107

QY 91 IQILGVKTSRFLQCRPDGALYGSLLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPNGK 150
DB 108 VSRIGVDSGLYLGWNDKGILYSEKLTSE-CIFREQEENWNTYSSN-----YKHGNT 161

QY 151 -----SPHRDPAPRGPAR-----FLPLGLPALPE 176
DB 162 GRRYFVALNKDGTDRDQAGSKRRQKQKTHFLPRPVDPERVPE 202

RESULT 12
Q90XQ5 PRELIMINARY; PRT; 124 AA.
AC Q90XQ5;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Fibroblast growth factor 4 (Fragment).

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OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11555861;
RX MEDLINE=21439472; Weinstein M., Tassava R.A.;
RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
and semi-quantitative RT-PCR expression studies.";
J. Exp. Zool. 290:529-540 (2001).
RL EMBL; AF360984; AAL16957.1; -.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
FT NON_TER 1
SQ SEQUENCE 124 AA; 14161 MW; 919CE10E9F66CEF3 CRC64;

Query Match      15.0%; Score 167.5; DB 13; Length 124;
Best Local Similarity 35.1%; Pred. No. 9.9e-08;
Matches 39; Conservative 23; Mismatches 44; Indels 5; Gaps 3;

QY 60 HLEIREDTGCGAADQSPESLILQALKALPGVITQILGVKTSRFLQCRPDGALYGSLLHFDPE 119
DB 13 HVQVLDPGRHGHMSESYSLLEISPVVERGVVSILOVKSALFLAMNRRKLYGSKQYN-E 71

QY 120 ACSFRELLLEDGYNVYQSEAH-GLPLHLPNG--KSPHRDPAPRGPARFLP 166
DB 72 ECKFKETLLANNYNAYESRQYFGMYIALSKNGRTKGRNVSPTMNVTHFLP 122

RESULT 13
Q8C7A8 PRELIMINARY; PRT; 211 AA.
AC Q8C7A8;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Fibroblast growth factor 20.
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=22354683; PubMed=12466851;
RA the FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK052233; BAC34892.1; -.
DR MGD; MGI:1891346; Fgf20.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 211 AA; 23614 MW; 6CFA714BD4F6CDFE CRC64;

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Query Match 14.8%; Score 165; DB 11; Length 211;
Best Local Similarity 34.4%; Pred. No. 3.3e-07;
Matches 55; Conservative 16; Mismatches 65; Indels 24; Gaps 6;
QY 32 PDSPLPFGGVRORVLYTDDAQOEAHLEIREDCVTGGA-ADQSPESLLQALKKPGV 90
DB 52 PGSVETLAHLGILRRRLQC-----RTGHLQILPDGIVGQTRQDHSLGLFISVAVGL 107
QY 91 IQILGVKTSFLCQPDGALYSLHFDPEACSFRELLLEDGYNVYQSEAH-----GLPLH 145
DB 108 VSRGVDSGLYGNMDKGLYSEKLTSE-CIFREQFEENWYNYSSNIYKHGDTGRYF 166
QY 146 LPGNKSHRDPAPRGPAPR-----FLPLGLPPALPE 176
DB 167 VALNK-----DQTPRDGARSKHQKFTHEFLPRPVDPERVPE 202
RESULT 14
Q8R5L7 PRELIMINARY; PRT; 247 AA.
AC Q8R5L7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor14.
GN FGF14.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
QY 24 GACQAHPIPDSSPLPFGGVRORVLYTDDAQ-----QTEAHLEIREDCVTGGA 73
DB 38 GLCNGNLVDIFSQRIFG--LKKRLRRQDPQLKGIIVTRLYCRQGYLQHPDGLDGTK 95
QY 74 DQSPES-LLQLKALKPGVIOILGVKTSFLCQPDGALYSLHFDPEACSFRELLLEDGY 132
DB 96 DDSTNSTLNLIPVGLRVVAIQGVKTYIANGGEGYLPSELFTPE-CKFKESVFENY 154
QY 133 NVYQS-----EAHGLPLH-----LPGNKSHPDRPAPRGPAPRFLPLGLPPALPEPP 178
DB 155 VIYSSMLYRQESGRANFLGLNKEQVMKGNVKTTPA-----AHFLPKP-LEVAMYREP 209
SQ SEQUENCE 247 AA; 27720 MW; 427C3C760894996E CRC64;

Query Match 14.5%; Score 161; DB 11; Length 247;
Best Local Similarity 29.8%; Pred. No. 9.4e-07;
Matches 62; Conservative 28; Mismatches 80; Indels 38; Gaps 9;
QY 24 GACQAHPIPDSSPLPFGGVRORVLYTDDAQ-----QTEAHLEIREDCVTGGA 73
DB 38 GLCNGNLVDIFSQRIFG--LKKRLRRQDPQLKGIIVTRLYCRQGYLQHPDGLDGTK 95
QY 74 DQSPES-LLQLKALKPGVIOILGVKTSFLCQPDGALYSLHFDPEACSFRELLLEDGY 132
DB 96 DDSTNSTLNLIPVGLRVVAIQGVKTYIANGGEGYLPSELFTPE-CKFKESVFENY 154
QY 133 NVYQS-----EAHGLPLH-----LPGNKSHPDRPAPRGPAPRFLPLGLPPALPEPP 178
DB 155 VIYSSMLYRQESGRANFLGLNKEQVMKGNVKTTPA-----AHFLPKP-LEVAMYREP 209
QY 179 GILAPQPPDVGSSDPLSMVGPQGRSPS 206
DB 210 SL-----HDVGETVPKAGVTPSKTSAS 232
RESULT 15
Q8BST0 PRELIMINARY; PRT; 247 AA.
AC Q8BST0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Pituitary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK030616; BAC27049.1; -.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_HBGF.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 247 AA; 27720 MW; 427C3C760894996E CRC64;
Query Match 14.5%; Score 161; DB 11; Length 247;
Best Local Similarity 29.8%; Pred. No. 9.4e-07;
Matches 62; Conservative 28; Mismatches 80; Indels 38; Gaps 9;
QY 24 GACQAHPIPDSSPLPFGGVRORVLYTDDAQ-----QTEAHLEIREDCVTGGA 73
DB 38 GLCNGNLVDIFSQRIFG--LKKRLRRQDPQLKGIIVTRLYCRQGYLQHPDGLDGTK 95
QY 74 DQSPES-LLQLKALKPGVIOILGVKTSFLCQPDGALYSLHFDPEACSFRELLLEDGY 132
DB 96 DDSTNSTLNLIPVGLRVVAIQGVKTYIANGGEGYLPSELFTPE-CKFKESVFENY 154
QY 133 NVYQS-----EAHGLPLH-----LPGNKSHPDRPAPRGPAPRFLPLGLPPALPEPP 178
DB 155 VIYSSMLYRQESGRANFLGLNKEQVMKGNVKTTPA-----AHFLPKP-LEVAMYREP 209
QY 179 GILAPQPPDVGSSDPLSMVGPQGRSPS 206
DB 210 SL-----HDVGETVPKAGVTPSKTSAS 232
RESULT 16
Q90XQ1 PRELIMINARY; PRT; 111 AA.
AC Q90XQ1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 4 (Fragment).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=43114;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21439472; PubMed=11555861;
RA Christensen R.N.; Weinstein M.; Tassava R.A.;
RT "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT and semi-quantitative RT-PCR expression studies.";
RL J. Exp. Zool. 290:529-540 (2001).
DR EMBL; AF360988; AAL16961.1; -.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR008996; Cytok IL1_HBGF.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.

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DR PRINTS; PRO0262; IL1HBGF.
DR ProDom; PD000831; IL1 HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12607 MW; 4A3A52ED39001057 CRC64;

Query Match 14.4%; Score 160; DB 13; Length 111;
Best Local Similarity 37.4%; Pred. No. 4.2e-07;
Matches 34; Conservative 21; Mismatches 34; Indels 2; Gaps 2;

QY 60 HLEIRDTGVTGAADQSPESLLQKALPGVILGLVKTSLRFLCQPDGALYGLSHFDPE 119
DB 13 HVQVLPDGKIHGTHNENRYSLLEISFVERGVSVILGVKSALFLAMNRRKLYGSKQYS-E 71

QY 120 ACSFRELLEDGYNVQSEAH-GLPLHLPQN 149
DB 72 ECKFKPEPLANNYNAYESRQYFGMYTALSKN 102

RESULT 17
Q9EST9 PRELIMINARY; PRT; 212 AA.
AC Q9EST9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FGF-20.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
TISSUE=Brain;
RC MEDLINE=20490008; PubMed=11032730;
RA Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
RA Itoh N.; a novel neurotrophic factor, preferentially expressed in the
RA "Fgf-20," a novel neurotrophic factor, preferentially expressed in the
RT substantia nigra pars compacta of rat brain."
RL Biochem. Biophys. Res. Commun. 277:355-360(2000).
DR EMBL; AB020021; BAB13763.1; -.
DR FIR; JC7511; JC7511.
DR HSP; P31371; IG82.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_III_like.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1 HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 212 AA; 23537 MW; 4F858BEFE772B977 CRC64;

Query Match 14.4%; Score 160; DB 11; Length 212;
Best Local Similarity 33.8%; Pred. No. 9.6e-07;
Matches 54; Conservative 17; Mismatches 65; Indels 24; Gaps 6;

QY 32 PDSSFLQFGGQVRQRYLYTDDAQTEAHLREIDGTGVGA-ADQSPESLLQKALPGV 90
DB 52 PGSVELAHHLGILRRRLQYLC---RTGPHLQILPDGSGVQTRQDHSFLGILEFISVAVGL 107

QY 91 IQILGVKTSRLCQPDGALYGLSHFDPEACSFRELLEDGYNVQSEAH-----GLPLH 145
DB 108 VSIKGVDSGLYLMGNKGLYSEKLTSE-CIFREQFEENYNTYSSNIYKHGDTGRYF 166

QY 146 LPGNKSPHRDAPRGPAR-----FLPLPGLPALPE 176
DB 167 VALNK---DGTTPRGARSKRHKQKTHFLPRVPDVRVPE 202

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RESULT 18
Q9DFC9 PRELIMINARY; PRT; 191 AA.
AC Q9DFC9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 4.
GN FGF4.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=20433237; PubMed=10976049;
RA Grandel H., Draper B.W., Schulte-Merker S.;
RT "dackel acts in the ectoderm of the zebrafish pectoral fin bud to
RT maintain AER signaling."
RL Development 127:4169-4178(2000).
DR EMBL; AF283555; AAG13950.1; -.
DR HSP; P31371; IG82.
DR ZFIN; ZDB-GENE-001006-1; fgf4.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_III_like.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1 HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 191 AA; 21203 MW; D2B5F2FAD44B2289 CRC64;

Query Match 14.3%; Score 159.5; DB 13; Length 191;
Best Local Similarity 26.3%; Pred. No. 9.3e-07;
Matches 51; Conservative 27; Mismatches 69; Indels 47; Gaps 6;

QY 11 SGIMVSVLGLLIGACQAHPIPD-----SSPLQFGGQVRQ----- 46
DB 5 SALLPLVLGLMTSSVRCAPLPGHSGPVERRWETLYSRSLARIPGKRDISRDSYLTG 64

QY 47 ----RVLYTDDAQTEAHLREIDGTGVGAADQSPESLLQKALPGVILGLVKTSLRFL 102
DB 65 IKELRLRYCNVG--IGFHLQVLPCKKITGVHNNRYSLLEISFVERGVVTLFGVRSGLFV 122

QY 103 CQRPDGLYGLSHFDPEACSFRELLEDGYNVQSEAHGLPLHLP-----NKSP 152
DB 123 AMNSKGLYGEQFTNE-CKFREKLLANNYNAYESLAH-----PGMYIGLSKAGTKKG 175

QY 153 HRDPAPRGPARFLP 166
DB 176 NRVSTSTMTWTHFLP 189

RESULT 19
Q9IAI6 PRELIMINARY; PRT; 237 AA.
AC Q9IAI6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor homologous factor 4 isoform 1A
DE (Fragment).
GN FHF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=20112823; PubMed=10644718;
RA Munoz-Santjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199605; AAF31392.1; -.
DR HSP; P13171; IG82.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
FT NON_TER 1
SQ SEQUENCE 237 AA; 26816 MW; F13076736548BB22 CRC64;

Query Match 14.3%; Score 159; DB 13; Length 237;
Best Local Similarity 29.3%; Pred. No. 1.4e-06;
Matches 61; Conservative 30; Mismatches 79; Indels 38; Gaps 9;

QY 24 GACQAHPIPDSPLLQFGGVQRVRLYTDDAQ-----QTEHLEIREDDGTGGAA 73
DB 27 GLCNGNLVDIFSKVRIFG-LKKRRLRRQDPQLKGIVTRLYCRQGYILOMHPDGLDGYK 84
QY 74 DOSPES-LLQKALKPGVIQILGVKTSRFLCORPDGALYGLSLHFDPEACSFRELLLEDGY 132
DB 85 DSSNSTLFLNLPVGLRVVAGVKTGLYALNNEGFLYTSFLTPE-CKPKESVFENY 143
QY 133 NYYQS-----FAHGLPLH-----LPGNKSPPHDDAPRGPARFLPLGPPALPPP 178
DB 144 VIYSSMLYRQBSGRAWFLGNLKEGVQMKGNKVKTKPA----AHFLPKP-LEVAMYREP 198
QY 179 GILAPQPPDVGSSDPLSMVPSQGRSPS 206
DB 199 SL-----HDIGETVPKAGVTFKSTAS 221

RESULT 20
Q7ZZN4 PRELIMINARY; PRT; 208 AA.
AC Q7ZZN4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor 9.
GN FGF9.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RA Yoshioka H., Ishimaru Y., Sugiyama N., Taunekawa N., Noce T.,
RA Kasahara M., Morohashi K.;
RT "Mesonephric FGF9 is the initiation signal for Gonadal Organogenesis
RT in chick.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB108842; BAC7516.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 208 AA; 23382 MW; DC73CDB7329D36CA CRC64;

Query Match 14.2%; Score 157.5; DB 13; Length 208;
Best Local Similarity 27.6%; Pred. No. 2.2e-06;
Matches 53; Conservative 28; Mismatches 68; Indels 43; Gaps 8;

QY 34 SSPLLQFGGQ-----VRQRYLYTDDAQTEA-----HLEIREDDGTGGAAQSPESL 80
DB 61 SSPLAAGSGQSGLEQSSQSFQSPSGRRTSLYCRVGIGFHLQIYDPDGKVGSHANMLSV 120
QY 81 LQKALKPGVIQILGVKTSRFLCORPDGALYGLSLHFDPEACSFRELLLEDGYNYVQSEAH 140
DB 121 LEIFAVSQGIVGIRGVFSNFKLMSKGLHASAKFTDD-CKFRFRQENSYNYASAIH 179
QY 141 -----GLPLHLPGNKSPHRDPAPRG-----PARFLP-----LPGLP-----PAL 174
DB 180 RTEKTGREWYVALNK---RGKAKGCSPRVKPQHISTHFLPRFKQSEQPELSFTVTVPK 236
QY 175 PEPPGILAPQPP 186
DB 237 KKPPSPKPKIP 248
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Best Local Similarity 32.0%; Pred. No. 1.6e-06;
Matches 55; Conservative 21; Mismatches 69; Indels 27; Gaps 7;

QY 23 LGACQAHPIPDSPLLQFGGVQRVRLYTDDAQTEHLEIREDDGTGGAA-ADQSP 78
DB 37 LQKAEAGGLPRGPAVTDLHLKILRRQLYC-----RTGFHLEIFPNGTIQGTRODHRF 92
QY 79 SLLQKALKPGVIQILGVKTSRFLCORPDGALYGLSLHFDPEACSFRELLLEDGYNYVQSE 138
DB 93 GILEFISIAVGLSVIRGVDLSGLYGMNEKGLYSEKLTQE-CVFRQEQFEENWINTYSSN 151
QY 139 AH-----GLPLHLPGNKSPHRDPAPRGPAR-----FLPLGLPALPS 176
DB 152 LYKHVDTGRRYYVALNK-----DGTREGTRTKRHKFTHFLPRPVDPEKVP 199

RESULT 21
Q8NF90 PRELIMINARY; PRT; 268 AA.
AC Q8NF90;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor-5.
GN FGF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=21347229; PubMed=11454700;
RA Hanada K.-I., Perry-Lalley D.M., Ohnmacht G.A., Bettinotti M.P.,
RA Yang J.C.;
RT "Identification of fibroblast growth factor-5 as an overexpressed
RT antigen in multiple human adenocarcinomas.";
RL Cancer Res. 61:5511-5516(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Hanada K.-I., Yang J.C.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF535149; AAN04097.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 268 AA; 29550 MW; 28B7268B26781BCF CRC64;

Query Match 14.2%; Score 157.5; DB 4; Length 268;
Best Local Similarity 27.6%; Pred. No. 2.2e-06;
Matches 53; Conservative 28; Mismatches 68; Indels 43; Gaps 8;
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RESULT 22	
OC Q9W6A2	PRELIMINARY; PRT; 245 AA.
AC Q9W6A2	SEQUENCE FROM N.A.
DT 01-NOV-1999	(TRENBLrel. 12, Created)
DT 01-NOV-1999	(TRENBLrel. 12, Last sequence update)
DT 01-OCT-2003	(TRENBLrel. 25, Last annotation update)
DE Fibroblast growth factor 13 isoform 1S	(Fibroblast growth factor homologous factor 2 isoform 1T+1S').
GN FGf13 OR FGF-2.	(Chicken).
OS Gallus Gallus	(Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	
OC NCBI_TaxID=9031;	
EN [1]	
RP SEQUENCE FROM N.A.	PubMed=9847253;
RX MEDLINE=99065510;	PubMed=9847253;
RA Munoz-Sanjuan I., Simandl B.K., Fallon J.F., Nathans J.;	
RT "Expression of chicken fibroblast growth factor homologous factor (FGF)-1 and of differentially spliced isoforms of FGF-2 during development and involvement of FGF-2 in chicken limb development."	
RL development 126:409-421(1999).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Brain;	
RX MEDLINE=20112823;	PubMed=10644718;
RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;	
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors Is Generated by Alternative Promoter Usage and Differential Splicing."	
RL J. Biol. Chem. 275:2589-2597(2000).	
DR EMBL; AF108755; AAD21576.1; -.	
DR EMBL; AF199611; AAF31398.1; -.	
DR HSSP; P31371; 1G82.	
DR GO; GO:0008083; F: growth factor activity; IEA.	
DR InterPro; IPR008996; Cytok IL1-like.	
DR InterPro; IPR002348; IL1_HBGF.	
DR Pfam; PF00167; FGF; 1.	
DR PRINTS; PR00262; IL1HBGF.	
DR ProDom; PD000831; IL1_HBGF; 1.	
DR SMART; SM00442; FGF; 1.	
DR PROSITE; PS00247; HBGF_FGF; 1.	
SQ SEQUENCE 245 AA; 27605 MW; DA0DAFEDBA1B8F28 CRC64;	
Query Match 14.0%; Score 155.5; DB 13; Length 245;	
Best Local Similarity 29.4%; Pred. No. 3e-06;	
Matches 53; Conservative 26; Mismatches 72; Indels 29; Gaps 7;	
QY 24 GACQAHPIPDSSPLQFGQVQRVY-----LYTDDAQQTAEHLREIDGTGVAADQ 75	
Db 36 GSCDKNKLVFSRVLFGSKRRRRPEPQLGIIVTKLYSRQGYHLQLQADGTIDGTKEE 95	
QY 76 -SPESLLQLKALPGVIQILGKTSFLQRPDGLYGLSLHFDPEACSFRELLLEDGYNV 134	
Db 96 DSYTYTLNLIPLVGLRVVA:QGVQTKLYLANSEGYLTSEHTTPE-CKPKSIFENYVT 154	
QY 135 Y-----QSEAGHLPILH-----PGNKSPhRDPAFPGPAPFPLPLGPPALPEPGI 180	
Db 155 YSSMIYRQQSGRGWYGLNKEGIMKGNHVKNKFA-----AHFLPKP-LKVAMYKEPSL 209	
RESULT 23	
QY95L12	PRELIMINARY; PRT; 208 AA.
AC Q95L12	
DT 01-DEC-2001	(TRENBLrel. 19, Created)
DT 01-DEC-2001	(TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003	(TRENBLrel. 25, Last annotation update)
DE Fibroblast growth factor 9.	
GN FGF9.	
OS Sus scrofa (Pig).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	
OC NCBI_TaxID=9823;	
EN [1]	
RP SEQUENCE FROM N.A.	
RA Paradis V., Silversides D.W.;	
RT "Sus scrofa fgf9 cDNA."	
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AY033825; AAK61609.2; -.	
DR GO; GO:0008083; F: growth factor activity; IEA.	
DR InterPro; IPR008996; Cytok IL1-like.	
DR InterPro; IPR002348; IL1_HBGF.	
DR Pfam; PF00167; FGF; 1.	
DR PRINTS; PR00262; IL1HBGF.	
DR ProDom; PD000831; IL1_HBGF; 1.	
DR SMART; SM00442; FGF; 1.	
DR PROSITE; PS00247; HBGF_FGF; 1.	
SQ SEQUENCE 208 AA; 23454 MW; 05FD0E2048CCC5E5 CRC64;	
Query Match 13.9%; Score 155; DB 6; Length 208;	
Best Local Similarity 32.5%; Pred. No. 2.7e-06;	
Matches 52; Conservative 19; Mismatches 65; Indels 24; Gaps 6;	
QY 32 PDSSPLQFGQVQRVLYTDDAQQTAEHLREIDGTGGA-ADQSPESLLQLKALPGV 90	
Db 49 PAVTDLHLKILRRRLQY----RTGFHLFIFFNGTIQGRKHRSRFGILEFISIAVGL 104	
QY 91 IQILGVKTSFLQRPDGLYGLSLHFDPEACSFRELLLEDGYNVQSEAH-----GLPLH 145	
Db 105 VSIRGVDSGLYGMNEKELYSKLTQE-CVTFREQFENYNYSSNLYKXVDGTGRFFY 163	
QY 146 LPGNKSPHRDPAPRGPAP-----FLPLGLPPALPE 176	
Db 164 VALNK-----DCTPREGTETKHKQFTHELPRPVDPKVPE 199	
RESULT 24	
QY9PVY1	PRELIMINARY; PRT; 208 AA.
AC Q9PVY1	
DT 01-MAY-2000	(TRENBLrel. 13, Created)
DT 01-MAY-2000	(TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003	(TRENBLrel. 25, Last annotation update)
DE XFGF-20.	
GN XFGF-20.	
OS Xenopus laevis (African clawed frog).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
OC Xenopodinae; Xenopus.	
OC NCBI_TaxID=8335;	
EN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=99373151; PubMed=10441498;	
RA Koga C., Adachi N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,	
RA Tei H., Sakaki Y., Kurokawa T., Shiohara K., Yokoyama K.K.;	
RT "Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevis."	
RL Biochem. Biophys. Res. Commun. 261:756-765(1999).	
DR EMBL; AB012615; BAA83474.1; -.	
DR PIR; JC7082; JC7082.	
DR HSSP; P31371; 1G82.	
DR GO; GO:0008083; F: growth factor activity; IEA.	
DR InterPro; IPR008996; Cytok IL1-like.	
DR InterPro; IPR002348; IL1_HBGF.	
DR Pfam; PF00167; FGF; 1.	
DR PRINTS; PR00262; IL1HBGF.	
DR ProDom; PD000831; IL1_HBGF; 1.	
DR SMART; SM00442; FGF; 1.	
DR PROSITE; PS00247; HBGF_FGF; 1.	
SQ SEQUENCE 208 AA; 23438 MW; 268881D36E757D4D CRC64;	
Query Match 13.7%; Score 153; DB 13; Length 208;	
Best Local Similarity 31.5%; Pred. No. 4.1e-06;	
Matches 53; Conservative 22; Mismatches 65; Indels 28; Gaps 7;	

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QY 27 QAHPIPOSP--LLQFGQVQRYLYTDDAQCTAHLEIREDTGVGGA-AQSPESLIQL 83
Db 42 QSERLSRAPSDELHQILRRQLYC-----RTGFHLQILPDGNGVQGRQDHSRFGILIEF 97
QY 84 KALKPGVQIIGVTSRFLQCPDQALYGLSHFDPEACSFRELLLEDGYNVYQSEAHGLP 143
Db 98 ISVALGIVSIRGVDITGLYGMNDKGLFGSEKLISE-CIFREQFEENWNTYSSN----- 151
QY 144 LHLFGNK-----SPHRDPAPRGPAPR-----FLPLGLPALPE 176
Db 152 LYKHGDSGRYFVALNKDGTDRGTRAKRHOKFTHTFLPRVPDPEKVE 199

RESULT 25
Q8R4X0
ID Q8R4X0 PRELIMINARY; PRT; 211 AA.
AC Q8R4X0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor-like factor-4D (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu C., Dib-Hajj S.D., Waxman S.G.;
RT "Fibroblast growth factor homologous factor-4D.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348523; AAL83904.1; -.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG FGF; 1.
FT NON TER 1
SQ SEQUENCE 211 AA; 23346 MW; 046C18019C63EBA3 CRC64;

Query Match 13.7%; Score 153; DB 11; Length 211;
Best Local Similarity 32.7%; Pred. No. 4.2e-06;
Matches 53; Conservative 21; Mismatches 62; Indels 26; Gaps 7;

QY 60 HLEIREDTGVGAADQSPES--LLQKALKPGVQIQLGVKTSRFLCQRPDQALYGLSHFD 118
Db 46 YLQHPDGDALDGTDDSTNSTLFLNLPVGLRVVAIQVKTGLYIANGEGYLYPSELFTF 105

QY 119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSHPRDPAPRGP 164
Db 106 E-CFKESVFENYVYIYSSMLYRQGESGRAWFLGNKEGQVMKGNRVKTKPEA----- 160

QY 165 LPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPQGRSPS 206
Db 161 LPKP-LEVAMRYEPL-----HDVGETVPKAGVTFSKSTAS 196

RESULT 26
O89096
ID O89096 PRELIMINARY; PRT; 252 AA.
AC O89096;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor 14 (FHF-4B).
GN FGF14.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

QY 27 QAHPIPOSP--LLQFGQVQRYLYTDDAQCTAHLEIREDTGVGGA-AQSPESLIQL 83
Db 42 QSERLSRAPSDELHQILRRQLYC-----RTGFHLQILPDGNGVQGRQDHSRFGILIEF 97
QY 84 KALKPGVQIIGVTSRFLQCPDQALYGLSHFDPEACSFRELLLEDGYNVYQSEAHGLP 143
Db 98 ISVALGIVSIRGVDITGLYGMNDKGLFGSEKLISE-CIFREQFEENWNTYSSN----- 151
QY 144 LHLFGNK-----SPHRDPAPRGPAPR-----FLPLGLPALPE 176
Db 152 LYKHGDSGRYFVALNKDGTDRGTRAKRHOKFTHTFLPRVPDPEKVE 199

RESULT 25
Q8R4X0
ID Q8R4X0 PRELIMINARY; PRT; 211 AA.
AC Q8R4X0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor-like factor-4D (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu C., Dib-Hajj S.D., Waxman S.G.;
RT "Fibroblast growth factor homologous factor-4D.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF348523; AAL83904.1; -.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG FGF; 1.
FT NON TER 1
SQ SEQUENCE 211 AA; 23346 MW; 046C18019C63EBA3 CRC64;

Query Match 13.7%; Score 153; DB 11; Length 211;
Best Local Similarity 32.7%; Pred. No. 4.2e-06;
Matches 53; Conservative 21; Mismatches 62; Indels 26; Gaps 7;

QY 60 HLEIREDTGVGAADQSPES--LLQKALKPGVQIQLGVKTSRFLCQRPDQALYGLSHFD 118
Db 46 YLQHPDGDALDGTDDSTNSTLFLNLPVGLRVVAIQVKTGLYIANGEGYLYPSELFTF 105

QY 119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSHPRDPAPRGP 164
Db 106 E-CFKESVFENYVYIYSSMLYRQGESGRAWFLGNKEGQVMKGNRVKTKPEA----- 160

QY 165 LPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPQGRSPS 206
Db 161 LPKP-LEVAMRYEPL-----HDVGETVPKAGVTFSKSTAS 196

RESULT 26
O89096
ID O89096 PRELIMINARY; PRT; 252 AA.
AC O89096;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor 14 (FHF-4B).
GN FGF14.
OS Mus musculus (Mouse), and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX NCBI_TaxID=10090, 10116;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse; STRAIN=C57BL/6J; TISSUE=Cerebellum, and Diencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Mouse, and Rat; TISSUE=Brain;
RX MEDLINE=98267141; PubMed=9602045;
RA Yamamoto S., Mikami T., Ohbayashi N., Ohta M., Itoh N.;
RT "Structure and expression of a novel isoform of mouse FGF homologous
factor (FHF)-4.";
RL Biochim. Biophys. Acta 1398:38-41 (1998).
DR EMBL; AK035974; BAC29263.1; -.
DR EMBL; AK079100; BAC37540.1; -.
DR EMBL; AB008908; BAA31544.1; -.
DR EMBL; AB008907; BAA31543.1; -.
DR HSSP; P31371; 1G82.
DR MGI; MGI:109189; Fgf14.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG FGF; 1.
SQ SEQUENCE 252 AA; 28364 MW; 281781EEBA63AB44 CRC64;

Query Match 13.7%; Score 153; DB 11; Length 252;
Best Local Similarity 32.7%; Pred. No. 5.2e-06;
Matches 53; Conservative 21; Mismatches 62; Indels 26; Gaps 7;

QY 60 HLEIREDTGVGAADQSPES--LLQKALKPGVQIQLGVKTSRFLCQRPDQALYGLSHFD 118
Db 87 YLQHPDGDALDGTDDSTNSTLFLNLPVGLRVVAIQVKTGLYIANGEGYLYPSELFTF 146

QY 119 EACSFRELLLEDGYNVYQS-----EAHGLPLH-----LPGNKSHPRDPAPRGP 164
Db 147 E-CFKESVFENYVYIYSSMLYRQGESGRAWFLGNKEGQVMKGNRVKTKPEA----- 201

QY 165 LPLGLPALPEPPGILAPQPPDVGSSDPLSMVGPQGRSPS 206
Db 202 LPKP-LEVAMRYEPL-----HDVGETVPKAGVTFSKSTAS 237

RESULT 27
Q8VCY9
ID Q8VCY9 PRELIMINARY; PRT; 245 AA.
AC Q8VCY9;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor 13.
GN FGF13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018238; AAHL8238.1; -.
DR MGI; MGI:109178; Fgf13.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
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DR InterPro; IPR002348; ILL_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILL_HBGF.
DR ProDom; PD000831; ILL_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 245 AA; 27587 MW; 5B96D41AC3A3DF78 CRC64;

Query Match 13.7%; Score 152.5; DB 11; Length 245;
Best Local Similarity 29.6%; Pred. No. 5.6e-06;
Matches 53; Conservative 25; Mismatches 72; Indels 29; Gaps 7;

Qy 25 ACQAHPIPDSPILQFGQVQRQY-----LYTDDAQQAHLREDTGTGGADQ- 75
Db 37 SCQKKNLNVSRVLFSGKRRRRPPQLKGIWTKLYSRQGYHLQAOAGTIDGTDED 96
Qy 76 SPESLLQKALKPGVQIILGVKTSRFLCQPDGALYGLSHFDPEACSFRELLLEDGYNVY 135
Db 97 STYTLFNLIPVGLRVVAIQGVQTKLYLNMNSEGYLYTSEHFTPE-CKFKESVFENYVTV 155

Qy 136 -----QSEAHGLPLH-----PGNKSHPDPAPRGPAPRFLPLGLPALPEPPI 180
Db 156 SSMYRQQSGRWYGLNKEGEIMKGNHVKNKPA-----AHFLPKP-LKVAMYKEPSL 209

RESULT 28
Q9ERQ5 PRELIMINARY; PRT; 207 AA.
AC Q9ERQ5; (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE FGF-16 protein.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Sontag D.P.; Cattini P.A.;
RT "Cloning and biological function of FGF-16 in the heart."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF292104; AAG29501.1; -.
DR HSSP; P31371; 1G82.
DR MGD; MGI:1931627; Fgf16.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR InterPro; IPR008996; CytoK_ill_like.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILL_HBGF.
DR ProDom; PD000831; ILL_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;

Query Match 13.6%; Score 151.5; DB 11; Length 207;
Best Local Similarity 32.6%; Pred. No. 5.6e-06;
Matches 61; Conservative 20; Mismatches 75; Indels 31; Gaps 8;

Qy 3 SDTGTGHEHSLVSVLAGLLGACQAHPIPDSPILQFGQVQRQYLYTDDAQQAHL 62
Db 28 ADSGPFNLNRL-----GQLEGKLGKSGPTDFAHL---KGIILRRQYLC-----RTGFHLE 74

Qy 63 IREDGTGVGAA-DQSPESLLQKALKPGVQIILGVKTSRFLCQPDGALYGLSHFDPEAC 121
Db 75 IFPNGVTHGTRHDHSPGILIEFISLAVGLISIRGVDSGLYGNMNGELYSKGLTRE-C 133

Qy 122 SFRELLLEDGYNVQSAHGLPLHLPGNK-----SPHRDPAPRGPAPR-----FLPLP 168
Db 134 VFREQFEENWNTY---ASALYKHSDSERQYVVALNKDGSFREGYRTKHKQTHFLPRP 190

Qy 169 GLPPALP 175
Db 191 VDPSKLP 197

RESULT 29
Q86YN7 PRELIMINARY; PRT; 252 AA.
AC Q86YN7; (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Fibroblast growth factor 14 isoform 1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Bonner T.I.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY188178; AA031806.1; -.
DR GO; GO:0008083; F.growth factor activity; IEA.
DR InterPro; IPR008996; CytoK_ill_like.
DR InterPro; IPR002348; ILL_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILL_HBGF.
DR ProDom; PD000831; ILL_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 252 AA; 28462 MW; 305B0B9A3F56D577 CRC64;

Query Match 13.6%; Score 151; DB 4; Length 252;
Best Local Similarity 32.7%; Pred. No. 8e-06;
Matches 53; Conservative 20; Mismatches 63; Indels 26; Gaps 7;

Qy 60 HLEIREDTGVGAADQSPES-LLQKALKPGVQIILGVKTSRFLCQPDGALYGLSHFD 118
Db 87 YLQMHDPGALDGTGDDSTNLTFLNLPVGLRVVAIQGVQTKLYLNMNGEGYLYPSELFT 146

Qy 119 EACSFRELLLEDGYNVQY-----EAHGLPLH-----LPGNKSHPDPAPRGPAPR 164
Db 147 E-CKFKESVFENYVYSSMLYRQESGRANFLGLNKEGQAMGNVKKTPA-----AHF 201

Qy 165 LPLGLPALPEPPIILAPQPDVGVSSDPLSMVGFSGRSPS 206
Db 202 LPKP-LEVAMYREPSL-----HDVGETVPKPGVTPSKTSAS 237

RESULT 30
Q9IAI5 PRELIMINARY; PRT; 253 AA.
AC Q9IAI5; (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE Fibroblast growth factor homologous factor 4 isoform 1B.
GN FHF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112823; PubMed=10644718;
RA Munoz-Sanjuan I.; Smallwood P.M.; Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
Is Generated by Alternative Promoter Usage and Differential
Splicing."
RT J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199606; AAF31393.1; -.

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Qy 156 PAPER---GPARFLPL 167
Db 152 QKTRRKN TSAHFLEP 166

RESULT 32
Q95K97 PRELIMINARY; PRT; 208 AA.
ID Q95K97 AC Q95K97
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Medulla oblongata;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RA "Isolation of full-length cDNA clones from macaque brain cDNA
RA libraries."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB063051; BAB60779.1; -.
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Hypothetical protein.
SQ SEQUENCE 208 AA; 23466 MW; 0766A787609B3661 CRC64;

Query Match 13.5%; Score 150; DB 6; Length 208;
Best Local Similarity 30.4%; Pred. No. 7.8e-06;
Matches 41; Conservative

Qy 42 GQVQRVLYTDDAQOETAHLEIREDDGTGVGNADQS-PESLLQALKPGVQILGVKTSR 100
Db 75 GDVWRWRKLF-----FTKYFLKIEKNGKVGSTKENCPSVILLETISVEIGVAVKAINSY 130

Qy 101 FLCQRPDCALYGSLHFDPEACSFLELLEDGYNVYQS---EAHGLPLH--LPGNKSPPHRD 155
Db 131 YLAWNKKGLYGSKEFNND-CKLKERIEENGYNVYASFNWQHNGRQMYVALNGKAPRRG 189

Qy 156 PAPER---GPARFLPL 167
Db 190 QKTRRKN TSAHFLEP 204

RESULT 33
Q9ERW3 PRELIMINARY; PRT; 192 AA.
ID Q9ERW3 AC Q9ERW3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 13.
GN FGF13.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal root ganglion;
RA Xiao H., Huang Q., Zhang F., Guo C., Chen Z., Han Z., Zhang X.;
RA "Rattus norvegicus fibroblast growth factor 13."
PT

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Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AF271786; AAG15492.1; -.

HSSP; P31371; 1G82.

GO; GO:0008083; F: growth factor activity; IEA.

InterPro; IPR008996; Cytok IL1 like.

InterPro; IPR002348; IL1_HBGF.

Pfam; PF00167; FGF; 1.

PRINTS; PR00262; IL1HBGF.

ProDom; PD000831; IL1_HBGF; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

SEQUENCE 192 AA; 21504 MW; 7736A3671677B263 CRC64;

Query Match 13.3%; Score 148.5; DB 11; Length 192;

Best Local Similarity 33.8%; Pred. No. 3.7e-06;

Matches 46; Conservative 17; Mismatches 52; Indels 21; Gaps 6;

QY 60 HLEIRDTGVGAADQ-SPESILQALKPGVILQGVKTSRFLCPDPDGLYSLHFD 118

DB 27 HQLQADGTIDTKEDSTYTLFNLIPGLRVAVLQGVQTKLYLAMNSEGYLTSEHFT 86

QY 119 EACSFRELLEDGYNYV-----QSEAHGLPLHL-----PKNKSPHRDPAPRGARF 164

DB 87 E-CKFESVFENYTYSSMYRQOQSGRWYGLNKEGEIMKGNVKKPKA----AHF 141

QY 165 LPLGLPPALPEPPGI 180

DB 142 LPKP-LKVAMYKEPSL 156

RESULT 34

Q9IA13 PRELIMINARY; PRT; 199 AA.

ID Q9IA13

AC Q9IA13

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Fibroblast growth factor 2 isoform 1Q+1Y.

GN FGF-2.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI_TaxID=9031;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112823; PubMed=10644718;

RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;

RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors Is Generated by Alternative Promoter Usage and Differential Splicing";

RT J. Biol. Chem. 275:2589-2597(2000).

RL EMBL; AF199610; AAF31397.1; -.

DR HSSP; P31371; 1G82.

DR GO; GO:0008083; F: growth factor activity; IEA.

DR InterPro; IPR008996; Cytok IL1 like.

DR InterPro; IPR002348; IL1_HBGF.

DR Pfam; PF00167; FGF; 1.

DR PRINTS; PR00262; IL1HBGF.

DR ProDom; PD000831; IL1_HBGF; 1.

DR SMART; SM00442; FGF; 1.

DR PROSITE; PS00247; HBGF FGF; 1.

DR SEQUENCE 199 AA; 22316 MW; FCEC93ABFCEDE22C CRC64;

Query Match 13.3%; Score 147.5; DB 13; Length 199;

Best Local Similarity 31.3%; Pred. No. 1.2e-05;

Matches 51; Conservative 21; Mismatches 64; Indels 27; Gaps 7;

QY 33 DSSPLQFGGVORRYLTDDAQQTAEHLEIREDTGVGAADQ-SPESILQALKPGVI 91

DB 13 DASKEPQLKGVTKLY-----SRQYHQLQADGTIDGTEEDSSVTLFNLIPVGLRV 66

Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AF271786; AAG15492.1; -.

HSSP; P31371; 1G82.

GO; GO:0008083; F: growth factor activity; IEA.

InterPro; IPR008996; Cytok IL1 like.

InterPro; IPR002348; IL1_HBGF.

Pfam; PF00167; FGF; 1.

PRINTS; PR00262; IL1HBGF.

ProDom; PD000831; IL1_HBGF; 1.

SMART; SM00442; FGF; 1.

PROSITE; PS00247; HBGF FGF; 1.

SEQUENCE 192 AA; 21504 MW; 7736A3671677B263 CRC64;

Query Match 13.3%; Score 148.5; DB 11; Length 192;

Best Local Similarity 33.8%; Pred. No. 3.7e-06;

Matches 46; Conservative 17; Mismatches 52; Indels 21; Gaps 6;

QY 60 HLEIRDTGVGAADQ-SPESILQALKPGVILQGVKTSRFLCPDPDGLYSLHFD 118

DB 27 HQLQADGTIDTKEDSTYTLFNLIPGLRVAVLQGVQTKLYLAMNSEGYLTSEHFT 86

QY 119 EACSFRELLEDGYNYV-----QSEAHGLPLHL-----PKNKSPHRDPAPRGARF 164

DB 87 E-CKFESVFENYTYSSMYRQOQSGRWYGLNKEGEIMKGNVKKPKA----AHF 141

QY 165 LPLGLPPALPEPPGI 180

DB 142 LPKP-LKVAMYKEPSL 156

RESULT 34

Q9IA13 PRELIMINARY; PRT; 199 AA.

ID Q9IA13

AC Q9IA13

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Fibroblast growth factor 2 isoform 1Q+1Y.

GN FGF-2.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OC NCBI_TaxID=9031;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112823; PubMed=10644718;

RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;

RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors Is Generated by Alternative Promoter Usage and Differential Splicing";

RT J. Biol. Chem. 275:2589-2597(2000).

RL EMBL; AF199610; AAF31397.1; -.

DR HSSP; P31371; 1G82.

DR GO; GO:0008083; F: growth factor activity; IEA.

DR InterPro; IPR008996; Cytok IL1 like.

DR InterPro; IPR002348; IL1_HBGF.

DR Pfam; PF00167; FGF; 1.

DR PRINTS; PR00262; IL1HBGF.

DR ProDom; PD000831; IL1_HBGF; 1.

DR SMART; SM00442; FGF; 1.

DR PROSITE; PS00247; HBGF FGF; 1.

DR SEQUENCE 199 AA; 22316 MW; FCEC93ABFCEDE22C CRC64;

Query Match 13.3%; Score 147.5; DB 13; Length 199;

Best Local Similarity 31.3%; Pred. No. 1.2e-05;

Matches 51; Conservative 21; Mismatches 64; Indels 27; Gaps 7;

QY 33 DSSPLQFGGVORRYLTDDAQQTAEHLEIREDTGVGAADQ-SPESILQALKPGVI 91

DB 13 DASKEPQLKGVTKLY-----SRQYHQLQADGTIDGTEEDSSVTLFNLIPVGLRV 66

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RN RP SEQUENCE FROM N.A.
RA Zhang Y., Zhou Y., Peng X., Yuan J., Qiang B.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AF411527; AAL05875.1; -.
DR GO: 0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 208 AA; 23433 MW; D6C77E96D4885C10 CRC64;

Query Match 13.2%; Score 147; DB 4; Length 208;
Best Local Similarity 29.6%; Pred. No. 1.5e-05;
Matches 40; Conservative 32; Mismatches 49; Indels 14; Gaps 6;

QY 42 GQVQRVLYTDDAQOTEAHLEIREDTGVGAADQS-PESLLQKALKPGVIQILGVKTSR 100
DB 75 GDVVRKRLFS-----FTKYFLKIEKNGKVGSTKKENCPSYLEITSVEIGAVAKAINS 130
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
DB 131 YLANRKGKLYSGKEFNND-CKLKERIEENGYNVYASFNWQHNGRQMYVALNGKGPARG 189
QY 156 PAPR---GPARFLPL 167
DB 190 QKTRKNTSAHFLPM 204

RESULT 37
Q804S4 PRELIMINARY; PRT; 236 AA.
AC Q804S4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor-like protein (Fragment).
GN FGF-2.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN RP SEQUENCE FROM N.A.
RA Reed K.M.;
RL "FHF-2 in the turkey (Meleagris gallopavo).";
RE Anim. Biotechnol. 0:0-0(2003).
DR EMBL; AF540440; AA033291.1; -.
DR GO: 0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR NON TER 1
SQ SEQUENCE 236 AA; 26670 MW; 748ED02C414DDC01 CRC64;

Query Match 13.0%; Score 144.5; DB 13; Length 236;
Best Local Similarity 33.1%; Pred. No. 2.9e-05;
Matches 45; Conservative 18; Mismatches 52; Indels 21; Gaps 6;

QY 60 HLEIREDTGVGAADQ-SPEILLQKALKPGVIQILGVKTSRFT-CQRPDGLYSLHFD 118
DB 71 HLQLOADTIDGTKEEDSYTFENLIPVGLRVAIQGVOTKLYLANNSEGLYTSSEHTP 130
QY 119 EACSFRELLLEDGYNVY-----QSEAHGLPLH-----PGNKSHPRPAPGPARF 164
DB 131 E-CKPKESVFENYVYSSMIYRQQSGRQYGLNKEGIMKGNHVKNKPA-----AHF 185

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QY 165 LPLPGLPALPEPRGT 180
DB 186 LKXP-LKVANYKEPSL 200

RESULT 38
O42407 PRELIMINARY; PRT; 212 AA.
AC O42407
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN RP SEQUENCE FROM N.A.
RA MEDLINE-97330690; PubMed-9187149;
RX Chuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
RA Yoshioka H., Kuwana T., Nohno T., Yamasaki M., Itoh N., Noji S.;
RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
RT of the chick limb bud through interaction with FGF8, an apical
RT ectodermal factor."
RL Development 124:2235-2244(1997).
DR EMBL; D86333; BA424945.1; -.
DR HSSP; P31371; IG82.
DR GO: 0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;

Query Match 12.9%; Score 144; DB 13; Length 212;
Best Local Similarity 28.9%; Pred. No. 2.8e-05;
Matches 39; Conservative 30; Mismatches 52; Indels 14; Gaps 5;

QY 42 GQVQRVLYTDDAQOTEAHLEIREDTGVGAADQS-PESLLQKALKPGVIQILGVKTSR 100
DB 79 GDVVRKRLYS---YNKYFLKIEKNGKVGSTKKENCPSYLEITSVEIGVAVKSIKSNY 134
QY 101 FLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQS-----EAHGLPLHLPGNKSPHRD 155
DB 135 YLANRKGKLYSGKEFNND-CKLKERIEENGYNVYASLNKWKNGRQMFVALNGRGATKRG 193
QY 156 PAPR---GPARFLPL 167
DB 194 QKTRKNTSAHFLPM 208

RESULT 39
Q9N1B9 PRELIMINARY; PRT; 213 AA.
AC Q9N1B9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 10.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN RP SEQUENCE FROM N.A.
RE TISSUE=Endometrium;

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Wed Mar 3 08:19:48 2004

QY 158 -----PRGPAR-----FLPLP 168
DB 238 WYIGDKRGRSRKGRNVKPESSAHLPLP 267
Search completed: March 2, 2004, 16:07:17
Job time : 89.0833 secs

RX MEDLINE=20411101; PubMed=10952944;
RA Chen C., Spencer T.E., Bazer F.W.;
RT "Fibroblast growth factor-10: A stromal mediator of epithelial
function in the ovine uterus";
RL Biol. Reprod. 63:959-966(2000).
DR EMBL; AF213396; AAF25944.1; -.
DR HSP; P31371; I982.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1 HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 213 AA; 23768 MW; C347149A81C15634 CRC64;

Query Match 12.9%; Score 143.5; DB 6; Length 213;
Best Local Similarity 31.1%; Pred. No. 3.2e-05;
Matches 42; Conservative 30; Mismatches 48; Indels 15; Gaps 7;
QY 42 GQVQRVLYTDDAQTEAHLEIREDTGVGGAADQS--PESLLQLKALKPGVIGILGVKTSR 100
DB 81 GDVWRKLFES---FTKYFKI-ENKVGSGTKKENCPSILLEITSVEIGVAVKAINS 135
QY 101 FLCQRPDGLYGLSLHDPDPCSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
DB 136 YLAMNKKGLYSGKEFNND-CKLERIEGNYNTYASFNWQHNGRMVYVALNGKGA 194
QY 156 PAPR---GPAREFLP 167
DB 195 QKTRKNTSAHFLPM 209

RESULT 40
Q8I6J7 PRELIMINARY; PRT; 268 AA.
AC Q8I6J7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fibroblast growth factor 3/7/10/22.
GN CF-FGF3/7/10/22.
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22259793; PubMed=12373588;
RA Satou Y., Imai K.S., Satoh N.;
RT "Pgf genes in the basal chordate Ciona intestinalis";
RL Dev. Genes Evol. 212:432-438(2002).
DR EMBL; AB086094; BAC22066.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 268 AA; 30873 MW; 9187484AEBB5457D CRC64;

Query Match 12.7%; Score 141.5; DB 5; Length 268;
Best Local Similarity 29.3%; Pred. No. 6.5e-05;
Matches 44; Conservative 23; Mismatches 50; Indels 33; Gaps 6;
QY 41 GQVQRVLYTDDAQTEAHLEIREDTGVGGAADQSPELILQLKALP-GVIGILGVKTS 99
DB 129 GGDREMYELY---NRNHVFIEIKDGKVRGYSNKSPQTEIEVQSVAAAGVIRFYSPSTG 184
QY 100 RFLCORPDGLYGLSLHDPDPCSFRELLLEDGYNVYQSEAHGLPLHLPNGKSPHRDPA-- 157
DB 185 RYLANMRHSLYASNRKIDCFVE-RWQDFYATYRS-----LHQPGNRRRRRKARE 237

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:51:17 ; Search time 20.0292 Seconds
(without alignments)
543.341 Million cell updates/sec

Title: US-10-060-765-4

Perfect score: 1113

Sequence: 1 MDSDETFGHSGLVWSVLG.....SSDFLSMVGPSQGRSPSYAS 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1113	100.0	209	1 FGFL_HUMAN	Q9nsal1 homo sapien
2	793.5	71.3	210	1 FGFL_MOUSE	Q9j1n1 mus musculus
3	265	23.8	216	1 FGFL_HUMAN	Q95750 mus musculus
4	249.5	22.4	251	1 FGFL_MOUSE	Q9epc2 mus musculus
5	235.5	21.2	251	1 FGFL_HUMAN	Q8v182 rattus norv
6	222.5	20.0	251	1 FGFL_MOUSE	Q9gvr9 homo sapien
7	206.5	18.6	218	1 FGFL_MOUSE	O35622 mus musculus
8	179	16.1	245	1 FGFL_MOUSE	P05524 mus musculus
9	177.5	15.9	239	1 FGFL_HUMAN	P11487 homo sapien
10	177	15.9	206	1 FGFL_BOVIN	P48803 bos taurus
11	176.5	15.9	208	1 FGFL_HUMAN	P10767 homo sapien
12	174	15.6	187	1 FGFL_HUMAN	P48805 xenopus lae
13	170.5	15.3	208	1 FGFL_MOUSE	P21658 mus musculus
14	167	15.0	266	1 FGFL_MOUSE	P48807 rattus norv
15	165	14.8	194	1 FGFL_MOUSE	P48804 gallus gall
16	164	14.7	264	1 FGFL_MOUSE	P15656 mus musculus
17	163.5	14.7	192	1 FGFL_XENLA	P48806 xenopus lae
18	163.5	14.7	206	1 FGFL_HUMAN	P08620 homo sapien
19	161	14.5	211	1 FGFL_HUMAN	Q9np95 homo sapien
20	160.5	14.4	256	1 FGFL_MOUSE	P48802 brachydanio
21	159	14.3	247	1 FGFL_HUMAN	Q92915 homo sapien
22	157	14.1	208	1 FGFL_HUMAN	P31371 homo sapien
23	157	14.1	208	1 FGFL_MOUSE	P36364 rattus norv
24	156.5	14.1	208	1 FGFL_MOUSE	P54130 mus musculus
25	155.5	14.0	155	1 FGFL_MOUSE	P34004 mesocricetu
26	154.5	13.9	155	1 FGFL_MOUSE	P10935 mus musculus
27	153.5	13.8	202	1 FGFL_MOUSE	P11403 mus musculus
28	153	13.7	247	1 FGFL_MOUSE	P70379 mus musculus
29	153	13.7	268	1 FGFL_HUMAN	P12034 homo sapien
30	152.5	13.7	245	1 FGFL_MOUSE	P70377 mus musculus
31	150.5	13.5	207	1 FGFL_HUMAN	O43320 homo sapien
32	150	13.5	208	1 FGFL_HUMAN	O15520 homo sapien
33	150	13.5	215	1 FGFL_MOUSE	P70492 rattus norv

34	148	13.3	209	1 FGFL_MOUSE	O35565 mus musculus
35	146.5	13.2	155	1 FGFL_HUMAN	P05230 homo sapien
36	146.5	13.2	207	1 FGFL_MOUSE	O54769 rattus norv
37	146	13.1	237	1 FGFL_XENLA	P36386 xenopus lae
38	144.5	13.0	155	1 FGFL_BOVIN	P03968 bos taurus
39	143.5	12.9	152	1 FGFL_MOUSE	P20002 sus scrofa
40	143	12.8	209	1 FGFL_XENLA	Q91875 xenopus lae
41	142	12.8	220	1 FGFL_CHICK	P48801 gallus gall
42	141.5	12.7	245	1 FGFL_HUMAN	Q92913 homo sapien
43	141	12.7	170	1 FGFL_HUMAN	O9hct0 homo sapien
44	141	12.7	194	1 FGFL_SHEEP	P48808 ovis aries
45	140	12.6	194	1 FGFL_CANFA	P79150 canis fami

ALIGNMENTS

RESULT 1	FGFL_HUMAN	STANDARD	PRT	209 AA
AC	Q9NSAI			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196)			
GN	FGF21			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20461777; PubMed=10858549;			
RA	Nishimura T., Nakatake Y., Konishi M., Itoh N.;			
RT	"Identification of a novel FGF, FGF-21, preferentially expressed in the liver."			
RL	Biachim. Biophys. Acta 1492:203-206(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309;			
RA	Clark H.F., Gurney A.J., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."			
RL	Genome Res. 13:2285-2270(2003).			
CC	- - SIMILARITY: Belongs to the heparin-binding growth factors family.			
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CC	EMBL; AB021975; BAA99415.1; -			
DR	EMBL; AY359086; AAQ89444.1; -			
DR	HSSP; P03968; IBAR			
DR	Genew; HGNC:3678; FGF21			
DR	GO; GO:0005576; C:extracellular; TAS			
DR	GO; GO:0005625; C:soluble fraction; TAS			
DR	GO; GO:0007267; P:cell-cell signaling; TAS			
DR	GO; GO:0007165; P:signal transduction; TAS			
DR	InterPro; IPR008996; Cytok_IL1_like			

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DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR PRODOM: PD000831; IL1 HBGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 209
FT CONFLICT 23 23
FT SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;

Query Match 100.0%; Score 1113; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 7.7e-75;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSDETFEHSGLVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTFAH 60
DB 1 MDSDETFEHSGLVSVLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTFAH 60
QY 61 LEIREDTGVCAGADQSPESLQKALKEGVILGVKTSRFLCORPDGALYGSLEHFDPEA 120
DB 61 LEIREDTGVCAGADQSPESLQKALKEGVILGVKTSRFLCORPDGALYGSLEHFDPEA 120
QY 121 CSFRELLEEDGVNYVQSEAHGLPLHLPGNKGSPHRDPAPRGPARFLPLGLPALPEPPGI 180
DB 121 CSFRELLEEDGVNYVQSEAHGLPLHLPGNKGSPHRDPAPRGPARFLPLGLPALPEPPGI 180
QY 181 LAPQPDVGSDDPLSMVGFSGQSRSPSYAS 209
DB 181 LAPQPDVGSDDPLSMVGFSGQSRSPSYAS 209

RESULT 2
FGFL MOUSE STANDARD; PRT; 210 AA.
ID FGFL MOUSE STANDARD; PRT; 210 AA.
AC Q9JUN1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Fibroblast growth factor-21 precursor (FGF-21).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadohira K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

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RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also
CC expressed in the thymus at lower levels.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB025718; BAA99416.1; -
CC EMBL; AK007574; BAB25115.1; -
CC HSP; P03968; IBAR.
CC MGD; MGI:1861377; Fgf21.
CC InterPro; IPR008996; Cytok IL1-like.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; IL1HBGF.
CC PRODOM; PD000831; IL1 HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 210
FT SEQUENCE 210 AA; 23237 MW; AB02AAB6477E6F0 CRC64;

Query Match 71.3%; Score 793.5; DB 1; Length 210;
Best Local Similarity 78.9%; Pred. No. 1.8e-51;
Matches 157; Conservative 10; Mismatches 31; Indels 1; Gaps 1;

QY 12 GLWYS-VLAGLLGACQAHPIPDSSPLLQFGQVQRQRYLYTDDAQQTFAHLEIREDTGTVG 70
DB 12 GLWYRLLLAVELLGVYQAYIPDSSPLLQFGQVQRQRYLYTDDAQQTFAHLEIREDTGTV 71
QY 71 GAADQSPESLQKALKEGVILGVKTSRFLCORPDGALYGSLEHFDPEACSFRELLEL 130
DB 72 GAHRSPELLELXALKEGVILGVKASRFLCQPDGALYGSLEHFDPEACSFRELLEL 131
QY 131 GYNYVQSEAHGLPLHLPGNKGSPHRDPAPRGPARFLPLGLPALPEPPGILAPQPDVGS 190
DB 132 GYNYVQSEAHGLPLHLPGNKGSPHRDPAPRGPARFLPLGLPALPEPPGILAPQPDVGS 191
QY 191 SDPLSMVGFSGQSRSPSYAS 209
DB 192 SDPLSMVGFSGQSRSPSYAS 210

RESULT 3
FGFJ HUMAN STANDARD; PRT; 216 AA.
ID FGFJ HUMAN STANDARD; PRT; 216 AA.
AC O95750;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibroblast growth factor-19 precursor (FGF-19) (UNQ0334/PRO0533).
GN FGF19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99132028; PubMed=9931477;
RA Nishimura T., Utsunomiya Y., Hoshikawa M., Ohuchi H., Itoh N.;
RT "Structure and expression of a novel human FGF, FGF-19, expressed in

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Wed Mar 3 08:19:48 2004

the fetal brain.";
 RL Biochim. Biophys. Acta 1444:148-151(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RA Xie M.-H., Holcomb I., Deuel B., Dowd P., Huang A., Vagts A.,
 RA Foster J., Brush J., Gu Q., Liang J., Hillan K., Goddard A.,
 RA Gurney A.L.;
 RT "FGF-19, a novel fibroblast growth factor with unique specificity for
 RT FGF4.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin L.B., Ioshizuka S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May be involved in brain development during
 CC embryogenesis.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed only in fetal brain.
 CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC
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 CC
 CC EMBL; AB018122; BAA75500.1; -
 CC EMBL; AF110400; AAD45973.1; -
 CC EMBL; AY358302; AAQ88669.1; -
 CC EMBL; BC017664; AAH17664.1; -
 CC HSP; P09038; IBFG.
 CC Genew; HGNC:3675; FGF19.
 CC MIM; 603891; -
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC InterPro; IPR008996; Cytok_III_like.

DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; IL1_HBGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KW Growth factor; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 216 FIBROBLAST GROWTH FACTOR-19.
 SQ SEQUENCE 216 AA; 24002 MW; E0BCBC9C220F9832 CRC64;
 Query Match 23.8%; Score 265; DB 1; Length 216;
 Best Local Similarity 36.3%; Pred. No. 8.5e-13;
 Matches 77; Conservative 27; Mismatches 82; Indels 26; Gaps 9;
 QY 11 SGLWVSVLAGLLIGACQAHPIPDSSPLQF--GGVQRVLYTDDAQ-QTEAHLREEDG 67
 DB 14 AGLWLAV-AGRPLA-----FSDAGPHVHYGWDPIRLRHLYTSGPHGLSCFLIRADG 66
 QY 68 TVGGAADQSPESILQLKALPGVIQLGVKTSFLCQRPDGPALYGSIHFDPEACSFRELL 127
 DB 67 VDCARQGSASHLSLEIKAVLRITVAIKGVHSVRYLCMGADGKMGQLLYSEEDCAFEET 126
 QY 128 LEDGVNYVQSEAHGLPLHLPNGKSPHRDPAPRGPALPLPLCLPALP---EPGI--- 180
 DB 127 RPDGVNVRSEKHLRPLVSLSSAKQ-RQLYKNRG---FLPLSHFLPLMLPMVPEEDLRGH 182
 QY 181 ----LAPQPPDVGSDDPLSMV-GPSQGRSPSY 207
 DB 183 LESDMFSSPLETSDMDPFGLVLTGLEAVRSPSF 214
 RESULT 4
 PFNM_MOUSE
 ID FGM_MOUSE STANDARD; PRT; 251 AA.
 AC Q9BPC2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibroblast growth factor-23 precursor (FGF-23).
 GN FGF23.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20490027; PubMed=11032749;
 RA Yamashita T., Yoshioka M., Itoh N.;
 RT "Identification of a novel fibroblast growth factor, FGF-23,
 RT preferentially expressed in the ventrolateral thalamic nucleus of the
 RT brain.";
 RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/c; TISSUE=Embryo;
 RX MEDLINE=20517346; PubMed=11062477;
 RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J.,
 RA Lorenz-Depiereux B., Grabowski M., Meitinger T., Strom T.M.;
 RT "Autosomal dominant hypophosphataemic rickets is associated with
 RT mutations in FGF23.";
 RL Nat. Genet. 26:345-348(2000).
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- TISSUE SPECIFICITY: Mainly expressed in the brain and thymus at
 CC low levels. In brain; preferentially expressed in the
 CC ventrolateral thalamic nucleus.
 CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC
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 CC
 CC EMBL; AB018122; BAA75500.1; -
 CC EMBL; AF110400; AAD45973.1; -
 CC EMBL; AY358302; AAQ88669.1; -
 CC EMBL; BC017664; AAH17664.1; -
 CC HSP; P09038; IBFG.
 CC Genew; HGNC:3675; FGF19.
 CC MIM; 603891; -
 CC GO; GO:0007399; P:neurogenesis; TAS.
 CC InterPro; IPR008996; Cytok_III_like.

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EMBL; AB037889; BAB13478.1; -
EMBL; AF263536; AAG09916.1; -
PIR; JC7513; JC7513.
HSP; P03968; IBAR.
MGD; MGI:1891427; Fgf23.
InterPro; IPR008996; Cytok IL1_like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1_HBGF; 1.
SMART; SM00442; FGF; 1.
ProSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 251
FT SEQUENCE 251 AA; 27757 MW; 110C1F2C735DC360 CRC64;
SQ

Query Match 22.4%; Score 249.5; DB 1; Length 251;
Best Local Similarity 35.1%; Pred. No. 1.4e-11;
Matches 73; Conservative 27; Mismatches 85; Indels 23; Gaps 8;

QY 12 GLWVSVLAGLLGACQ---AHPIPDSSPLL--QFGQVQRQRYLYTDDAQOQTEAHLEIRE 66
Db 3 GTCRLVGVLCVCSIGTARAYEDTSPLLGNSWGLT---HLVTATA-RTSYHLQIHRD 58
QY 67 GTVGGADQSPESLLQKALKPGVIOILGVKTSRFLCQPDGALYGLSHDFPEACSFREL 126
Db 59 GHVDGTPTHTIYSALMITSDEAGSVITGAMTRFLCMLDRLGNIFGSHFSPENCKRQW 118
QY 127 LLEDGVNYQSEAHGLPLHLPGNK---SPHRDPAPRGAPRL-----PLPGLPPALPEP 177
Db 119 TLENGYDVLSQKHVYLSGRKRIFFQGTNPFPF--SQFLARNEVPLLFHYTARPR 176
QY 178 PGILAPQPPDVGSSDPLSMVGPQGRSP 205
Db 177 HTRSAEDPPE---RDPLNLKPRPRATP 201

RESULT 5
FGFN RAT
ID FGFN RAT STANDARD; PRT; 251 AA.
AC Q8VI82;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23).
GN FGF23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.
RT "Rattus norvegicus fgf23.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 251
FT SEQUENCE 251 AA; 27911 MW; 35A229E1B3900593 CRC64;
SQ

Query Match 21.2%; Score 235.5; DB 1; Length 251;
Best Local Similarity 34.1%; Pred. No. 1.4e-10;
Matches 71; Conservative 28; Mismatches 86; Indels 23; Gaps 8;

QY 12 GLWVSVLAGLLGACQ---AHPIPDSSPLL--QFGQVQRQRYLYTDDAQOQTEAHLEIRE 66
Db 3 GACRLVGVLCVCSIGTARAYSDTSPLLGNSWGLT---HLVTATARN--YHLQIHRD 58
QY 67 GTVGGADQSPESLLQKALKPGVIOILGVKTSRFLCQPDGALYGLSHDFPEACSFREL 126
Db 59 GHVDGTPTHTIYSALMITSDEAGSVVIGAMTRFLCMLDRLGNIFGSHFSPENCKRQW 118
QY 127 LLEDGVNYQSEAHGLPLHLPGNK---SPHRDPAPRGAPRL-----PLPGLPPALPEP 177
Db 119 TLENGYDVLSQKHVYLSGRKRIFFQGTNPFPF--SQFLARNEVPLLFHYTARPR 176
QY 178 PGILAPQPPDVGSSDPLSMVGPQGRSP 205
Db 177 HTRSAEDPPE---RDPLNLKPRPRATP 201

RESULT 6
FGFN HUMAN
ID FGFN HUMAN STANDARD; PRT; 251 AA.
AC Q9GZV9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibroblast growth factor-23 precursor (FGF-23) (Tumor-derived hypophosphatemia inducing factor) (UNQ3027/PRO9828).
GN FGF23 OR HYPP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20490027; PubMed=11032749;
RA Yamashita T., Yoshio M., Itoh N.;
RT "Identification of a novel fibroblast growth factor, FGF-23, preferentially expressed in the ventrolateral thalamic nucleus of the brain.";
RL Biochem. Biophys. Res. Commun. 277:494-498(2000).
RN [2]
RP SEQUENCE FROM N.A., VARIANTS ADHR GLN-176; GLN-179 AND TRP-179, AND VARIANT MET-239.
RX MEDLINE=20517346; PubMed=11062477;
RA White K.E., Evans W.E., O'Riordan J.L.H., Speer M.C., Econs M.J., Lorenz-DePiereux B., Grabowski M., Meitinger T., Strom T.M.;
RT "Autosomal dominant hypophosphataemic rickets is associated with mutations in FGF23.";
RL Nat. Genet. 26:345-348(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21267444; PubMed=11344269;
RA Shimada T., Mizutani S., Muto T., Yoneya T., Hino R., Takeda S., Takeuchi Y., Fujita T., Fukumoto S., Yamashita T.;
RT "Cloning and characterization of FGF23 as a causative factor of tumor-induced osteomalacia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6500-6505(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
-1- SUBCELLULAR LOCATION: Secreted (Potential).
-1- DISEASE: Defects in FGF23 are the cause of autosomal dominant
hypophosphataemic rickets (ADHR) [MIM:193100]. ADHR is
characterized by low serum phosphorus concentrations, rickets,
osteomalacia, leg deformities, short stature, bone pain and dental
abscesses.
-1- SIMILARITY: Belongs to the heparin-binding growth factors family.

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EMBL; AB037973; BAB13477.1; -;
EMBL; AF263537; AAG09917.1; -;
EMBL; AB047858; BAB58889.1; -;
EMBL; AY358323; BAA088689.1; -;
HSSP; P03968; 1AFC.
DR GENE; HGNC:3680; FGF23.
DR MIM; 605380; -;
DR MIM; 193100; -;
DR GO; GO:0005615; C:extracellular space; NAS.
DR GO; GO:0030154; P:cell differentiation; NAS.
DR GO; GO:0008996; Cytok IL1-like.
DR InterPro; IPR008996; Cytok IL1-like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1_HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE NEG.
KW Growth factor; Signal; Disease mutation; Polymorphism.
FT SIGNAL 1 24 POTENTIAL
FT CHAIN 25 251 FIBROBLAST GROWTH FACTOR-23.
FT VARIANT 176 176
FT VARIANT 179 179
FT VARIANT 179 179
FT VARIANT 239 239
FT VARIANT 239 239
FT SEQUENCE 251 AA; 27954 MW; 6093BD0C50C2489 CRC64;
Query Match 20.0%; Score 222.5; DB 1; Length 251;
Best Local Similarity 30.8%; Pred. No. 1.3e-09;
Matches 68; Conservative 36; Mismatches 70; Indels 47; Gaps 9;
13 LWSVSLAGLL-LGACQAHPTDPSPLL--PFGGQVORVLYTDDAQOATEAHLREIDGTV 69
8 LWCALCSVCMSVIRAY--PNASPLIGSSWGLI--HLYTAFARN--YHLQHKNGHV 61
70 GGAADQSPESLQLKLPKGVQILGVKTSRFLCORPDGALYGLSHLFDPCACSFRELLLE 129
62 DGAPHQTIYSALMRSEADAGFVITGVMSRYLWDFRGNFGSHYDFDPCRCFQHTLE 121
130 DGVNVYQSEAHGLPHLPLGNKSPHRDPAPGPAFLPLGLPGALPEPP----- 178
122 NGYDVTHSPQYHFLVSL-----GRAKRAFLPGMNP-----PPYSQFLSRNEI 164

179 ---GILAPOP-----PDVGSDDLPLSMVGPSCQGRSPSYAS 209
165 PLIHENTPPIRHRTRSAEDSDERDLNVLKPRARMTAPAS 205
RESULT 7
FGFP_MOUSE STANDARD; PRT; 218 AA.
ID FGFP_MOUSE
AC O35622;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibroblast growth factor-15 precursor (FGF-15).
GN FGF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9745424; PubMed=9310317;
RA McWhirter J.R., Goulding M., Weiner J.A., Chun J., Murie C.;
RT "A novel fibroblast growth factor gene expressed in the developing
nervous system is a downstream target of the chimeric homeodomain
oncoprotein E2A-Pbx1".
RL Development 124:3221-3232 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Bojunga N., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gnarowski P.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";


```
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=89239468; PubMed=2470007;
RA Brooks S., Smith R., Casey G., Dickson C., Peters G.;
RT "Sequence organization of the human int-2 gene and its expression in
RT teratocarcinoma cells.";
RL Oncogene 4:429-436(1989).
CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC or send an email to license@isb-sib.ch).
CC EMBL: X14445; CAA32615.1; -.
DR PIR: S04742; S04742.
DR HSP; P31371; IG82.
DR Genew; HGNC:3681; FGF3.
DR MIM; 164950; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR PROTO-ONCOGENE; Growth factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 17
FT CHAIN 18 239
FT CARBOHYD 65
FT SEQUENCE 239 AA; 26886 MW; 8DBEF17D2B2E3C63 CRC64;
SQ
Query Match 15.9%; Score 177.5; DB 1; Length 239;
Best Local Similarity 29.7%; Pred. No. 2.4e-06;
Matches 51; Conservative 23; Mismatches 57; Indels 41; Gaps 6;
QY 41 GQGVQRVLYTDDAQOQTEAHLEIREDTGVAADQSPESLLQKALPGVILGKTSR 100
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
40 GGAPEPRKLYC----ATKYLQHPSGRVNGSLNSAYSILTEITAVEGVIAIRGLFSGR 95
QY 101 FLCQPDGALYGLHFDPAACSFRELLLDGQVNVYQSEAHGLPLPGNKSHPDRPAP-- 158
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
96 YLAMNKRGLYASRHSAB-CEVERIHELGYNTYASRLYRTVSSTPGAR---RQPSAER 151
QY 159 -----RGPAP-----FLP-----LPGLPPALPEPPG 179
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
152 LNVSVNGKGRPRGPKTRTKQSLFLPRVLDHDMVRLQSLGPPPG 203
RESULT 10
FGF4_BOVIN
ID_FGF4_BOVIN STANDARD; PRT; 206 AA.
AC P48803;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibroblast growth factor-4 precursor (FGF-4) (Heparin secretory
DE transforming protein) (HST) (HBGF-4).
GN FGF4 OR HST.
OS Bos taurus (Bovine).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=96032369; PubMed=7557455;
RA Yu J.C., Dessebra A.J., Wang L.M., Fleming T.P., Chedid M.,
RA Miki T., Heidaran M.A.;
RT "An unexpected transforming gene in calf-thymus carrier DNA: bovine
RT hst.";
RL Gene 162:333-334(1995).
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC or send an email to license@isb-sib.ch).
CC EMBL: U15969; AAA91622.1; -.
DR HSP; P31371; IG82.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR PROTO-ONCOGENE; Growth factor; Mitogen; Signal.
FT SIGNAL 1 29
FT CHAIN 30 206
FT SEQUENCE 206 AA; 22041 MW; F9B7A8606E56613 CRC64;
SQ
Query Match 15.9%; Score 177; DB 1; Length 206;
Best Local Similarity 32.1%; Pred. No. 2.2e-06;
Matches 52; Conservative 23; Mismatches 75; Indels 12; Gaps 5;
QY 14 WSVIAGLILGACQAHPIEDSPILLQFGQV-----RQVLYTDDAQOQTEAHLEIREDTG 68
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
46 WESLVAASLSLAGLPVAAQPKAAVQSGAGDYLGLKRLRLYCNVG--IGFHLQVLPDGR 103
QY 69 VGGAAQSPESLLQKALPGVILGKTSRFLCQRPDGLYGLHFDPAACSFRELL 128
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
104 IGVHADTSDLSLELSPVERGVSVIFGVASFFVAMSSRGLYGSFPFTDE-CRPREILL 162
QY 129 EDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAKPGAPARELP 166
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
163 PNNYNAYCEDRHPGPFIALSKNGKAKNGKRVSPMKVTHFLP 204
RESULT 11
FGF6_HUMAN
ID_FGF6_HUMAN STANDARD; PRT; 208 AA.
AC P10767;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibroblast growth factor-6 precursor (FGF-6) (HST-2).
GN FGF6 OR HST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91360279; PubMed=1886714;
RA Coulier F., Batoz M., Marics I., de Lapeyriere O., Birnbaum D.;
RT "Putative structure of the FGF6 gene product and role of the signal
RT peptide.";
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QY      85 ALKPGVQILGVKTSRFLQCPDGLYGLSHLHFDPEACSFRELLLEGGYNYQSEAH-----140
Db      123 AVSQGIVGIRGVFNSKFLAMSKKGLHASAKFTDD--CKFRERFOESYNTYASIAHRTK 181
QY      141 -GLPLHLPGNKSHPRDAPRG-----PAREFLP-----LPGLP-----PALPEPP 178
Db      182 TGREWYVALNK---RGKAKGCSPRVKPQHVSHFLPRFKQSEQPELSFTVTVPKKKPP 238
QY      179 GILAPOPPDVGSSDPLSMVGPQGRSPS 206
Db      239 ---RPWKPKV-----PLS---PSR-RSPS 255

RESULT 15
ID_FGF4_CHICK STANDARD; PRT; 194 AA.
AC P48804; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE Fibroblast growth factor-4 precursor (FGF-4) (HBGF-4).
GN FGF4 OR FGF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
ON NCBI_TaxID=9031;
RX SEQUENCE FROM N.A. (ISOFORM LONG).
RA MEDLINE=95021713; PubMed=7935794;
RT "A positive feedback loop coordinates growth and patterning in the
RL Nature 371:609-612(1994).
CC -!- FUNCTION: MAY BE THE ENDOGENOUS RIDGE SIGNAL FOR LIMB DEVELOPMENT.
CC RECIPROCAL INTERACTIONS MAY CREATE A POSITIVE FEEDBACK LOOP
CC BETWEEN SONIC HEDGEHOG (SHH) AND FGF4.
CC -!- TISSUE SPECIFICITY: POSTERIOR RIDGE.
CC -!- INDUCTION: BY retinoic acid.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U14654; AAA58706.1; -.
CC PIR; S78506; I50710.
CC HSSP; P09038; 1BFF.
CC InterPro; IPR008996; Cytok IL1-like.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; IL1HBGF.
CC ProDom; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Mitogen; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 194 FIBROBLAST GROWTH FACTOR-4.
SQ SEQUENCE 194 AA; 21642 MW; 5D44245BE97E664A CRC64;

Query Match 14.8%; Score 165; DB 1; Length 194;
Best Local Similarity 27.3%; Pred. No. 1.6e-05;
Matches 53; Conservative 29; Mismatches 68; Indels 44; Gaps 7;

QY      11 SGLWVSLVAGLL-LGACQAHPIP-----DSSP 36
Db      5 AALLPALLGLLWPGAVRGPPGRLPPGPRQRWDAAALFARSVARLPAERDAARDGY 64

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QY      37 LILQFGQVRQRYLYTDDAQQTAAHLEIRDEGTVGGAADQSPESLLQKALKKPGVTOILGV 96
Db      65 LL--GKRLRLYCNVG--IGFHIQVLPDGRIDGIHSENRYSLLEISPVRGVWIFGV 119
QY      97 KTSRFLQCPDGLYGLSHLHFDPEACSFRELLLEGGYNYQSEAH-GLPLHLPGN---KSP 152
Db      120 RSLGFLVAMNSKGLYGSTHVNDK-CKFKELLFPNNYNAYESRIYPGMYIALSKNGRTKKG 178
QY      153 HRDPAPRGPARFLP 166
Db      179 NKVSPMTVTTHLP 192

RESULT 16
ID_FGF5_MOUSE STANDARD; PRT; 264 AA.
AC P15656; O88925;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5).
GN FGF5 OR FGF-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX SEQUENCE FROM N.A. (ISOFORM LONG).
RA MEDLINE=90201563; PubMed=2318343;
RT "Isolation of cDNAs encoding four mouse FGF family members and
RL characterization of their expression patterns during embryogenesis."
RN Dev. Biol. 138:454-463(1990).
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=C57BL/6;
RX MEDLINE=91045929; PubMed=1700424;
RA Haub O., Drucker B., Goldfarb M.;
RT "Expression of the murine fibroblast growth factor 5 gene in the
RT adult central nervous system."
RL Proc. Natl. Acad. Sci. U.S.A. 87:8022-8026(1990).
RN (3)
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RA MEDLINE=99003286; PubMed=9786939;
RX Ozawa K., Suzuki S., Asada M., Tomooka Y., Li A.J., Yoneda A.,
RA Komi A., Imamura T.;
RT "An alternatively spliced fibroblast growth factor (FGF)-5 mRNA is
RT abundant in brain and translates into a partial agonist/antagonist for
RT FGF-5 neurotrophic activity."
RL J. Biol. Chem. 273:29262-29271(1998).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P15656-1; Sequence=Displayed;
CC Name=Short; Synonym=FGF-5S;
CC IsoId=P15656-2; Sequence=VSP_001520, VSP_001521.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC
CC EMBL; M30643; AAA96698.1; -.
CC EMBL; M37823; AAB02660.1; -.
CC EMBL; M37821; AAB02660.1; JOINED.
CC EMBL; M37822; AAB02660.1; JOINED.
CC EMBL; M37821; AAB02659.1; ALT SEQ.
CC EMBL; AB016516; BAA33737.1; -.
CC PIR; A36207; A36207.

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HSP; P09038; 1BFG.
MGI:95519; FGF5.
InterPro; IPR008996; Cytok IL1 like.
InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.
PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1_HBGF; 1.
SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HGF FGF; 1.
KW Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 264 FIBROBLAST GROWTH FACTOR-5.
FT DOMAIN 53 59 POLY-SER.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 118 121 ILEI -> QIVG (in isoform Short).
FT VARSPLIC 122 264 /FTId=VSP_001520.
FT Missing (in isoform Short).
FT /FTId=VSP_001521.
FT SEQUENCE 264 AA; 29103 MW; FGA9C8153EE923D1 CRC64;
Query Match 14.7%; Score 164; DB 1; Length 264;
Best Local Similarity 28.6%; Pred. No. 2,6e-05;
Matches 58; Conservative 25; Mismatches 78; Indels 42; Gaps 7;
QY 34 SSPLQLFGQVQRQLYLTDAAQTEA-----HLEIRDGVGGADQSPESLIQLK 84
DB 63 ASFGSGSGSEHSSFWQSPSGRRGTGLYCRVIGFHLQIYDPGVKNGSHEASVLSILEIF 122
QY 85 ALKPGVQILGVKTRFLCORPDGALYGLSLHFDPEACSFRELLLEDGVNVYQSEAH--- 140
DB 123 AVSQGIVGIRGVFSNKKFLAMSKKKGLHSAKFTDD-CKFRERFQNSVNTYASAIHRTK 181
QY 141 -GLPLHLPCKNSPHRDPAPRG-----PARFLP-----LFLGPLALPEPPGILAP 183
DB 182 TGREWTVALNK---RGKARGCSPRVKQHVHSTHFLPRFKQSEQLSFTVTVPKKPP 238
QY 184 QPDDVGSDFLSVMVGFSGQSRPS 206
DB 239 VKPKVPLSQP-----RRSPS 253
RESULT 17
ID_FGF_XENLA STANDARD; PRT; 192 AA.
AC P48806; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DR 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor 4-II precursor (FGF-4-II) (HBGF-4-II)
DS Embryonic fibroblast growth factor II) (XFGF-II).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
NCBI TaxID=8355;
RX [1]
RX MEDLINE=92315916; PubMed=1618138;
RA Isaacs H.V., Tannahill D., Slack J.M.W.;
RT "Expression of a novel FGF in the Xenopus embryo. A new candidate
RT inducing factor for mesoderm formation and anteroposterior
RT specification."
RL Development 114:711-720(1992).
CC -!- FUNCTION: GOOD CANDIDATE FOR AN INDUCING FACTOR WITH POSSIBLE
CC ROLES BOTH IN MESODERM INDUCTION AT THE BLASTULA STAGE AND IN THE
CC FORMATION OF THE ANTEROPOSTERIOR AXIS AT THE GASTRULA STAGE.
CC -!- SUBCELLULAR LOCATION: Secreted (probable).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC (HST) AND FROM KARPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC	
CC ACTIVITY.	
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
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CC use by non-profit institutions as long as its content is in no way	
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CC or send an email to license@isb-sib.ch).	
CC -----	
CC EMBL; J02986; AAB59555.1; -	
CC EMBL; M17446; AAB59473.1; -	
CC PIR; A28417; TVHUS.	
CC PDB; 1I17; 15-AUG-01.	
CC Genew; HGNC:3682; FGF4.	
CC MIM; 164980; -	
CC GO; GO:0005576; C:extracellular; TAS.	
CC GO; GO:0008083; F:growth factor activity; TAS.	
CC GO; GO:0007267; P:cell-cell signaling; TAS.	
CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.	
CC GO; GO:0007165; P:signal transduction; TAS.	
CC InterPro; IPR008996; Cytok III like.	
CC InterPro; IPR002348; IL1_HBGF.	
CC Pfam; PF00167; FGF; 1	
CC PRINTS; PR00262; IL1HBGF.	
CC PRODOM; PD000831; IL1_HBGF; 1.	
CC SMART; SM00442; FGF; 1.	
CC PROSITE; PS00247; HBGF FGF; 1.	
KW Proto-oncogene; Growth factor; Mitogen; Signal; 3D-structure.	
FT SIGNAL 1 27 POTENTIAL.	
FT CHAIN 28 206 FIBROBLAST GROWTH FACTOR-4.	
SQ SEQUENCE 206 AA; 22047 MW; CTFD54A0272A1569 CRC64;	
Query Match 14.7%; Score 163.5; DB 1; Length 206;	
Best Local Similarity 36.9%; Pred. No. 2.2e-05;	
Matches 41; Conservative 19; Mismatches 46; Indels 5; Gaps 3;	
Qy 60 HLETRDVTGGAADQSPESLLQKALPGVQILGVTSFLCPDPGALYGLSHDPPE 119	
Db 95 HLAQLEDGRIGCAHADTRDSLLSLSPVGVSVIFGVASRFVAMSSKGKLYGSPFFTDE 154	
Qy 120 ACSREILLEGYNYQSEAH-GLPLHLPGN--KSPHRDPAKPGPARFLP 166	
Db 155 -CTFKEILLPNNAYESIKYTPGMFIALSKNGTKKGNVSVPTMKVTHFLP 204	
RESULT 19	
FGFK_HUMAN	
ID FGFK_HUMAN STANDARD; PRT; 211 AA.	
AC Q9NFP5;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Fibroblast growth factor-20 (FGF-20).	
GN FGF20.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=20374469; PubMed=10913340;	
RA Kirikoshi H., Sagara N., Saitoh T., Tanaka K., Sekihara H.,	
RA Shikawa K., Katoh M.	
RT "Molecular cloning and characterization of human FGF-20 on chromosome	
RT 8p21.3-p22."	
RL Biochem. Biophys. Res. Commun. 274:337-343(2000).	
RP [2]	
RP SEQUENCE FROM N.A.	
RA Itoh N.	
RP Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.	
RESULT 20	
FGF3_BRARE	
ID FGF3_BRARE STANDARD; PRT; 256 AA.	
AC P48802;	
DT 01-FEB-1996 (Rel. 33, Created)	
DT 01-FEB-1996 (Rel. 33, Last sequence update)	
DT 01-NOV-1997 (Rel. 35, Last annotation update)	
DE Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3).	
GN FGF3 OR FGF-3.	
OS Brachydanio rerio (Zebrafish) (Danio rerio).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC Cyprinidae; Danio.	
OX NCBI_TaxID=7955;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=96204005; PubMed=8622866;	
RA Kiefer P., Strahle U., Mason I., Dickson C.;	
RT "Secretion and mitogenic activity of zebrafish FGF3 reveal	
RT intermediate properties relative to mouse and Xenopus homologues."	
RL Oncogene 12:1503-1511(1996).	
CC -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).	
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.	
CC -----	
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CC -----	
CC EMBL; AB044277; BAB03633.1; -	
CC EMBL; AB030648; BAB03530.1; -	
CC PIR; JC7353; JC7353.	
CC HSSP; P31371; IG82.	
CC Genew; HGNC:3677; FGF20.	
CC MIM; 605558; -	
CC GO; GO:0005576; C:extracellular; TAS.	
CC GO; GO:0005625; C:soluble fraction; TAS.	
CC GO; GO:0007267; P:cell-cell signaling; TAS.	
CC GO; GO:0007165; P:signal transduction; TAS.	
CC InterPro; IPR008996; Cytok III like.	
CC InterPro; IPR002348; IL1_HBGF.	
CC Pfam; PF00167; FGF; 1	
CC PRINTS; PR00262; IL1HBGF.	
CC PRODOM; PD000831; IL1_HBGF; 1.	
CC SMART; SM00442; FGF; 1.	
CC PROSITE; PS00247; HBGF FGF; 1.	
KW Growth factor.	
SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;	
Query Match 14.5%; Score 161; DB 1; Length 211;	
Best Local Similarity 33.1%; Pred. No. 3.4e-05;	
Matches 53; Conservative 19; Mismatches 64; Indels 24; Gaps 6;	
Qy 32 PDSSPLQFGQVQRVLYTDDAQTEAHLEIREDTGVGGA-ADQSPESLLQKALPGV 90	
Db 52 PGAQAHLHGIILRRRLQYC----RTGFHLQILPDGVSQGTRODHSIFGILFISVAVGL 107	
Qy 91 IQILGVKTSFLCPDPGALYGLSHDPPEACSFLELLEDGYNVYQSEAH-----GLPLH 145	
Db 108 VSRGVDSGLYGLNDKGLYGSSEKLTSE-CIFREQFEENWYNTSSNIYKHGDTGRYF 166	
Qy 146 LPGNKSPHRDPAKPGPAR-----FLPLGLPPALPE 176	
Db 167 VALNK----DGTTRDGRGSRKHQKFTFLPRPVDPERVPE 202	
RESULT 20	
FGF3_BRARE	
ID FGF3_BRARE STANDARD; PRT; 256 AA.	
AC P48802;	
DT 01-FEB-1996 (Rel. 33, Created)	
DT 01-FEB-1996 (Rel. 33, Last sequence update)	
DT 01-NOV-1997 (Rel. 35, Last annotation update)	
DE Fibroblast growth factor-3 precursor (FGF-3) (HBGF-3).	
GN FGF3 OR FGF-3.	
OS Brachydanio rerio (Zebrafish) (Danio rerio).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC Cyprinidae; Danio.	
OX NCBI_TaxID=7955;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=96204005; PubMed=8622866;	
RA Kiefer P., Strahle U., Mason I., Dickson C.;	
RT "Secretion and mitogenic activity of zebrafish FGF3 reveal	
RT intermediate properties relative to mouse and Xenopus homologues."	
RL Oncogene 12:1503-1511(1996).	
CC -!- FUNCTION: POTENT MITOGEN AND TRANSFORMING AGENT (BY SIMILARITY).	
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.	
CC -----	
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QY	179	GILAPQPDVGGSDPFLSMVGFSPQCRSPS	206
	:	:	:
	:	:	:
Db	210	SL-----HDVGETVPKPGVTFSKTSAS	232

RESULT 22

ID	FCF9 HUMAN	STANDARD;	PRT;	208 AA.
AC	P31371;			
DT	01-JUL-1993	(Rel. 26, Created)		
DT	01-OCT-1994	(Rel. 30, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	DE	Glia-activating factor precursor (GAF) (Fibroblast growth factor-9) (FGF-9) (HBGF-9).		
GN	GN	FGF9.		

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain;
RX MEDLINE=93309459; PubMed=8321227;
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property.";
RL Mol. Cell. Biol. 13:4251-4259(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-26 AND 34-54.
RC TISSUE=Glial tumor;
RX MEDLINE=93151105; PubMed=8428960;
RA Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Sasada R.,
RA Kondo T., Kurokawa T.;
RT "Novel secretory heparin-binding factors from human glioma cells
RT (glia-activating factors) involved in glial cell growth.
RT Purification and biological properties.";
RL J. Biol. Chem. 268:2857-2864(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.60 ANGSTROMS).
RX MEDLINE=21127675; PubMed=11223514;
RA Hecht H.-J., Adar R., Hofmann B., Bogin O., Weich H., Yayon A.;
RT "Structure of fibroblast growth factor 9 shows a symmetric dimer with
RT unique receptor- and heparin-binding interfaces.";
RL Acta Crystallogr. D 57:378-384(2001).
CC -!- FUNCTION: May have a role in glial cell growth and differentiation
CC during development, gliosis during repair and regeneration of
CC brain tissue after damage, differentiation and survival of
CC neuronal cells, and growth stimulation of glial tumors.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Glial cells.
CC -!- PTM: Three molecular species were found (30 kDa, 29 kDa and 25
CC kDa), cleaved at Leu-4, Val-13 and Ser-34 respectively. The
CC smaller ones might be products of proteolytic digestion.
CC Furthermore, there may be a functional signal sequence in the 30
CC kDa species which is uncleavable in the secretion step.
CC -!- PTM: N-glycosylated.
CC -!- DISEASE: The continuous overexpression of GAFS may lead to
CC malignant cell growth caused by an autocrine loop.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC -!- DATABASE: NAME=Red Systems' cytokine source book: FGF9;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=199".
CC -----
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CC -----
CC EMBL; D14838; BAA03572.1; -;
DR EMBL; AL139378; CAC17692.1; -;
DR PIR; A48137; A48137.
DR PDB; 1G82; 07-MAR-01.
DR PDB; 1IHK; 02-MAY-01.
DR Genew; HGNC:3687; FGF9.
DR MIM; 600921; -;
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008083; F:growth factor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
KW Glycoprotein; 3D-structure.
FT PROPEP 1 3
FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 79 79 N-LINKED (GLCNAC...).
FT CONFLICT 24 26 VLP -> SLL (IN REF. 2).
FT CONFLICT 34 34 S -> A (IN REF. 2).
FT HELIX 54 61
FT TURN 62 62
FT STRAND 63 68
FT TURN 69 71
FT STRAND 72 76
FT TURN 78 79
FT STRAND 82 85
FT HELIX 91 93
FT STRAND 95 101
FT TURN 102 103
FT STRAND 104 109
FT TURN 110 112
FT STRAND 115 118
FT TURN 120 121
FT STRAND 124 127
FT HELIX 132 134
FT STRAND 136 140
FT STRAND 146 154
FT TURN 156 158
FT STRAND 161 163
FT STRAND 166 166
FT TURN 168 169
FT STRAND 172 172
FT HELIX 175 177
FT TURN 180 181
FT HELIX 183 185
FT STRAND 187 190
FT HELIX 194 196
FT HELIX 198 200
FT TURN 201 202
SQ SEQUENCE 208 AA; 23440 MW; F32A0E7106EF59C9 CRC64;
Query Match 14.1%; Score 157; DB 1; Length 208;
Best Local Similarity 31.2%; Pred. No. 6:5e-05;
Matches 59; Conservative 20; Mismatches 72; Indels 38; Gaps 8;
QY 3 SDETPGHSGLWVSVLAGLLGACQAHPIPDSSPLIQFGQVQRVLYITDDAQTEAHLR 62
DB 34 SDHLGQSEAG-----GLPRG-----PAVTDLHLKGLRRRLQYLC---RTGFHLE 75
QY 63 IREDGTGGA-ADOSPESLLQLKALPGVITQILGVKTSRFLCQRPDGLALYGLHFDPEAC 121
DB 76 IFPNGITQGTQRKHSRFGILEFISIAVLGVSIRGVDSGLYGLMNEKELYSEKLTQE-C 134
QY 122 SFRELLEDGVNYYQSEAH-----GLFLHLPGNKSPHRDPAPGPAPR-----FLPL 167
DB 135 VFREQFENWNYTSSNLYKHVDIGRYYVALNK-----DGTPTREGTRTKRQKFTFLPR 190
QY 168 PGLPPALPE 176
DB 191 PVDPDKVPE 199
RESULT 23
FGF9 RAT ID FGF9 RAT STANDARD; PRT; 208 AA.
AC P36364;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)

01-NOV-1997 (Rel. 35, Last annotation update)
 Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
 (FGF-9) (HBGF-9).
 FGF9 OR FGF-9.
 Rattus norvegicus (Rat).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Brain;
 MEDLINE=93309459; PubMed=8321227;
 Miyamoto M., Naruo K.-I., Sako C., Matsumoto S., Kondo T.,
 Kurakawa T.;
 Molecular cloning of a novel cytokine cDNA encoding the ninth member
 of the fibroblast growth factor family, which has a unique secretion
 property.";
 Mol. Cell. Biol. 13:4251-4259(1993).
 -!- FUNCTION: May have a role in glial cell growth and differentiation
 during development, gliosis during repair and regeneration of
 brain tissue after damage, differentiation and survival of
 neuronal cells, and growth stimulation of glial tumors.
 -!- SUBCELLULAR LOCATION: Secreted.
 -!- TISSUE SPECIFICITY: Brain and kidney.
 -!- PTM: N-glycosylated.
 -!- SIMILARITY: Belongs to the heparin-binding growth factors family.

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 or send an email to license@isb-sib.ch).

 EMBL; D14839; BAA03573.1; --
 HSSP; P31371; IG82.
 InterPro; IPR008996; Cytok IL1_like.
 InterPro; IPR002348; IL1_HBGF.
 DR PFam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; IL1_HBGF; 1.
 DR SMART; SMO0442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor; Differentiation; Mitogen; Heparin-binding;
 Glycoprotein.
 FT PROPEP 1 3 BY SIMILARITY.
 FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
 FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 208 AA; 23413 MW; 4A3CE894DF643EB CRC64;

 Query Match 14.1%; Score 157; DB 1; Length 208;
 Best Local Similarity 31.2%; Pred. No. 6.5e-05;
 Matches 59; Conservative 20; Mismatches 72; Indels 38; Gaps 8;

 QY 3 SDTGFHSGHGVSVIAGLLIGACQAHIPDSSPLPGFGGVRORYLYTDDAQTEAHLE 62
 DB 34 SDHLQSQEAG-----GLPRG-----PAVTDLHKILIRRRQLYC-----RTGFHLE 75

 QY 63 TREDTGVGA-ADQSPESILQLKALKPGVIOILGVKTSRFLCQPDGALYGLSLHFDPEAC 121
 DB 76 IFPNGTIOQTRKDHGRFGILEFISTAVGLSVIRGYDSGLYLGMEKGLYSEKLTQ-C 134

 QY 122 SPRELLLEDGVNYQSEAH-----GLPHLPONKSPHRDPRGPAR-----FLPL 167
 DB 135 VFRQFEENWYNTSYNSLYKHDVTGRRYVALNK---DGTPREGTRTKRQKFTFLPR 190

 QY 168 PGLPPALPE 176
 DB 191 PVEDPKVPE 199

RESULT 24

DR	PROSITE; PS00247; HBGF FGF; 1.	Matches	48; Conservative	12; Mismatches	62; Indels	15; Gaps	5;
KW	Growth factor; Differentiation; Mitogen; Heparin-binding;						
KW	Glycoprotein.						
FT	PROPEP	1	3	BY SIMILARITY.			
FT	CHAIN	4	208	GLIA-ACTIVATING FACTOR.			
FT	CARBOHYD	79	79	N-LINKED (GLNAC...) (POTENTIAL).			
SQ	SEQUENCE	208 AA;	23440 MW;	8BDELEEDFB70979E CRC64;			
	Query Match	14.1%;	Score 156.5;	DB 1;	Length 208;		
	Best Local Similarity	32.0%;	Pred. No. 7.1e-05;				
	Matches	55; Conservative	21; Mismatches	69; Indels	27; Gaps	7;	
QY	23 LGACQAHPIPDSS---SPLLQGGQVRORYLYTDDAQOQTEAHLEIREDTGVGGA-ADQSPH 78						
DB	37 LGQSEAGGLPRGPAVTDLDHLKLRRLQYLC---RTGFHLEIFPNGTIQGTRKHRSF 92						
QY	79 SLQLKALKKPGVIOILGKTSRFLCQPDGALYGLSLHFDPEACSFRELLLEDGNNVYQSE 138						
DB	93 GILFISIAVLGNSIRGVDGLYLGMEKGLYSEKLTQE-CVFRQPFENWNTYSSN 151						
QY	139 AH-----GLPLHLFPGNKSHPHDPAPRGPAPR-----FLPLPLPALPE 176						
DB	152 LYKHVDIGRRYYVALNK---DGTREGTRTKRHKQKTHFLPLRPVDPDKVPE 199						
RESULT 25							
FGF1 MESAU							
ID	FGF1 MESAU STANDARD; PRT; 155 AA.						
AC	P34004; 1994 (Rel. 28, Created)						
DT	01-FEB-1994 (Rel. 28, Last sequence update)						
DT	28-FEB-2003 (Rel. 41, Last annotation update)						
DE	Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (AFGF).						
DE	growth factor) (AFGF).						
GN	FGF1 OR FGF-1.						
OS	Mesocricetus auratus (Golden hamster).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;						
OC	Mesocricetus.						
OX	NCBI_TaxID=10036;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=90270291; PubMed=1693366;						
RA	Hall J.A., Harris M.A., Malark M., Mansson P.E., Zhou H., Harris S.R.;						
RT	"Characterization of the hamster DDT-1 cell afGF/HBGF-I gene and cDNA and its modulation by steroids.";						
RL	J. Cell. Biochem. 43:17-26(1990).						
CC	-!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.						
CC	-!- SUBUNIT: Monomer.						
CC	-!- MISCELLANEOUS: This protein binds heparin, although less strongly than does bFGF.						
CC	-!- SIMILARITY: Belongs to the heparin-binding growth factors family.						
DR	PIR; A60721; A60721.						
DR	HSSP; P05230; 1RML.						
DR	InterPro; IPR008996; Cytok IL1-like.						
DR	InterPro; IPR002348; IL1_HBGF.						
DR	Pfam; PF00167; FGF; 1.						
DR	PRINTS; PR00262; IL1HBGF.						
DR	ProDom; PD000831; IL1_HBGF; 1.						
DR	SMART; SM00442; FGF; 1.						
DR	PROSITE; PS00247; HBGF FGF; 1.						
KW	Growth factor; Mitogen; Angiogenesis; Heparin-binding.						
FT	PROPEP	1	15	BY SIMILARITY.			
FT	CHAIN	16	155	HEPARIN-BINDING GROWTH FACTOR 1.			
FT	BINDING	24	28	HEPARIN (POTENTIAL).			
FT	BINDING	113	116	HEPARIN (POTENTIAL).			
SQ	SEQUENCE	155 AA;	17403 MW;	41ESEC760E412CC5 CRC64;			
	Query Match	14.0%;	Score 155.5;	DB 1;	Length 155;		
	Best Local Similarity	35.0%;	Pred. No. 6.1e-05;				

QY	41 GQVRORYLYTDDAQOQTEAHLEIREDTGVGGAADQSPH-LQLKALKKPGVIOILGKTS 99						
DB	21 GNYKPKLYCSNGGH---FLRILPDGTVDRSDQHIQQLSASAGSEVVIKTEIG 77						
QY	100 RFLCQRPDGLYGLSLHFDPEACSFRELLLEDGNNVYQSEAHGLPLHLPGNKSHPHDPAPR 159						
DB	78 QYLAAMDTSGLLYGS-QTPNEECFLERLEENHYNTYTSKKHAEKNWFGVGLKK--NGSCKR 134						
QY	160 GPAR-----FLPLP 168						
DB	135 GPRTHYGQKAILFLPLP 151						
RESULT 26							
FGF1 MOUSE							
ID	FGF1 MOUSE STANDARD; PRT; 155 AA.						
AC	P10935;						
DT	01-JUL-1989 (Rel. 11, Created)						
DT	01-JUL-1989 (Rel. 11, Last sequence update)						
DT	28-FEB-2003 (Rel. 41, Last annotation update)						
DE	Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast growth factor) (AFGF).						
DE	growth factor) (AFGF).						
GN	FGF1 OR FGF-1 OR FGFA.						
OS	Mus musculus (Mouse), and						
OS	Rattus norvegicus (Rat).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.						
OX	NCBI_TaxID=10090, 10116;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	SPECIES=Mouse;						
RX	MEDLINE=89240051; PubMed=2470029;						
RA	Goodrich S., Yan G.C., Bahrenburg K., Mansson P.E.;						
RT	"The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1)."						
RL	Nucleic Acids Res. 17:2867-2867(1989).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RX	SPECIES=Mouse;						
RX	MEDLINE=90201563; PubMed=2318343;						
RA	Hebert J.M., Basilico C., Goldfarb M., Haub O., Martin G.R.;						
RT	"Isolation of cDNAs encoding four mouse FGF family members and characterization of their expression patterns during embryogenesis.";						
RL	Dev. Biol. 138:454-463(1990).						
RN	[3]						
RP	SEQUENCE FROM N.A.						
RX	SPECIES=Mouse;						
RX	MEDLINE=97128312; PubMed=8972905;						
RA	Madiai F., Hackshaw K.V., Chiu I.M.;						
RT	"Cloning and characterization of the mouse Fgf-1 gene.";						
RL	Gene 179:231-236(1996).						
RN	[4]						
RP	SEQUENCE FROM N.A.						
RX	SPECIES=Mouse; STRAIN=BALB/c;						
RX	MEDLINE=97094746; PubMed=8939980;						
RA	Alam K.Y., Frostholt A., Hackshaw K.V., Evans J.E., Rotter A.,						
RA	Chiu I.M.;						
RT	"Characterization of the 1B promoter of fibroblast growth factor 1 and its expression in the adult and developing mouse brain.";						
RL	J. Biol. Chem. 271:30263-30271(1996).						
CC	-!- FUNCTION: The heparin-binding growth factors are angiogenic agents in vivo and are potent mitogens for a variety of cell types in vitro. There are differences in the tissue distribution and concentration of these 2 growth factors.						
CC	-!- SUBUNIT: Monomer.						
CC	-!- SIMILARITY: Belongs to the heparin-binding growth factors family.						
CC	-!- SIMILARITY: Belongs to the heparin-binding growth factors family.						
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EMBL; X14232; CAA32448.1; -	EMBL; M30641; AAA37618.1; -
EMBL; U36457; AAC52969.1; JOINED.	EMBL; U36457; AAC52969.1; JOINED.
EMBL; U36458; AAC52969.1; JOINED.	EMBL; U67610; AAC52907.1; -
PIR; D37360; D37360.	PIR; S04147; S04147.
HSSP; P05230; LRML.	MGI; MGI:95515; Fgf1.
InterPro; IPR008996; Cytok IL1_like.	InterPro; IPR002348; IL1_HBGF.
Pfam; PF00167; FGF; 1.	PRINTS; PR00262; IL1HBGF.
ProDom; PD000831; IL1_HBGF; 1.	SMART; SM00442; FGF; 1.
PROSITE; PS00247; HBGF_FGF; 1.	Growth factor; Mitogen; Angiogenesis; Heparin-binding.
PROPEP 1	15
CHAIN 16	155
BINDING 24	28
BINDING 113	116
SEQUENCE 155 AA; 17418 MW; 8880E4FF0FAA161 CRC64;	
Query Match	13.9%; Score 154.5; DB 1; Length 155;
Best Local Similarity	34.3%; Pred. No. 7.2e-05;
Matches 48; Conservative 13; Mismatches 64; Indels 15; Gaps 5;	
y	38 LQFGVQVRVLYTDDAQCTEAHLREIDGTGVGAADQSPESL-LQLKALPGVVIQLGV 96
b	18 LPLGNVKKPLLYCSNGH---FLRLPGTVDGTRDSQHIQLQSAESAGEVVIKGT 74
y	97 KTSRFTQCPDPDGGALYGLSHFDPEACFRLELLEDGVNVQSAHGLPLHPGNKSPHRDP 156
b	75 ETGQYLAMTEGLLYGS-QTPNEECFLERLEENHYNTYTSKHAENKMFVGLKK--NGS 131
y	157 APRGPAPR-----PLPLP 168
b	132 CKRGPRTHYGQKAILFLPLP 151
RESULT 27	
GF4 MOUSE	
D	GF4 MOUSE STANDARD; PRT; 202 AA.
C	P11403; P15657;
T	01-JUL-1989 (Rel. 11, Created)
T	01-JUL-1989 (Rel. 11, Last sequence update)
T	28-FEB-2003 (Rel. 41, Last annotation update)
T	Fibroblast growth factor-4 precursor (FGF-4) (K-fibroblast growth factor) (HBGF-4).
E	FGF4 OR FGF-4 OR KFGF.
N	Mus musculus (Mouse).
S	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
O	NCBI TaxID:10090;
X	[1]
X	NCBI TaxID:10090;
R	SEQUENCE FROM N.A.
R	MEDLINE=89296455; PubMed=2740210;
R	Dickson C.;
R	"The mouse homologue of hst/k-FGF: sequence, genome organization and location relative to int-2.;"
R	Nucleic Acids Res. 17:4037-4045(1989).
R	[2]
R	SEQUENCE FROM N.A.
R	MEDLINE=90201563; PubMed=2318343;
R	Hebert J.M., Basilio C., Goldfarb M., Haub O., Martin G.R.;
R	"Isolation of cDNAs encoding four mouse FGF family members and characterization of their expression patterns during embryogenesis.;"
R	Dev. Biol. 138:454-463(1990).

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MEDLINE=20246297; PubMed=10786625;
Yanamoto S., Mikami T., Konishi M., Itoh N.;
"Stage-specific expression of a novel isoform of mouse FGF-14 (FHF-4)
in spermatocytes.";
Biochim. Biophys. Acta 1490:121-124(2000).
-!- FUNCTION: Probably involved in nervous system development and
function.
-!- SURCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=1;
IsoId=p70379-1; Sequence=Displayed;
Name=2; Synonyms=FGF-14C;
IsoId=p70379-2; Sequence=VSP 001530;
-!- TISSUE SPECIFICITY: Brain and testis; widely distributed in the
developing nervous system. In adult, high levels in the granular
layer of the cerebellum, less in hippocampus and olfactory bulb.
-!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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EMBL: U66204; AAB18920.1; -.
EMBL: ABC29498; BAA89483.1; -.
HSSP: P31371; IG82.
MGD: MGI:109189; Fgf14.
InterPro: IPR008996; CytoK IL1 like.
InterPro: IPR002348; IL1_HBGF.
Pfam: PF00167; FGF; 1.
PRINTS: PR00262; IL1HBGF.
ProDom: PD000831; IL1_HBGF; 1.
SMART: SM00442; FGF; 1.
PROSITE: PS00247; HBGF FGF; 1.
Growth factor; Alternative splicing.
FT VARSPILC 1 84
Missing (in isoform 2).
/FTID=VSP_001530.
SQ SEQUENCE 247 AA; 27764 MW; 372C6FCBDC72FDA CRC64;
Query Match 13.7%; Score 153; DB 1; Length 247;
Best Local Similarity 32.7%; Pred.No. 0.00015;
Matches 53; Conservative 21; Mismatches 62; Indels 26; Gaps 7;
QY 60 HLEIRDGTGGADQSPES-LLQLKALKPGVLIQILGKTSRFLCQPDGALYGSLLHFD 118
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
82 YLQMHFPGALDGTGKDDNSTLFLNLPVGLRVAIQGVKTLGYIAMNGEGVLYSELSFT 141
::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
119 EACSFRELLEDGNYVYQS-----EAHGLFLH-----LPQKSGPHRDPA 164
142 E-CKFESVENYVIYSSMLYRQESGRAWFLGNKEGVQMKGNRVKTKTKEA----AHF 196
Dy 165 LPLFGLPPALPEPGHILAPOPPDVGSSDPLSMVGPSQGRSPS 206
197 LPXP-LEVAMYREPSL-----HDVGETVPKAGVTPSKTSAS 232
QY
Dy
RESULT 29
ID_FGFS_HUMAN STANDARD; PRT: 268 AA.
AC P12034; O75846;
DT 01-OCT-1989 (Rel. 12, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
Dy Fibroblast growth factor-5 precursor (FGF-5) (HBGF-5) (Smag-82).
GN FGF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
OX NCBI TaxID=9606;

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DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 268
FT DOMAIN 49 52
FT DOMAIN 55 62
FT DOMAIN 110 110
FT CARBOHYD 120 123
FT VARSPPLIC 124 268
FT VARSPPLIC 124 268
FT Missing (in isoform Short).
FT /FTID=VSP_001518.
FT R -> I (IN REF. 1).
FT CONFLICT 42 42
FT CONFLICT 83 86
FT CONFLICT 86 86
FT PSGR -> LGA (IN REF. 2).
SQ SEQUENCE 268 AA; 29526 MW; 08F4268B26781E9D CRC64;

Query Match 13.7%; Score 153; DB 1; Length 268;
Best Local Similarity 28.1%; Pred. No. 0.00017;
Matches 55; Conservative 27; Mismatches 74; Indels 40; Gaps 8;

QY 34 SSPLQLQFGQ--VRQRYLYTDDAQTEA-----HLEIREDTGVGGAADQSPESL 80
DB 61 SSPAASLQSGSLGEGSQSGFQSGRRRTGSLYCRVIGFHLQIYDPDGKNGSHEANMLSV 120
QY 81 LQKALKPGVQIILGVKTSRFLCQRPDQALYGLSHFDPEACSFRELLLEDGYNVYQSEAH 140
DB 121 LEIFAVSGQVIGIRGVFNKFLAMSKKLHASAKFTDD-CKFRERPOENSNTYASAIH 179
QY 141 -----GLPLHLPGNKSHPDRDPAPRG-----PARPLP-----LPGLPPALPEPG 179
DB 180 RTEKTGWEYVALNK--RGKAKGCSPRVKPQHISTHLPFRKQSEQPELSFTVTYPEK 236
QY 180 ILAPOPDPVSGSDPLS 195
DB 237 KNPPSP--IKSKIPLS 250

RESULT 30
ID FGFG MOUSE STANDARD; PRT; 245 AA.
AC P03377; O35338;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Fibroblast growth factor-13 (FGF-13) (Fibroblast growth factor
DE homologous factor 2) (FHF-2).
GN FGFI3 OR FHF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=96382556; PubMed=8790420;
RA Smallwood P.M., Munoz-Sanjuan I., Tong P., Macke J.P.,
RA Hendry S.H., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.;
RT "Fibroblast growth factor (FGF) homologous factors: new members of
RT the FGF family implicated in nervous system development.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:9850-9857(1996).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=97376484; PubMed=9232594;
RA Hartung H., Feldman B., Lovic H., Coulter F., Birnbaum D.,
RA Goldfarb M.;
RT "Murine FGF-12 and FGF-13: expression in embryonic nervous system,
RT connective tissue and heart.";
RL Mech. Dev. 64:31-39(1997).
CC -!- FUNCTION: Probably involved in nervous system development and
CC function.
CC -!- TISSUE SPECIFICITY: Brain, eye and heart; in embryonic brain,
CC present in all divisions of the central and peripheral nervous
CC system and it is at least 5 times more abundant than other FHPs.

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CC In adult, most abundant in hippocampus.
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC
CC EMBL; U66202; AAB18918.1; -.
CC EMBL; AF020737; AAB71606.1; -.
CC HSSP; P31371; IG82.
CC MGD; MGI:109178; Fgfl3.
CC InterPro; IPR008996; Cytok IL1-like.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; IL1HBGF.
CC PRODOM; PD000831; IL1_HBGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor.
FT CONFLICT 2 2 MISSING (IN REF. 2).
FT CONFLICT 199 199 L -> Q (IN REF. 2).
FT CONFLICT 245 AA; 27617 MW; 5B96D41C190975DD CRC64;
SQ SEQUENCE 245 AA; 27617 MW; 5B96D41C190975DD CRC64;

Query Match 13.7%; Score 152.5; DB 1; Length 245;
Best Local Similarity 23.6%; Pred. No. 0.00017;
Matches 53; Conservative 25; Mismatches 72; Indels 29; Gaps 7;

QY 25 AQAHPTDPSPLQFGQVQRV-----LYTDDAQTEAHLEIREDTGVGGAADQ- 75
DB 37 SCDKNLVNFSRVKLFSGKRRRPPQLKGVTKLYSRQCYHLQADGTIDTKDED 96
QY 76 SPESLLQKALKPGVQIILGVKTSRFLCQRPDQALYGLSHFDPEACSFRELLLEDGYNVY 135
DB 97 STYTLFNLIPVGLRVVALQGVQTKLYLAMNSEGYLYTSEHFTPE-CKFKESVFENYVTV 155
QY 136 -----QSEAHGLPLHL-----PGNKSHPDRDPAPRGPARPLPGLPPALPEPGI 180
DB 156 SSMIVRQQSGRGWYLGKNGEIMKGNHVKNKPA----AHFLKP-LKVAMYKEPSL 209

RESULT 31
ID FGFG HUMAN STANDARD; PRT; 207 AA.
AC O43320;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGFI6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamanoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -!- FUNCTION: Induces hepatocellular proliferation. Has no biological
CC effect on the heart (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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CC -----
 CC EMBL; AB009391; BAA24956.1; -
 CC PIR; JC5941; JC5941.
 CC HSPF; P31371; 1382.
 CC Genew; HGNC:3672; FGF16.
 CC MIM; 603724; -
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0008083; F:growth factor activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0007397; P:histogenesis and organogenesis; TAS.
 CC GO; GO:0008152; P:metabolism; TAS.
 CC GO; GO:0009266; P:response to temperature; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR008996; Cytok IL1-like.
 CC InterPro; IPR002348; IL1_HBGF.
 CC Pfam; PF00167; FGF; 1
 CC PRINTS; PR00262; IL1HBGF.
 CC ProDom; PD000831; IL1_HBGF; 1.
 CC SMART; SM00442; FGF; 1.
 CC PROSITE; PS00247; HBGF_FGF; 1.
 CC Growth factor.
 CC CAROBYD 78 78 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 207 AA; 23759 MW; 78AD160BDA8B5F8 CRC64;

Query Match 13.5%; Score 150.5; DB 1; Length 207;
 Best Local Similarity 32.6%; Pred. No. 0.00019;
 Matches 61; Conservative 20; Mismatches 75; Indels 31; Gaps 8;
 QY 3 SDETFEHSGLWVSVIAGLLIGACQAHPIPPSSPLQFGGVRORYLYTDDAQTEAHLE 62
 DB 28 ADSPGFLNERL-----CQIEGKLGQSGPTDFAHL---KGIILRRQLYC-----RIGFHLE 74
 QY 63 IREDGTWGAA-DQSPESLLQKALKPGVIOILGVKTSRFLCORPDGALYGLSLHFPDPEAC 121
 DB 75 IFPNTGTVGTHDHSRFGILFISLAVGLISIRGVDGSLGLGMNERGELYSKKLTRE-C 133
 QY 122 SFRELLDGVNVYQSEAHGLPLPGNK-----SPHRDPAPRGPAR-----FLPLP 168
 DB 134 VEREQFEENWYNTYAST---LYKHSDSERQYVVALNKGDSREGYRTKRHXQFTFLPRP 190
 QY 169 GLPPALP 175
 DB 191 VDPSKLP 197

RESULT 32
 FGFA HUMAN STANDARD; PRT; 208 AA.
 AC O15520;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Fibroblast growth factor-10 precursor (FGF-10) (Keratinocyte growth
 DE factor 2).
 DE FGF10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=97435285; PubMed=9287324;
 RA Emoto H., Tagashira S., Mattei M.-G., Yamasaki M., Hashimoto G.,
 RA Katsumata T., Negro T., Nakatsuka M., Birnbaum D., Coulier F.,
 RA Itoh N.;
 RT "Structure and expression of human fibroblast growth factor-10.";
 RL J. Biol. Chem. 272:23191-23194 (1997).

RN SEQUENCE FROM N.A.
 RP TISSUE=Lung;
 RC Jimenez P.A., Gruber J.R., Liu B., Feng P., Florence C., Blunt A.,
 RA Huddleston K.A., Telliska M., Alfonso P., Coleman T.A., Ornitz D.M.,
 RA Dillon P.A., Duan R.D.;
 RA "Cutaneous wound healing by keratinocyte growth factor 2.";
 RT Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: COULD BE A GROWTH FACTOR ACTING IN THE PROCESS OF WOUND
 CC HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER
 CC SIMILAR TO FGF-7.
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
 CC -----
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EMBL; AB002097; BAA22331.1; -
 EMBL; U67918; AAB61991.1; -
 PDB; 1NUN; 04-MAR-03.
 Genew; HGNC:3666; FGF10.
 MIM; 602115; -
 GO; GO:0005615; C:extracellular space; TAS.
 GO; GO:0008083; F:growth factor activity; TAS.
 GO; GO:0007397; P:histogenesis and organogenesis; TAS.
 GO; GO:0000074; P:regulation of cell cycle; TAS.
 InterPro; IPR008996; Cytok IL1-like.
 InterPro; IPR002348; IL1_HBGF.
 Pfam; PF00167; FGF; 1.
 PRINTS; PR00262; IL1HBGF.
 ProDom; PD000831; IL1_HBGF; 1.
 SMART; SM00442; FGF; 1.
 PROSITE; PS00247; HBGF_FGF; 1.
 Growth factor; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 37
 FT CHAIN 38 208
 FT DOMAIN 52 62
 FT CAROBYD 51 51 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CAROBYD 196 196 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 208 AA; 23436 MW; COA0705C108680B3 CRC64;
 SQ
 Query Match 13.5%; Score 150; DB 1; Length 208;
 Best Local Similarity 30.4%; Pred. No. 0.00021;
 Matches 41; Conservative 31; Mismatches 49; Indels 14; Gaps 6;
 QY 42 GQVRQRYLYTDDAQTEAHLEIREDTGVGGADQS-PESLLQKALKPGVIOILGVKTSR 100
 DB 75 GDVWRKILFS---FTKYFLKIKKNGKVGSGKNCPSYILEITVSVEIGVAVKAINS 130
 QY 101 FLCQRPDGLYGLSLHFPDPEACSFRELLDGVNVYQSEAHGLPLH-LPGNKSPPRD 155
 DB 131 YLAWNKKGLYGSKEFNND-CKLKERIEGNYNTYASFNWQHNGRQMYVALNGKGPARG 189
 QY 156 PAPR---GPARFLPL 167
 DB 190 QKTRKNTSAHFLPM 204
 RESULT 33
 FGFA RAT STANDARD; PRT; 215 AA.
 ID FGFA RAT
 AC P70492;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibroblast growth factor-10 precursor (FGF-10).
 DE FGF10.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Wistar;
 RA MEDLINE=96279129; PubMed=8663172;
 RA Yamasaki M., Miyake A., Tagashira S., Itoh N.;
 RT "Structure and expression of the rat mRNA encoding a novel member of
 RT the fibroblast growth factor family";
 RL J. Biol. Chem. 271:15918-15921(1996).
 CC -1- FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
 CC HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER
 CC SIMILAR TO FGF-7.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: PREFERENTIALLY EXPRESSED IN THE LUNG IN
 CC ADULTS.
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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 CC EMBL; D79215; BAAL1468.1; -;
 DR HSPF; P31371; IG82.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; IL1_HBGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor; Glycoprotein; Signal.
 KW SIGNAL 1 36 FIBROBLAST GROWTH FACTOR-10.
 FT CHAIN 37 215
 FT DOMAIN 51 69 POLY-SER. (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 215 AA; 24029 MW; 93778EFA6FC0866A CRC64;
 Query Match 13.5%; Score 150; DB 1; Length 215;
 Best Local Similarity 30.4%; Pred. No. 0.0022;
 Matches 41; Conservative 31; Mismatches 49; Indels 14; Gaps 6;
 QY 42 GGVORLYLTDDAQOQTEAHLEIREDTGVGAADQS-PESLLQKALKPGVIOILGVKTSR 100
 Db 82 GGVWRKLFES-----FTKYLTKKNGKVSCTKNECPYSILEITSVEIGWAVKAINSY 137
 QY 101 FLCQRPDGLYSLHDPACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
 Db 138 YLAMNKKGLYSGKEFNND-CKLKERIEENGYNTYASFNWQHNGROMYVALNGKGPARG 196
 QY 156 PAPR---GPARFLPL 167
 Db 197 QKTRRNTSAHFLEPM 211
 RESULT 34
 FGFA MOUSE STANDARD; PRT; 209 AA.
 AC O35565;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibroblast growth factor-10 precursor (FGF-10) (Keratinocyte growth
 DE factor 2).
 GN FGF10.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97473538; PubMed=9332392;
 RA Tagashira S., Harada H., Katsumata T., Itoh N., Nakatsuka M.;
 RT "Cloning of mouse FGF10 and up-regulation of its gene expression
 RT during wound healing";
 RL Gene 197:399-404(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RA Duan D.R., Florence C.;
 RA Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: COULD BE A GROWTH FACTOR ACTIVE IN THE PROCESS OF WOUND
 CC HEALING. ACTS AS A MITOGEN IN THE LUNG. MAY ACT IN A MANNER
 CC SIMILAR TO FGF-7.
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed abundantly in embryos and the lung,
 CC and at much lower levels in brain and heart.
 CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
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 CC EMBL; D89080; BAA22836.1; -;
 DR EMBL; U94517; AAD00761.1; -;
 DR HSPF; P31371; IG82.
 DR MGD; MGI:1099809; Fgf10.
 DR GO; GO:0001759; P:induction of an organ; IMP.
 DR GO; GO:0009887; P:organogenesis; IMP.
 DR InterPro; IPR008996; Cytok IL1 like.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD000831; IL1_HBGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 DR Growth factor; Glycoprotein; Signal.
 KW SIGNAL 1 36 FIBROBLAST GROWTH FACTOR-10.
 FT CHAIN 37 209
 FT DOMAIN 52 63 POLY-SER. (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 209 AA; 23597 MW; 7FD22227BF4943CC CRC64;
 Query Match 13.3%; Score 148; DB 1; Length 209;
 Best Local Similarity 30.4%; Pred. No. 0.0003;
 Matches 41; Conservative 30; Mismatches 50; Indels 14; Gaps 6;
 QY 42 GGVORLYLTDDAQOQTEAHLEIREDTGVGAADQS-PESLLQKALKPGVIOILGVKTSR 100
 Db 76 GGVWRKLFES-----FTKYLTKKNGKVSCTKNECPYSILEITSVEIGWAVKAINSY 131
 QY 101 FLCQRPDGLYSLHDPACSFRELLLEDGYNVYQS---EAHGLPLH--LPGNKSPHRD 155
 Db 132 YLAMNKKGLYSGKEFNND-CKLKERIEENGYNTYASFNWQHNGROMYVALNGKGPARG 190
 QY 156 PAPR---GPARFLPL 167
 Db 191 QKTRRNTSAHFLEPM 205
 RESULT 35
 FGFI HUMAN STANDARD; PRT; 155 AA.
 ID -FGFI HUMAN
 AC P05230; P07502;
 DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
DE growth factor) (AFGF) (Beta-endothelial cell growth factor) (ECGF-
DE beta).
DN FGF1 OR FGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=86261805; PubMed=3523756;
RA Jaye M., Hawk R., Burgess W., Ricca G.A., Chiu I.-M., Ravera M.W.,
RA O'Brien S.J., Modi W.S., Maciag T., Drohan W.N.;
RA "Human endothelial cell growth factor: cloning, nucleotide sequence,
RT and chromosome localization.";
RL Science 233:541-545(1986).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=89343957; PubMed=2474753;
RA Wang W.P., Lehtoma K., Varban M.L., Krishnan I., Chiu I.M.;
RA "Cloning of the gene coding for human class I heparin-binding growth
RT factor and its expression in fetal tissues.";
RL Mol. Cell. Biol. 9:2387-2395(1989).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain stem;
RX MEDLINE=90265618; PubMed=1693186;
RA Chiu I.M., Wang W.P., Lehtoma K.;
RA "Alternative splicing generates two forms of mRNA coding for human
RT heparin-binding growth factor 1.";
RL Oncogene 5:755-762(1990).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=90073637; PubMed=2590193;
RA Mergia A., Fischer E., Graves D., Tumolo A., Miller J.,
RA Gospodarowicz D., Abraham J.A., Shipley G.D., Fiddes J.C.;
RA "Structural analysis of the gene for human acidic fibroblast growth
RT factor.";
RL Biochem. Biophys. Res. Commun. 164:1121-1129(1989).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=92019819; PubMed=1717925;
RA Wang W.P., Quick D., Balcerzak S.P., Needleman S.W., Chiu I.M.;
RA "Cloning and sequence analysis of the human acidic fibroblast growth
RT factor gene and its preservation in leukemia patients.";
RL Oncogene 6:1521-1529(1991).
RN [6]
RN SEQUENCE FROM N.A.
RX MEDLINE=92202857; PubMed=1372643;
RA Li Y.L., Kha H., Golden J.A., Migchielsen A.A.J., Goetzl E.J.,
RA Turk E.J.;
RA "An acidic fibroblast growth factor protein generated by alternate
RT splicing acts like an antagonist.";
RL J. Exp. Med. 175:1073-1080(1992).
RN [7]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RN SEQUENCE OF 1-154 FROM N.A.
RX MEDLINE=94069734; PubMed=7504343;
RA Zhao X.M., Yeoh T.K., Hiebert M., Frist W.H., Miller G.G.;
RT "The expression of acidic fibroblast growth factor (heparin-binding
RT growth factor-1) and cytokine genes in human cardiac allografts and T
RT cells.";
RL Transplantation 56:1177-1182(1993).
RN [9]
RN SEQUENCE OF 1-40 FROM N.A.
RX MEDLINE=90365758; PubMed=2393407;
RA Crumley G., Dionne C.A., Jaye M.;
RT "The gene for human acidic fibroblast growth factor encodes two
RT upstream exons alternatively spliced to the first coding exon.";
RL Biochem. Biophys. Res. Commun. 171:7-13(1990).
RN [10]
RN SEQUENCE OF 16-155.
RX MEDLINE=86296647; PubMed=2427112;
RA Harper J.W., Struydom D.J., Lobb R.R.;
RT "Human class I heparin-binding growth factor: structure and homology
RT to bovine acidic brain fibroblast growth factor.";
RL Biochemistry 25:4097-4103(1986).
RN [11]
RN SEQUENCE OF 16-155.
RX MEDLINE=86295741; PubMed=3527167;
RA Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
RT "The complete amino acid sequence of human brain-derived acidic
RT fibroblast growth factor.";
RL Biochem. Biophys. Res. Commun. 138:611-617(1986).
RN [12]
RN SEQUENCE OF 16-155.
RX MEDLINE=87048871; PubMed=3778488;
RA Gautschi-Sova P., Mueller T., Boehlen P.;
RT "Amino acid sequence of human acidic fibroblast growth factor.";
RL Biochem. Biophys. Res. Commun. 140:874-880(1986).
RN [13]
RN SEQUENCE OF 16-47.
RX MEDLINE=86186784; PubMed=3964259;
RA Gimenez-Gallego G., Conn G., Hatcher V.B., Thomas K.A.;
RT "Human brain-derived acidic and basic fibroblast growth factors:
RT amino terminal sequences and specific mitogenic activities.";
RL Biochem. Biophys. Res. Commun. 135:541-548(1986).
RN [14]
RN SEQUENCE OF 16-49.
RX MEDLINE=86275260; PubMed=3732516;
RA Gautschi P., Frater-Schroeder M., Boehlen P.;
RT "Partial molecular characterization of endothelial cell mitogens from
RT human brain: acidic and basic fibroblast growth factors.";
RL FEBS Lett. 204:203-207(1986).
RN [15]
RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96194129; PubMed=8652550;
RA Blaber M., Disalvo J., Thomas K.A.;
RT "X-ray crystal structure of human acidic fibroblast growth factor.";
RL Biochemistry 35:2086-2094(1996).
RN [16]
RN STRUCTURE BY NMR OF 24-155.
RX MEDLINE=94358885; PubMed=7521397;
RA Pineda-Lucena A., Gimenez M.A., Nieto J.L., Santoro J., Rico M.,
RA Gimenez-Gallego G.;
RT "1H-NMR assignment and solution structure of human acidic fibroblast
RT growth factor activated by inositol hexasulfate.";
RL J. Mol. Biol. 242:81-98(1994).
RN [17]
RN STRUCTURE BY NMR OF 24-155.
RP

[illegible]

canine hearts."; Eur. J. Biochem. 181:67-73 (1989).
 [9]
 SEQUENCE OF 1-18 FROM N.A.
 Philippe J.M., Renaud F., Desset S., Laurent M.;
 Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
 [10]
 X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 MEDLINE=91095983; PubMed=1702556;
 Zhu X., Komiya H., Chirino A., Faham S., Fox G.M., Arakawa T.,
 Hsu B.T., Rees D.C.;
 "Three-dimensional structures of acidic and basic fibroblast growth
 factors";
 Science 251:90-93 (1991).
 -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
 in vivo and are potent mitogens for a variety of cell types in
 vitro. There are differences in the tissue distribution and
 concentration of these 2 growth factors.
 -!- SUBUNIT: Monomer.
 -!- MISCELLANEOUS: This protein binds heparin, although less strongly
 than does bFGF.
 -!- SIMILARITY: Belongs to the heparin-binding growth factors family.

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 EMBL; M13439; AAA30516.1; -
 EMBL; X13221; CAA31610.1; -
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 EMBL; M35608; AAA30517.1; -
 EMBL; X66446; CAA47063.1; -
 EMBL; M97660; AAA30563.1; -
 EMBL; M97661; AAA30564.1; -
 EMBL; JH0613; GKBOA.
 PIR; JH0613; GKBOA.
 PDB; 1BAR; 31-OCT-93.
 DR PDB; 1APC; 31-OCT-93.
 InterPro; IPR008996; Cytok IL1-like.
 InterPro; IPR002348; IL1_HBGF.
 Pfam; PF00167; FGF; 1.
 PRINTS; PR00262; IL1HBGF
 ProDom; PD000831; IL1_HBGF; 1.
 SMART; SM00442; FGF; 1.
 PROSITE; PS00247; HBGF_FGF; 1.
 Growth factor; Mitogen; Angiogenesis; Heparin-binding; Acetylation;
 3D-structure.
 PROPEP 1 15
 CHAIN 2 155
 CHAIN 16 155
 CHAIN 22 155
 MOD RES 2 2
 BINDING 24 28
 BINDING 113 116
 TURN 23 24
 STRAND 27 31
 TURN 32 35
 STRAND 36 37
 STRAND 39 40
 TURN 42 43
 STRAND 45 47
 TURN 52 53
 TURN 56 57
 STRAND 59 65
 TURN 66 67
 STRAND 68 73
 TURN 74 76
 STRAND 79 79
 STRAND 82 82
 TURN 84 85
 ENDOTHELIAL CELL GROWTH FACTOR BETA.
 HEPARIN-BINDING GROWTH FACTOR 1.
 ENDOTHELIAL CELL GROWTH FACTOR ALPHA.
 ACETYLTATION.
 HEPARIN (POTENTIAL).
 HEPARIN (POTENTIAL).
 15
 155
 155
 155
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 116
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87 91 89
 FT STRAND 91 91
 FT HELIX 96 104
 FT STRAND 100 107
 FT TURN 106 114
 FT STRAND 110 117
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 FT TURN 128 132
 FT STRAND 131 134
 FT STRAND 134 137
 FT HELIX 135 141
 FT TURN 140 145
 FT HELIX 143 151
 FT STRAND 147 151
 SQ SEQUENCE 155 AA; 17493 MW; F6366641F189F9BFD CRC64;
 Query Match 13.0%; Score 144.5; DB 1; Length 155;
 Best Local Similarity 35.0%; Pred. No. 0.00039;
 Matches 49; Conservative 12; Mismatches 64; Indels 15; Gaps 5;
 QY 38 LQFGGQVRQRYLYTDDAQTEAHLEIREDDGTGVTGAADQSPESL-LQKALKPGVITQILGV 96
 Db 18 LPLGNYKPKLLYCSNGY---FLRLLPDGTVDTGDKRSQDHIQQLCAESIGEVYIKST 74
 QY 97 KTSRFLCQRPDGLYGSIHFPDRCSPFRELLEDGYNVYQSEAHCLPLHLPNKNSPHERDP 156
 Db 75 ETGQFLAMTDGLLYGS-QTPNEECLFLERLEENHYNTYISKGAHKHFWGLKNGR-- 131
 QY 157 APRGPAP-----FLRLP 168
 Db 132 SKLGPRTFHGQKAILFLPLP 151
 RESULT 39
 ID_FGF1_PIG STANDARD; PRT; 152 AA.
 AC P20002;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Heparin-binding growth factor 1 precursor (HBGF-1) (Acidic fibroblast
 growth factor) (AFGF) (Alpha-endothelial cell growth factor)
 DE (Fragment).
 GN FGF1 OR FGF-1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92062117; PubMed=1719973;
 RA Schmidt M., Sharma H.S., Schott R.J., Schaper W.;
 RT "Amplification and sequencing of mRNA encoding acidic fibroblast
 growth factor (aFGF) from porcine heart."
 RL Biochem. Biophys. Res. Commun. 180:853-859 (1991).
 RN [2]
 RP SEQUENCE OF 22-41.
 RX MEDLINE=89231704; PubMed=2714282;
 RA Quinkler W., Maasberg M., Bernotat-Danielowski S., Luethe N.,
 RA Sharma H.S., Schaper W.;
 RT "Isolation of heparin-binding growth factors from bovine, porcine and
 canine hearts."
 RL Eur. J. Biochem. 181:67-73 (1989).
 CC -!- FUNCTION: The heparin-binding growth factors are angiogenic agents
 in vivo and are potent mitogens for a variety of cell types in
 vitro. There are differences in the tissue distribution and
 concentration of these 2 growth factors.
 CC -!- SUBUNIT: Monomer.

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RESULT 40
FGF9 XENLA
ID FGF9 XENLA STANDARD; PRT; 209 AA.
Q91875;
AC
DT DT 01-NOV-1997 (Rel. 35, Created)
DT DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE DE Gla-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE DE (FGF-9) (HBGF-9) (XFGF-9).
DE GN FGF9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97006698; PubMed=8853991;
RX Song J., Slack J.M.W.;
RA "XFGF-9; a new fibroblast growth factor from Xenopus embryos.";
RL Dev. Dyn. 206:427-436(1996).
CC -1- FUNCTION: May have a role
CL in muscle development and neural

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Search completed: March 2, 2004, 16:05:24
Job time : 21.0292 secs

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OM protein - protein search, using sw model

Run on: March 2, 2004, 16:00:38 ; Search time 29.6083 Seconds
(without alignments)
678.999 Million cell updates/sec

Title: US-10-060-765-4
Perfect score: 1113
Sequence: 1 MDSDETGFHSLWVSLAG.....SSDPLSMVGPQGRSPSYAS 209

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	249.5	22.4	251	2	fibroblast growth
2	179	16.1	245	1	transforming prote
3	177.5	15.9	239	1	fibroblast growth
4	176.5	15.9	208	2	fibroblast growth
5	174	15.6	187	2	embryonic fibrobla
6	173	15.5	206	2	fibroblast growth
7	170.5	15.3	208	2	fibroblast growth
8	167	15.0	266	2	fibroblast growth
9	165	14.8	194	2	fibroblast growth
10	164	14.7	264	2	embryonic fibrobla
11	163.5	14.7	192	2	fibroblast growth
12	163.5	14.7	206	1	fibroblast growth
13	161	14.5	211	2	fibroblast growth
14	160.5	14.4	256	2	fibroblast growth
15	160	14.4	212	2	fibroblast growth
16	157	14.1	208	2	fibroblast growth
17	157	14.1	208	2	fibroblast growth
18	155.5	14.0	155	1	acidic fibroblast
19	154.5	13.9	155	2	acidic fibroblast
20	154.5	13.9	155	2	acidic fibroblast
21	153.5	13.8	202	1	fibroblast growth
22	153	13.7	208	2	fibroblast growth
23	150.5	13.5	207	2	fibroblast growth
24	148.5	13.3	267	1	acidic fibroblast
25	146.5	13.2	155	1	acidic fibroblast
26	146.5	13.2	207	2	transforming prote
27	146	13.1	237	1	acidic fibroblast
28	144.5	13.0	155	1	acidic fibroblast
29	143.5	12.9	152	2	acidic fibroblast

30 142 12.8 194 2 S26049 fibroblast growth
31 142 12.8 220 2 I50588 fibroblast growth
32 141 12.7 194 2 S49501 keratinocyte growt
33 140 12.6 194 2 I48610 fibroblast growth
34 139 12.5 194 1 A36301 basic fibroblast g
35 138 12.4 189 2 A48834 basic fibroblast g
36 135 12.1 155 1 A40117 basic fibroblast g
37 131.5 11.8 155 2 JW0055 acidic fibroblast
38 127.5 11.5 155 2 A60130 acidic fibroblast
39 127 11.4 164 2 S31622 basic fibroblast g
40 124 11.1 413 2 H88481 protein let-756 li
41 122 11.0 154 2 A31674 basic fibroblast g
42 122 11.0 154 2 C37360 basic fibroblast g
43 122 11.0 168 2 JG0184 fibroblast growth
44 121 10.9 137 2 I46711 fibroblast growth
45 121 10.9 146 1 S00185 basic fibroblast g

ALIGNMENTS

RESULT 1

JC7513
fibroblast growth factor-23 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7513
R:Yamashita, T.; Yoshioka, M.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 494-498, 2000
A:Title: Identification of a novel fibroblast growth factor, FGF-23, preferentially expr
A:Reference number: JC7513; MUID:20490027; PMID:11032749
A:Contents: Embryo
A:Accession: JC7513
A:Molecule type: mRNA
A:Residues: 1-251 <YAM>
A:Cross-references: DDBJ:AB037889
C:Comment: This factor, a secreted protein, acts on proximal cells and plays roles in th
C:Genetics:
A:Gene: fgf-23
C:Keywords: nucleus

Query Match 22.4%; Score 249.5; DB 2; Length 251;
Best Local Similarity 35.1%; Pred. No. 8.4e-13; Indels 23; Gaps 8;
Matches 73; Conservative 27; Mismatches 85;

QY 12 GLWVSVLAGLLGACQ---AHPIDSSPLL--QFGQVQRVLYTDDAQTEAHLREI 66
DB 3 GTCRLVGVLCVCSLGTAAYPDTSPLGSNWGLT--HLYTATA-RTSYHLQIHRD 58
QY 67 GTVGGAAQSPESLLQLKALKPGVIOILGVKTSRFLCORPDGALYGLSHEDPEACSFREL 126
DB 59 GHVDGTPHOTIYSGALMITSEDAGSVITGAMTRFLCMDLHGNIFGLSHESPECKFRQW 118
QY 127 LLEDGNVVOSEAHGFLPHLPGNK---SPHRDPAPRGPAPFL-----PIPLGLPALPEP 177
DB 119 TLENGYDVVLSSKHVYLSGRAKRIFQPTNPPPP--SQFLARNEVPLLFHFTVPRR 176
QY 178 PGIAPQPPDVGSSDPLSLMVGPQGRSP 205
DB 177 HTRSADPPE---RDPLNLVKPRPRATP 201

RESULT 2

transforming protein (int-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C:Accession: A23930; S08157
R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dickson, C.
EMBO J. 5, 919-924, 1986
A:Title: Sequence, topography and protein coding potential of mouse int-2: a putative o
A:Reference number: A23930; MUID:86247582; PMID:3013624
A:Accession: A23930

A;Reference number: S23595; MUID:92315916; PMID:1618138

A;Accession: S23595

A;Molecule type: mRNA

A;Residues: 1-187 <ISA>

A;Cross-references: EMBL:X62593; NID:g64692; PIDN:CAA44479.1; PID:g64693

C;Superfamily: fibroblast growth factor

Query Match 15.8%; Score 174; DB 2; Length 187;
Best Local Similarity 34.8%; Pred. No. 6.5e-07;
Matches 48; Conservative 23; Mismatches 57; Indels 10; Gaps 5;

QY 33 DSSPLQFGQVQRVLYTDDAQTEAHLEIRDTGVGAADQSPESLLQKALKPGVQ 92
DB 54 DSYLL--GIKQRRLYCNVG--IGFHQVLPDGRNGHSENRYSLELSPEVGVVS 108
QY 93 ILGVKTSRFLCQPDGALYGLSLHFDPEACSFRELLLEDGYNVYQSEAH--GLPLHLPN-- 149
DB 109 LYGVKSGMFVAMNAKGLYGSRYFN--ECKFKETLLPNYNAVESRKYPGMYALGKNGR 167
QY 150 -KSPHRDPAPRGPARFLP 166
DB 168 TKKGNRVSPMTTLTHFLP 185

RESULT 6

JC4268
fibroblast growth factor 4 - bovine
N;Alternate names: transforming protein hst
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
C;Accession: JC4268
R;Yu, J.C.; DeSeabra, A.J.J.; Wang, L.M.; Fleming, T.P.; Chedid, M.; Miki, T.; Heidaran, Gene 162, 333-334, 1995
A;Title: An unexpected transforming gene in calf-thymus carrier DNA: Bovine hst.
A;Reference number: JC4268; MUID:96032369; PMID:7557455
A;Accession: JC4268
A;Molecule type: mRNA
A;Residues: 1-206 <YUJ>

A;Cross-references: GB:U15969
A;Note: The authors translated the codon GGC for residue 114 as Ser
C;Comment: This protein is a member of fibroblast growth factor family. The hst gene in C;Genetics:
A;Gene: hst
A;Introns: 113/3; 145/2
C;Superfamily: fibroblast growth factor
C;Keywords: thymus; transforming protein

Query Match 15.5%; Score 173; DB 2; Length 206;
Best Local Similarity 31.5%; Pred. No. 8.7e-07;
Matches 51; Conservative 23; Mismatches 76; Indels 12; Gaps 5;

QY 14 WVSVLGILLGACQHPIDSSPLQFGQV-----RQVLYTDDAQTEAHLEIRDTGT 68
DB 46 WESLVARSLLAGLVAAQPKAAVQSGAGDYLLGIKRLRLYCNVG--IGFHLQVLPDGR 103
QY 69 VGGAADQSPESLLQKALKPGVQILGVKTSRFLCQPDGALYGLSLHFDPEACSFRELL 128
DB 104 IGVVHATSDGLLELSPEVGVSGIFGVASFFVAMSGRGLYSGSPFTTDE--CRFREILL 162
QY 129 EDGYNVYQSEAH--GLPLHLPGN--KSPHRDPAPRGPARFLP 166
DB 163 PNNYNAVCEDRHPGPMFIALSKNGKAKGNRVSPMTKVTHTFLP 204

RESULT 7

SI4192
fibroblast growth factor 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-2000
C;Accession: SI4192; I49665; I49664
R;de Lapeyriere, O.; Rosnet, O.; Benharroch, D.; Raybaud, F.; Marchetto, S.; Planché, J. Oncogene 5, 823-831, 1990
A;Title: Structure, chromosome mapping and expression of the murine Fgf-6 gene.

A;Reference number: SI4192; MUID:90295275; PMID:2193291

A;Accession: SI4192

A;Molecule type: DNA

A;Residues: 1-208 <LAP>

A;Cross-references: EMBL:X51552

A;Note: It is uncertain whether Met-1 or Met-11 is the initiator

R;Ollendorff, V.; Rosnet, O.; Marics, I.; Birnbaum, D.; deLapeyriere, O.

Biochimie 74, 1035-1038, 1992

A;Title: Isolation and sequence of the murine Fgf6 cDNA.

A;Reference number: I49664; MUID:93120244; PMID:1477139

A;Accession: I49665

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 19-208 <RES>

A;Cross-references: GB:M92416; NID:gl93288; PIDN:AAA62261.1; PID:g666915

A;Accession: I49664

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-18 <RE2>

A;Cross-references: GB:M92415; NID:gl93286; PIDN:AAA62260.1; PID:gl93287

C;Genetics:

A;Gene: Fgf6

A;Introns: 116/1; 150/3

C;Superfamily: fibroblast growth factor

Query Match 15.3%; Score 170.5; DB 2; Length 208;
Best Local Similarity 36.4%; Pred. No. 1.4e-06;
Matches 36; Conservative 21; Mismatches 39; Indels 3; Gaps 2;

QY 42 GQVRQRYLTDDAQTEAHLEIRDTGVGAADQSPESLLQKALKPGVQILGVKTSRF 101
DB 81 GIKQRRLYCNVG--IGFHLQVDPDGRISGTHEENPYSLEISTVERGVVSDFGVKSALF 138

QY 102 LCQRPDGLYGLSLHFDPEACSFRELLLEDGYNVYQSEAH 140

DB 139 IAMNSKGRLYTTPSFHDE--CKFRETLTPNNYAYESDLY 176

RESULT 8

S68144
fibroblast growth factor 5 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: S68144
R;Hattori, Y.; Yamasaki, M.; Itoh, N.
Biochim. Biophys. Acta 1306, 31-33, 1996
A;Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel ti
A;Reference number: S68144; MUID:96201703; PMID:8611621

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-266 <HAT>

A;Cross-references: EMBL:D64085; NID:g992952; PIDN:BAAL0966.1; PID:g992953

C;Superfamily: fibroblast growth factor

Query Match 15.0%; Score 167; DB 2; Length 266;
Best Local Similarity 30.3%; Pred. No. 3.6e-06;
Matches 63; Conservative 26; Mismatches 69; Indels 50; Gaps 11;

QY 34 SSPLQFGQVQRVLYTDDAQTEA-----HLEIRDTGVGAADQSPESLLQLK 84
DB 63 ASPGQSGSGSEHSFQWSPSGRRTGLYCRVIGFHLQIYPDGKVGVSHEASVLSILEIF 122

QY 85 ALKPGVQILGVKTSRFLCQPDGALYGLSLHFDPEACSFRELLLEDGYNVYQSEAH---- 140
DB 123 AVSQGIVGIRGVFSNKFVAMSKGKCHASAKFTDD--CKFRFRFQENSINYASAIHRTK 181

QY 141 -GLPLHLPGNKSHPRDPAARG-----PARFLP-----LPGLP-----PALPEPP 178
DB 182 TGRWYVALNK--RGKAKGCSPRVXPQHVSTHFLFRKQSEQFELSFTVTVEKKKPP 238

QY 179 GILAPQPDVGVSSDPLSNMVGPSQGRSPS 206

A;Residues: 1-206 <YOS>
A;Cross-references: DDBJ:J02986; NID:g184430; PIDD:AA859555.1; PIDD:G386788
R;Taiba, M.; Yoshida, T.; Miyagawa, K.; Sakamoto, H.; Terada, M.; Sugimura, T.
Proc. Natl. Acad. Sci. U.S.A. 84, 2980-2984, 1987
c-myc: c-myc sequence of human transforming gene hat and identification of the coding

QY 146 LPGAHPHDPAPRGPAPR-----FLPLPGLPPALPE 176
DB 167 VALNK-----DGTDRGASRKHQKFTPLPRPVPDPVPE 202
RESULT 16
fibroblast growth factor 9 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66486
R:Seo, M.; Noguchi, K.
FEBS Lett. 370: 231-235, 1995
A:Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during indu
A:Reference number: S66486; MUID:95385801; PMID:7656983
A:Accession: S66486
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <SEO>
A:Cross-references: EMBL:D38258; NID:gl107458; PIDN:BAA07410.1; PID:gl107459
C:Superfamily: fibroblast growth factor
Query Match 14.1%; Score 157; DB 2; Length 208;
Best Local Similarity 31.2%; Pred. No. 1.7e-05;
Matches 59; Conservative 20; Mismatches 72; Indels 38; Gaps 8;
QY 3 SDETFEHSGLWVSVLGLLGCACQAHPIPPSSPLQFGQVQRORYLYTDDAQTEAHLE 62
DB 34 SDHLGQSEAG-----GLPRG-----PAVTDLDHLKGLRRRLQLYC-----RTGFHLE 75
QY 63 IREDGTGCGA-ADQSPESLIQALKPGVQIQLGKTSRFLCQRPDGLYGLSLHFDPEAC 121
DB 76 IFFNGTIQTRKDHRSRFGILFEISAVGLSVIRGVDGLYGMNEKGLYSEKLTQEC-C 134
QY 122 SFRELLEDGYNVYOSEAH-----GLPLHLPGNKSHPHDPAPRGPAPR-----FLPL 167
DB 135 VFREQFENWNTYSSNLYKHVDTRGRYYVALNK-----DGTFRGTRTKRHKQKFTHFLPR 190
QY 168 PGLPPALPE 176
DB 191 PVDPDKVPE 199
RESULT 17
fibroblast growth factor 9 - human
N:Alternate names: glia-activating factor
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A48137
R:Miyamoto, M.; Naruo, K.; Seko, C.; Matsumoto, S.; Kondo, T.; Kurokawa, T.
Mol. Cell. Biol. 13, 4251-4259, 1993
A:Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fib
A:Reference number: A48137; MUID:93309459; PMID:8321227
A:Accession: A48137
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-208 <MIY>
A:Cross-references: GB:D14838; NID:g391718; PIDN:BAA03572.1; PID:g391719
A:Experimental source: foreskin
A:Note: sequence extracted from NCBI backbone (NCBIN:134640, NCBI:P:134641)
C:Genetics:
A:Gene: GDB:PGF9
A:Cross-references: GDB:207221; OMIM:600921
A:Map position: 13q11-13q12
C:Superfamily: fibroblast growth factor
Query Match 14.1%; Score 157; DB 2; Length 208;
Best Local Similarity 31.2%; Pred. No. 1.7e-05;
Matches 59; Conservative 20; Mismatches 72; Indels 38; Gaps 8;
QY 3 SDETFEHSGLWVSVLGLLGCACQAHPIPPSSPLQFGQVQRORYLYTDDAQTEAHLE 62

DB 34 SDHLGQSEAG-----GLPRG-----PAVTDLDHLKGLRRRLQLYC-----RTGFHLE 75
QY 63 IREDGTGCGA-ADQSPESLIQALKPGVQIQLGKTSRFLCQRPDGLYGLSLHFDPEAC 121
DB 76 IFFNGTIQTRKDHRSRFGILFEISAVGLSVIRGVDGLYGMNEKGLYSEKLTQEC-C 134
QY 122 SFRELLEDGYNVYOSEAH-----GLPLHLPGNKSHPHDPAPRGPAPR-----FLPL 167
DB 135 VFREQFENWNTYSSNLYKHVDTRGRYYVALNK-----DGTFRGTRTKRHKQKFTHFLPR 190
QY 168 PGLPPALPE 176
DB 191 PVDPDKVPE 199
RESULT 18
acidic fibroblast growth factor - golden hamster
N:Alternate names: heparin-binding growth factor 1
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A60721
R:Hall, J.A.; Harris, M.A.; Malark, M.; Mansson, P.E.; Zhou, H.; Harris, S.E.
J. Cell. Biochem. 43, 17-26, 1990
A:Title: Characterization of the hamster DDT-1 cell aFGF/HGBF-I gene and cDNA and its m
A:Reference number: A60721; MUID:90270291; PMID:1693366
A:Accession: A60721
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-155 <HAL>
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding
Query Match 14.0%; Score 155.5; DB 1; Length 155;
Best Local Similarity 35.0%; Pred. No. 1.6e-05;
Matches 48; Conservative 12; Mismatches 62; Indels 15; Gaps 5;
QY 41 GGQVQRORYLYTDDAQTEAHLEIREDDGTGCGAADQSPESL-LQLKALKPGVQIQLGKTS 99
DB 21 GNYKPKLLYCSNGH---FLRIIPDGTGTRSDRSDHIOQLQLSAESAGEVIKGTETG 77
QY 100 RFLCQRPDGLYGLSLHFDPEACSFRELLEDGYNVYOSEAHGLPLHLPGNKSHPHDPAPR 159
DB 78 QYLAAMDYDGLYGS-QTPNEECLEFLERLEENHYNTYTSKKHAENKWFVGLKK--NGSKR 134
QY 160 GPAP-----FLPLP 168
DB 135 GPRTHYGQKAILFLPLP 151
RESULT 19
acidic fibroblast growth factor 1 - rat
N:Alternate names: heparin-binding growth factor 1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 16-Jul-1999
C:Accession: S04147
R:Goodrich, S.P.; Yan, G.C.; Bahrenburg, K.; Mansson, P.E.
Nucleic Acids Res. 17, 2867, 1989
A:Title: The nucleotide sequence of rat heparin binding growth factor 1 (HBGF-1).
A:Reference number: S04147; MUID:89240051; PMID:2470029
A:Accession: S04147
A:Molecule type: mRNA
A:Residues: 1-155 <GOO>
A:Cross-references: EMBL:X14232; NID:g56351; PIDN:CAA32448.1; PID:g56352
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; heparin binding
Query Match 13.9%; Score 154.5; DB 2; Length 155;
Best Local Similarity 34.3%; Pred. No. 1.9e-05;
Matches 48; Conservative 13; Mismatches 64; Indels 15; Gaps 5;
QY 38 LQFGQVQRORYLYTDDAQTEAHLEIREDDGTGCGAADQSPESL-LQLKALKPGVQIQLG 96

```

Db      18  LPLGNYKKPLKLYCSNGGH---FLRLPDGTVDGTRDSQDHIQLQLSAESAGEVVIKGT 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      97  KTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      75  ETQYILAMDTGELLYGS-QTPNEECFLERLEBNHNTYTSKKHAEKNWFVGLKK--NGS 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      157  APRGPAPAR-----FLPLP 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132  CKRGPRTHYGKAILFLPLP 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 20
D37360
acidic fibroblast growth factor - mouse
N:Alternate names: aFGF; FGF-1
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C:Accession: D37360; JCS231
R:Hebert, J.M.; Basillico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: D37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <HEB>
A:Cross-references: GB:M30641; NID:g1913284; PIDN:AAA37618.1; PID:G309236
R:Madijai, F.; Hackshaw, K.V.; Chiu, I.M.
Gene 179, 231-236, 1996
A:Title: Cloning and characterization of the mouse Fgf-1 gene.
A:Reference number: JCS231; MUID:97128312; PMID:8972905
A:Accession: JCS231
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155 <MAD>
A:Cross-references: GB:U36456
C:Comment: This protein is an inducer of neovascularization in angiogenic disease includ
C:Genetics:
A:Gene: Fgf-1
A:Introns: 57/1; 91/3
C:Superfamily: fibroblast growth factor

Query Match      13.9%; Score 154.5; DB 2; Length 155;
Best Local Similarity 34.3%; Pred. No. 1.9e-05;
Matches 48; Conservative 13; Mismatches 64; Indels 15; Gaps 5;

QY      38  LQFGGVRORYLTDQAQTEAHLEIREDTGVTGGAADQSPESI-LQLKALKPGVQILGV 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      18  LPLGNYKKPLKLYCSNGGH---FLRLPDGTVDGTRDSQDHIQLQLSAESAGEVVIKGT 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      97  KTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      75  ETQYILAMDTGELLYGS-QTPNEECFLERLEBNHNTYTSKKHAEKNWFVGLKK--NGS 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      157  APRGPAPAR-----FLPLP 168
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      132  CKRGPRTHYGKAILFLPLP 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 21
TVMSHS
fibroblast growth factor 4 - mouse
N:Alternate names: transforming protein hstf1; transforming protein k-FGF; transforming
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 17-Mar-2000
C:Accession: S04741; A37360
R:Brookes, S.; Smith, R.; Thurlow, J.; Dickson, C.; Peters, G.
Nucleic Acids Res. 17, 4037-4045, 1989
A:Title: The mouse homologue of hst/k-FGF: sequence, genome organization and location re
A:Reference number: S04741; MUID:89296455; PMID:2740210
A:Accession: S04741
A:Molecule type: DNA

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A:Residues: 1-202 <BRO>
A:Cross-references: GB:X14849; GB:M28516; NID:g52791; PIDN:CAA32967.1; PID:g52792
R:Hebert, J.M.; Basillico, C.; Goldfarb, M.; Haub, O.; Martin, G.R.
Dev. Biol. 138, 454-463, 1990
A:Title: Isolation of cDNAs encoding four mouse FGF family members and characterization
A:Reference number: A37360; MUID:90201563; PMID:2318343
A:Accession: A37360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166,'S',168-202 <HEB>
A:Cross-references: GB:M30642; NID:g193290; PIDN:AAA37619.1; PID:g309237
C:Genetics:
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match      13.8%; Score 153.5; DB 1; Length 202;
Best Local Similarity 34.2%; Pred. No. 3.1e-05;
Matches 38; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

QY      60  HLEIREDTGVTGGAADQSPESLQLKALKPGVQILGVKTSRFLCQRPDQALYGLSLHFDPE 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      91  HLQVLPDGRIGGVHADTRDSLLELSPVQGVGVIFGVASRFFVAMSSRCKLGVGPFETDE 150
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      120  ACSFRELLLEDGYNVYQSEAH-GLPLHLPGN---KSPHRDPAPRGPARFLP 166
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      151  -CKFXEILLPNYNAYEAYVGFMPFALSKNGRTKKNRVSPVTMKVTHFLP 200
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 22
JC7082
fibroblast somatotropin-20 - African clawed frog
N:Alternate names: fibroblast growth factor-20
C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7082
R:Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhashi, Y.; Sato, S.; Tei, H.; Sakak
Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A:Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus laevi
A:Reference number: JC7082; MUID:99373151; PMID:10441498
A:Accession: JC7082
A:Molecule type: mRNA
A:Residues: 1-208 <KOG>
A:Cross-references: DBJ:AB012615; NID:g5762261; PIDN:BA083474.1; PID:g5762262
C:Superfamily: fibroblast growth factor
C:Keywords: differentiation; fibroblast; growth factor; heparin binding

Query Match      13.7%; Score 153; DB 2; Length 208;
Best Local Similarity 31.5%; Pred. No. 3.5e-05;
Matches 53; Conservative 22; Mismatches 65; Indels 28; Gaps 7;

QY      27  QAHPIDSSSP--LQFGGVRORYLTDQAQTEAHLEIREDTGVTGGA-ADQSPESLLQL 83
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      42  QSERLSRSPSLSHLQILRRQLYC---RTGFHLQILPDGNGVQTRQDSRFGILEF 97
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      84  KALKPGVQILGVKTSRFLCQRPDQALYGLSLHFDPEACSFRELLLEDGYNVYQSEAHGLP 143
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      98  ISVAIGLVSIRGVDGLYGLMNDKGLFGLSEKLTSE-CIFREQFENWYNTYSSN----- 151
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      144  LHLPGNK-----SPHRDPAPRGPAR-----FLPLPLPALPE 176
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      152  LYKHGDSRRYFVALNKDGTFRDGTAKRHQKFTFLPRPVDPEKVE 199
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 23
JCS941
fibroblast growth factor 16 - human
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: JCS941
R:Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami,
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A:Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth fa

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RESULT 28

GKBOA

acidic fibroblast growth factor precursor - bovine
N/Alternate names: aFGF; eye-derived growth factor II; heparin-binding growth factor I;
C/Species: Bos primigenius taurus (cattle)
C/Date: 13-Aug-1986 #sequence revision 03-Feb-1994 #text change 19-Jan-2001
C/Accession: JH0613; S02102; S02065; S22065; A94281; S03953; A91010; A24477; B25
R/Renaud, F.; Desset, S.; Bugra, K.; Halley, C.; Philippe, J.M.; Courtois, Y.; Laurent,
Biochem. Biophys. Res. Commun. 184, 945-952, 1992
A/Title: Heterogeneity of 3' untranslated region of bovine acidic FGF transcripts.
A/Reference number: JH0613; MUID:92246990; PMID:1374244
A/Accession: JH0613
A/Molecule type: DNA
A/Residues: 58-155 <REN>
R/Halley, C.; Courtois, Y.; Laurent, M.
Nucleic Acids Res. 16, 10913, 1988
A/Title: Nucleotide sequence of bovine acidic fibroblast growth factor cDNA.
A/Reference number: S02102; MUID:89083506; PMID:3205724
A/Accession: S02102
A/Molecule type: mRNA
A/Residues: 1-155 <HAL>
A/Cross-references: EMBL:X13221; NID:g347; PIDN:CRAA31610.1; PID:g348
R/Alterio, J.; Halley, C.; Brou, C.; Soussi, T.; Courtois, Y.; Laurent, M.
FEBS Lett. 242, 41-46, 1988
A/Title: Characterization of a bovine acidic FGF cDNA clone and its expression in brain
A/Reference number: S02661; MUID:89078619; PMID:2849564
A/Accession: S02661
A/Molecule type: mRNA
A/Residues: 1-155 <ALT>
A/Cross-references: EMBL:X14032; NID:g322; PIDN:CRAA32192.1; PID:g323
R/Philippe, J.M.
submitted to the EMBL Data Library, May 1992
A/Reference number: S22065
A/Accession: S22065
A/Molecule type: mRNA
A/Residues: 1-18 <PHI>
A/Cross-references: EMBL:X66446; NID:g411; PIDN:CRAA47063.1; PID:g412
R/Abraham, J.A.; Merz, A.; Whang, J.L.; Tumolo, A.; Friedman, J.; Hjerrild, K.A.; Goss
Science 233, 545-548, 1986
A/Title: Nucleotide sequence of a bovine clone encoding the angiogenic protein, basic fi
A/Reference number: A94290; MUID:86261806; PMID:2425435
A/Accession: B24663
A/Molecule type: mRNA
A/Residues: 16-56 <ABR>
R/Gimenez-Gallego, G.; Rodkey, J.; Bennett, C.; Rios-Candelore, M.; DiSalvo, J.; Thomas,
Science 230, 1385-1388, 1985
A/Title: Brain-derived acidic fibroblast growth factor: complete amino acid sequence and
A/Reference number: A94281; MUID:86070224; PMID:4071057
A/Accession: A94281
A/Molecule type: protein
A/Residues: 16-155 <GIM>
R/Quinkler, W.; Maasberg, M.; Bernotat-Danielowaki, S.; Luethe, N.; Sharma, H.S.; Schape
Eur. J. Biochem. 181, 67-73, 1989
A/Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea
A/Reference number: S03953; MUID:89231704; PMID:2714282
A/Accession: S03953
A/Molecule type: protein
A/Residues: 16-45 <QUI>
R/Bohlen, P.; Esch, F.; Baird, A.; Gospodarowicz, D.
EMBO J. 4, 1951-1956, 1985
A/Title: Acidic fibroblast growth factor (FGF) from bovine brain: amino-terminal sequen
A/Reference number: A91010; MUID:86055750; PMID:4065099
A/Accession: A91010
A/Molecule type: protein
A/Residues: 16-30, 'X', 32-34, 'X', 36-44 <BOH>
R/Crabb, J.W.; Armes, L.G.; Carr, S.A.; Johnson, C.M.; Roberts, G.D.; Bordoli, R.S.; McK
Biochemistry 25, 4988-4993, 1986
A/Title: Complete primary structure of prostatropin, a prostate epithelial cell growth f
A/Reference number: A24477; MUID:87026586; PMID:3768327
A/Accession: A24477
A/Molecule type: protein

A/Residues: 2, 'GE', 5-155 <CRA>
R/Burgess, W.H.; Mehman, T.; Marshak, D.R.; Fraser, B.A.; Maciag, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 7216-7220, 1986
A/Title: Structural evidence that endothelial cell growth factor beta is the precursor of
A/Reference number: A94127; MUID:87016918; PMID:3532107
A/Accession: B25043
A/Molecule type: protein
A/Residues: 2-155 <BUR>
A/Note: this form was designated beta endothelial cell growth factor
A/Accession: C25043
A/Molecule type: protein
A/Residues: 16-155 <BU2>
A/Note: this form was designated acidic fibroblast growth factor
A/Accession: A25043
A/Molecule type: protein
A/Residues: 22-155 <BU3>
A/Note: this form was designated alpha endothelial cell growth factor
R/Strydom, D.J.; Harper, J.W.; Lobb, R.R.
Biochemistry 25, 945-951, 1986
A/Title: Amino acid sequence of bovine brain derived class 1 heparin-binding growth fact
A/Reference number: A24539; MUID:86187766; PMID:2421762
A/Accession: A24539
A/Molecule type: protein
A/Residues: 16-155 <STR>
R/Thomas, K.A.; Gimenez-Gallego, G.; Rios-Candelore, M.; DiSalvo, J.
J. Protein Chem. 6, 163-171, 1987
A/Title: Primary structure and mitogenic and angiogenic activities of brain-derived acic
A/Reference number: A60884
A/Accession: A60884
A/Molecule type: protein
A/Residues: 16-155 <THO>
R/Kuo, M.D.; Huang, S.S.; Huang, J.S.
J. Biol. Chem. 265, 16455-16463, 1990
A/Title: Acidic fibroblast growth factor receptor purified from bovine liver is a novel
A/Reference number: A37892; MUID:90375514; PMID:2168890
A/Accession: A37892
A/Molecule type: protein
A/Residues: 22-30, 'X', 32-38 <KU2>
A/Note: this form was designated brain-derived growth factor A
A/Accession: B37892
A/Molecule type: protein
A/Residues: 16-30, 'X', 32-40 <KUO>
A/Note: this sequence is an amino-terminal fragment of a form designated as brain-derive
R/Hill, C.E.; Belford, D.A.; Godovac-Zimmermann, J.; Hendry, I.A.
Brain Res. Dev. Brain Res. 63, 13-19, 1991
A/Title: Class 1 heparin binding growth factor promotes the differentiation but not the
A/Reference number: A61198; MUID:92164087; PMID:1724209
A/Accession: A61198
A/Molecule type: protein
A/Residues: 11-26; 28-50; 53-110, 'H', 112, 'NTY'; 134-155 <HIL>
R/Philippe, J.M.; Renaud, F.; Desset, S.; Laurent, M.; Mallet, J.; Courtois, Y.; Edwards
Biochem. Biophys. Res. Commun. 188, 843-850, 1992
A/Title: Cloning of two different 5' untranslated exons of bovine acidic fibroblast grow
A/Reference number: I46024; MUID:93075172; PMID:1280126
A/Accession: I46024
A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-18 <PH2>
A/Cross-references: EMBL:X66446; NID:g411; PIDN:CRAA47063.1; PID:g412
R/Sasaki, H.; Hoshi, H.; Hong, Y.M.; Suzuki, T.; Kato, T.; Sasaki, H.; Saito, M.; Youki,
J. Biol. Chem. 264, 17606-17612, 1989
A/Title: Purification of acidic fibroblast growth factor from bovine heart and its local
A/Reference number: A34477; MUID:90008933; PMID:2677012
A/Accession: A34477
A/Status: preliminary
A/Molecule type: protein
A/Residues: 16-24; 121-127; 134-143 <SAS>
A/Experimental source: heart
C/Comment: The acidic and basic fibroblast growth factors are the major endothelial-cell
ell types in vitro (although bFGF is 30-100 times more potent than aFGF in stimulating t
f these two growth factors.
C/Comment: This protein binds heparin, although less strongly than does bFGF.
C/Comment: There are some sequence similarities between residues 117-126 (a region flank

sidues 18-27) and bovine substance P beta (residues 98-107).

C;Genetics: HBGF-1
A;Gene: HBGF-1
A;Introns: 57/1; 91/3
C;Superfamily: fibroblast growth factor
C;Keywords: acetylated amino end; angiogenesis; growth factor; heparin binding; mitogen
F;2-155/Product: beta endothelial cell growth factor #status experimental <ECB>
F;16-155/Product: acidic fibroblast growth factor #status experimental <MAT>
F;22-155/Product: alpha endothelial cell growth factor #status experimental <BCA>
F;24-28,113-116/Region: heparin binding #status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 13.0%; Score 144.5; DB 1; Length 155;
Best Local Similarity 35.0%; Pred. No. 0.00012;
Matches 49; Conservative 12; Mismatches 64; Indels 15; Gaps 5;
Qy 38 LQFGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQSPESL-LQKALKPGVIQILGV 96
Db 18 LPLGNKPKLLYCSNGY---FLRILPDGTVGDKRSDQHIQLQCAESIGEVYIKST 74
Qy 97 KTSFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 156
Db 75 ETGQFLAMTDGLYGS-QTNEECFLERLEENHNTYISKKAERHWFVGLKNGR-- 131
Qy 157 APRGPAPR-----FLPLP 168
Db 132 SKLGPRTHFQKAILFLPLP 151

RESULT 29
JH0476
A;Molecule type: mRNA
A;Residues: 1-152 <SCH>
A;Cross-references: EMBL:X60317; NID:g1873; PIDN:CAA42869.1; PID:g1874
A;Experimental source: heart
A;Note: The hydrophobic core residues are packed around the internal symmetry axis
C;Comment: This protein belongs to the fibroblast growth factor family.
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor; heparin binding
F;22-28/Region: nuclear location signal
F;133/Binding site: heparin (lys) #status predicted

Query Match 12.9%; Score 143.5; DB 2; Length 152;
Best Local Similarity 33.6%; Pred. No. 0.00014;
Matches 46; Conservative 12; Mismatches 64; Indels 15; Gaps 5;
Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQSPESL-LQKALKPGVIQILGVKTS 99
Db 21 GNYKPKLLYCSNGH---FLRILPDGTVGDKRSDQHIQLQCAESIGEVYIKSTGTG 77
Qy 100 RFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 159
Db 78 QYLAAMTSLYGS-QTPSEECFLERLEENHNTYISKKAERHWFVGLKNGR--NGSCKR 134
Qy 160 GPAPR-----FLPLP 168
Db 135 GPRTHYQKAILFLPLP 151

RESULT 30
S26049
fibroblast growth factor 7 precursor - rat
N;Alternate names: keratinocyte growth factor
C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 16-Jul-1999
C;Accession: S26049; S78446
R;Yan, G.; Nikolaropoulos, S.; Wang, F.; McKeehan, W.L.
In Vitro Cell. Dev. Biol. 27, 437-438, 1991
A;Title: Sequence of rat keratinocyte growth factor (heparin-binding growth factor type
A;Reference number: S26049
A;Accession: S26049
A;Molecule type: mRNA
A;Residues: 1-194 <YAN>
A;Cross-references: EMBL:X56551
R;Yan, G.
submitted to the EMBL Data Library, February 1991

A;Reference number: S78446
A;Accession: S78446
A;Molecule type: mRNA
A;Residues: 1-16,'P',18-100,'M',102-123,'Q',125-150,'S',152-194 <YAN>
A;Cross-references: EMBL:X56551; NID:g56707; PIDN:CAA39892.1; PID:g56708
C;Superfamily: fibroblast growth factor
C;Keywords: extracellular protein; growth factor; heparin binding; mitogen
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-194/Product: fibroblast growth factor 7 #status predicted <MAT>

Query Match 12.8%; Score 142; DB 2; Length 194;
Best Local Similarity 27.5%; Pred. No. 0.00024;
Matches 39; Conservative 30; Mismatches 47; Indels 26; Gaps 6;
Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAAD-QSPESLQKALKPGVIQILGVKTS 99
Db 61 GGDIVRRLFC---RTQWYLRIDKRGKVGKTQMRNSYNIMEIRTVAVGIVAIGVESE 116
Qy 100 RFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAHGLPLHLPGNKSPHRDP 145
Db 117 YLLAMNKEGELYAKECN-EDCNFKLELLENHNTYISAKWTHSGGEMFVALNQGLP-- 173
Qy 146 LPGNKSPHRDPAPRGPAPRFLPL 167
Db 174 VKGKTKKEQKT----AHFLPM 191

RESULT 31
I50588
fibroblast growth factor 3 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000
C;Accession: I50588
R;Mahmood, R.; Kiefer, P.; Guthrie, S.; Dickson, C.; Mason, I.
Development 121, 1399-1410, 1995
A;Title: Multiple roles for FGF-3 during cranial neural development in the chicken.
A;Reference number: I50588; MUID:95309122; PMID:7789270
A;Accession: I50588
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-220 <MAH>
A;Cross-references: EMBL:Z47555; NID:9623215; PIDN:CAA87635.1; PID:g623216
C;Superfamily: fibroblast growth factor

Query Match 12.8%; Score 142; DB 2; Length 220;
Best Local Similarity 34.7%; Pred. No. 0.00028;
Matches 35; Conservative 20; Mismatches 40; Indels 6; Gaps 3;
Qy 41 GGQVRQRYLYTDDAQOQTEAHLEIREDTGVGAADQ-QSPESLQKALKPGVIQILGVKTS 99
Db 41 GGAFFFFLYC---ATKYHQLHPGGKINGTLEKNVSFSLITAVDVGIVAIGLFGSG 96
Qy 100 RFLCQRPDGLYSLHFDPEACSFRELLLEDGYNVYQSEAH 140
Db 97 KYLAAMKGRGLYASENYNTE-CEFVERTHELGYNTYASRLY 136

RESULT 32
S49501
keratinocyte growth factor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

R;Borja, A. Z.; Meijers, C.; Zeller, R.
Dev Biol. 157, 110-118, 1993
A;Title: Expression of alternatively spliced bFGF first coding exons and antisense mRNA
A;Reference number: A4834, MUID:39246053; PMID:7693281
A;Accession: A48634
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-189 <BOR>
A;Experimental source: embryo

A;Note: sequence extracted from NCBI backbone (NCBIN:131000, NCBI:131001)
R;Mittrani, E.; Gruenbaum, Y.; Shohat, H.; Ziv, T.
Development 109, 387-393, 1990
A;Title: Fibroblast growth factor during mesoderm induction in the early chick embryo.
A;Reference number: S23636; MUID:90382254; PMID:2401202
A;Accession: S23636
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 95-128 <MIT>
A;Cross-references: EMBL:X56804; NID:g62855; PIDN:CAA40139.1; PID:g62856
C;Superfamily: fibroblast growth factor

Query Match 12.4%; Score 138; DB 2; Length 189;
Best Local Similarity 35.4%; Pred. No. 0.0005;
Matches 40; Conservative 18; Mismatches 47; Indels 8; Gaps 5;

Qy 61 LEIRDEGTGGAADQS-PESLQLKALKPGVIQILGKTSRFLCQPDGALYSLHFDPE 119
Db 75 LRINPDGVDGVRKSDPHIKLQQAERGVSIGKVSANFLAMKEDGRLL-ALKCATE 133

Qy 120 ACSFRELLEDGYNVYQSEAHGLPHLPNGKSPHRDPAPR-GPAR-----FLPL 167
Db 134 ECFPFERLENNYTYRSRKYS-DWYVALKRTGYKPGKTPGQKAILFLPM 185

RESULT 36
A40117
basic fibroblast growth factor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A40117; A29618
R;Kimmelman, D.; Abraham, J.A.; Haaparanta, T.; Pallasi, T.M.; Kirschner, M.W.
Science 242, 1053-1056, 1988
A;Title: The presence of fibroblast growth factor in the frog egg: its role as a natural
A;Reference number: A40117; MUID:89058621; PMID:3194757
A;Accession: A40117
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <KIM>
A;Cross-references: GB:M18067; NID:g214177; PIDN:AAA49726.1; PID:g214178; GB:M21092
R;Kimmelman, D.; Kirschner, M.
Cell 51, 869-877, 1987
A;Title: Synergistic induction of mesoderm by FGF and TGF-beta and the identification of
A;Reference number: A29618; MUID:88052890; PMID:3479265
A;Accession: A29618
A;Molecule type: mRNA
A;Residues: 95-110,112-155 <KI2>
C;Superfamily: fibroblast growth factor
C;Keywords: growth factor

Query Match 12.1%; Score 135; DB 1; Length 155;
Best Local Similarity 33.0%; Pred. No. 0.00068;
Matches 38; Conservative 22; Mismatches 43; Indels 12; Gaps 5;

Qy 61 LEIRDEGTGGAADQS-PESL-LQLKALKPGVTQILGKTSRFLCQPDGALYSLHFDPE 119
Db 41 LRINSDGVDGGRKSDSHIKLQQAERGVSIGKVTANRYLAMKEDGRLL-TSLRCITD 99

Qy 120 ACSFRELLEDGYNVYQSEAHG-----LPLHLPNGKSPHRDPAPRGPAPR-----FLPL 167
Db 100 ECFPFERLEANNYTYRSRKYSYVVALKRTGQ---YKNGSSGTGQKAILFLPM 151

RESULT 37
JW0055
acidic fibroblast growth factor 1 precursor - sheep
N;Alternate names: FGF-1
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-Jan-2001
C;Accession: JW0055
R;Grieb, T.W.; Ring, M.; Brown, E.; Palmer, C.; Belle, N.; Donjerkovic, D.; Chang, H.; Y
Biochem. Biophys. Res. Commun. 246, 182-191, 1998
A;Title: Primary structure of ovine fibroblast growth factor-1 deduced by protein and cd

A;Reference number: JW0055; MUID:98262939; PMID:9600090
A;Accession: JW0055
A;Molecule type: mRNA
A;Residues: 1-155 <GRI>
C;Comment: This protein is a potent mitogenic factor for NIH 3T3 fibroblasts in the absence of serum.
C;Superfamily: fibroblast growth factor

Query Match 11.8%; Score 131.5; DB 2; Length 155;
Best Local Similarity 33.3%; Pred. No. 0.0013;
Matches 46; Conservative 14; Mismatches 67; Indels 11; Gaps 5;

Qy 38 LQFGQVQRVLYITDDAQTEAHLEIRDEGTGGAADQSPESL-LQLKALKPGVIQILGV 96

Db 18 LPLGNYKKPKLLYCSNGY---FLRILPDGVDGTRDSQHIQLQLYAESIGEVIYIKST 74

Qy 97 KTSRFLCQPDGALYSLHFDPEACSFRELLEDGYNVYQSEAHGLP---LHLPGNKSPH 153

Db 75 ETGQFLAMDTNGLLYGS-QTPSECLFLERLEENHYNTYISKHAENKWFGLKKGSSK 133

Qy 154 RDPAPRGPAPR---FLPLP 168

Db 134 LGPRTHFGQKAILFLPLP 151

RESULT 38

A60130

acidic fibroblast growth factor - chicken

N;Alternate names: endothelial cell growth factor

C;Species: Gallus gallus (chicken)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 16-Jul-1999

C;Accession: A60130; S02639

R;Schmuerch, H.; Risau, W.

Development 111, 1143-1154, 1991

A;Title: Differentiating and mature neurons express the acidic fibroblast growth factor (aFGF) in the developing chick brain.

A;Reference number: A60130; MUID:91347925; PMID:1715259

A;Accession: A60130

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-155 <SCH>

A;Cross-references: GB:S63263; NID:g234372; PIDN:AA19629.1; PID:g234373

R;Risau, W.; Gautschi-Sova, P.; Boehlen, P.

EMBO J. 7, 959-962, 1988

A;Title: Endothelial cell growth factors in embryonic and adult chick brain are related to basic fibroblast growth factor (bFGF).

A;Reference number: S02639; MUID:89296438; PMID:3402441

A;Accession: S02639

A;Molecule type: protein

A;Residues: 22-30,'X',32-44,'X',46-48 <RIS>

C;Superfamily: fibroblast growth factor

C;Keywords: growth factor

Query Match 11.5%; Score 127.5; DB 2; Length 155;
Best Local Similarity 32.6%; Pred. No. 0.0027;
Matches 45; Conservative 15; Mismatches 67; Indels 11; Gaps 5;

Qy 38 LQFGQVQRVLYITDDAQTEAHLEIRDEGTGGAADQSPESL-LQLKALKPGVIQILGV 96

Db 18 LPLGNYKKPKLLYCSNGH---FLRILPDGVDGTRDSQHIQLQLSAEDVGEVIYIKST 74

Qy 97 KTSRFLCQPDGALYSLHFDPEACSFRELLEDGYNVYQSEAHG-----LPLHLPNG-K 150

Db 75 ASGQYLAQMDTNGLLYGS-QLGPERCLFLERLEENHYNTYISKHADKNWFGVGLKKGNSK 133

Qy 151 SPHRDPAPRGPAPRFLPLP 168

Db 134 LGPRTHYGGKAILFLPLP 151

RESULT 39

S31622

basic fibroblast growth factor - short-tailed opossum (Monodelphis domestica) (fragment)

C;Species: Monodelphis domestica

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995

C;Accession: S31622

Search completed: March 2, 2004, 16:08:04
Job time : 30.6083 secs

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OM protein - protein search, using sw model

Run on: March 2, 2004, 16:02:23 ; Search time 2.6875 Seconds
(without alignments)
288.145 Million cell updates/sec

Title: US-10-060-765-8
Perfect score: 89
Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pap.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pap.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	181	4	US-09-390-207-5
2	89	100.0	209	4	US-09-390-207-2
3	57	64.0	1419	4	US-09-252-991A-31822
4	51	57.3	133	4	US-09-252-991A-22856
5	51	57.3	187	4	US-09-252-991A-18109
6	46	51.7	286	4	US-09-252-991A-29952
7	46	51.7	307	4	US-09-252-991A-21588
8	46	51.7	330	4	US-09-252-991A-25664
9	45	50.6	209	4	US-09-252-991A-30648
10	45	50.6	601	4	US-09-252-991A-23280
11	45	50.6	632	4	US-09-252-991A-24235
12	45	50.6	1294	2	US-08-819-288-3
13	45	50.6	1294	4	US-09-400-348-3
14	45	50.6	1321	1	US-08-261-822A-3
15	45	50.6	1321	5	PCT-US95-07744A-3
16	44.5	50.0	372	4	US-09-252-991A-32717
17	44	49.4	372	4	US-09-252-991A-23226
18	44	49.4	441	4	US-09-252-991A-27502
19	44	49.4	490	4	US-09-489-039A-8325
20	44	49.4	552	1	US-07-999-280A-22
21	44	49.4	552	1	US-07-999-280A-24
22	44	49.4	552	1	US-08-426-279-22
23	44	49.4	552	1	US-08-426-279-24
24	44	49.4	552	1	US-08-401-013-22
25	44	49.4	552	1	US-08-401-013-24
26	44	49.4	552	3	US-08-426-570-22
27	44	49.4	552	3	US-08-426-570-24

28	44	49.4	552	3	US-08-425-876-22	Sequence 22, Appl
29	44	49.4	552	3	US-08-425-876-24	Sequence 22, Appl
30	44	49.4	552	3	US-08-426-243-22	Sequence 24, Appl
31	44	49.4	552	3	US-08-426-243-24	Sequence 24, Appl
32	44	49.4	552	3	US-08-401-632-22	Sequence 22, Appl
33	44	49.4	552	3	US-08-401-632-24	Sequence 24, Appl
34	44	49.4	969	4	US-09-252-991A-26118	Sequence 26118, A
35	43	48.3	172	4	US-09-252-991A-22814	Sequence 22814, A
36	43	48.3	247	4	US-09-252-991A-22135	Sequence 22135, A
37	43	48.3	356	4	US-09-252-991A-26571	Sequence 26571, A
38	43	48.3	410	1	US-08-123-343A-5	Sequence 5, Appl
39	43	48.3	410	1	US-08-123-343A-7	Sequence 7, Appl
40	43	48.3	410	3	US-09-431-573-4	Sequence 4, Appl
41	43	48.3	410	3	US-09-431-573-5	Sequence 5, Appl
42	43	48.3	420	4	US-09-252-991A-30229	Sequence 30229, A
43	43	48.3	586	4	US-09-252-991A-28601	Sequence 28601, A
44	43	48.3	599	4	US-09-252-991A-17250	Sequence 17250, A
45	43	48.3	656	4	US-09-252-991A-25003	Sequence 25003, A

ALIGNMENTS

RESULT 1
US-09-390-207-5
; Sequence 5, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-5

Query Match 100.0%; Score 89; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 117 HLPGNKSPHRDPAPR 131

RESULT 2
US-09-390-207-2
; Sequence 2, Application US/09390207
; Patent No. 6504530
; GENERAL INFORMATION:
; APPLICANT: Thomason, Arlen
; APPLICANT: Liu, Benxian
; TITLE OF INVENTION: Fibroblast Growth Factor-Like Polypeptides
; FILE REFERENCE: 99-371
; CURRENT APPLICATION NUMBER: US/09/390,207
; CURRENT FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-390-207-2

Query Match 100.0%; Score 89; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18109
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-18109
 Query Match 57.3%; Score 51; DB 4; Length 187;
 Best Local Similarity 57.1%; Pred. No. 2.2;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAP 14
 DB 89 HRPGRHPRHDPAP 102
 RESULT 6
 US-09-252-991A-29952
 ; Sequence 29952, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 29952
 ; LENGTH: 286
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-29952
 Query Match 51.7%; Score 46; DB 4; Length 286;
 Best Local Similarity 53.3%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAP 15
 DB 35 HLPDRAHPRADPRPR 49
 RESULT 7
 US-09-252-991A-21588
 ; Sequence 21588, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 31822
 ; LENGTH: 1419
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-31822
 Query Match 64.0%; Score 57; DB 4; Length 1419;
 Best Local Similarity 66.7%; Pred. No. 2.5;
 Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAP 15
 DB 25 HLPRAQPHRRDPAP 39
 RESULT 4
 US-09-252-991A-22856
 ; Sequence 22856, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 22856
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-22856
 Query Match 57.3%; Score 51; DB 4; Length 133;
 Best Local Similarity 58.8%; Pred. No. 1.5;
 Matches 10; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
 QY 1 HLPGN--KSPHRDPAP 15
 DB 109 HRPCTAASEPHRSPAPR 125
 RESULT 5
 US-09-252-991A-18109
 ; Sequence 18109, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:

```

; SEQ ID NO 21588
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21588

Query Match      51.7%; Score 46; DB 4; Length 307;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGKNSPHRDPA 15
DB      100 PGRPRPGRPA 112

RESULT 8
US-09-252-991A-25664
; Sequence 25664, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25664
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25664

Query Match      51.7%; Score 46; DB 4; Length 330;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      3 PGKNSPHRDPA 15
DB      5 PAGRPRPGRPQR 17

RESULT 9
US-09-252-991A-30648
; Sequence 30648, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30648
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30648

Query Match      50.6%; Score 45; DB 4; Length 209;
Best Local Similarity 58.3%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGKNSPHRDPA 14

; SEQ ID NO 21588
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21588

Query Match      51.7%; Score 46; DB 4; Length 307;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGKNSPHRDPA 15
DB      100 PGRPRPGRPA 112

RESULT 8
US-09-252-991A-25664
; Sequence 25664, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25664
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25664

Query Match      50.6%; Score 45; DB 4; Length 601;
Best Local Similarity 53.3%; Pred. No. 60;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPA 15
DB      359 HLPDRAHPRRPA 373

RESULT 11
US-09-252-991A-24235
; Sequence 24235, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24235
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24235

Query Match      50.6%; Score 45; DB 4; Length 632;
Best Local Similarity 53.3%; Pred. No. 63;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPA 15
DB      16 HLPAGRAADHAFPA 30

RESULT 12
US-08-819-288-3
; Sequence 3, Application US/08819288
; Patent No. 5955652
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph
; APPLICANT: Alonso, Jose

```

```

; TITLE OF INVENTION: PLANT GENES FOR SENSITIVITY TO ETHYLENE
; TITLE OF INVENTION: AND PATHOGENS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5955652ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/819,288
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: UPN-2949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-819-288-3

Query Match 50.6%; Score 45; DB 2; Length 1294;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPA 13
Db 939 HLPNNKSGYWDPS 951

RESULT 14
US-08-261-822A-3
; Sequence 3, Application US/08261822A
; Patent No. 5650553
; GENERAL INFORMATION:
; APPLICANT: Ecker, Joseph R. et al.
; TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,822A
; FILING DATE: 17-JUN-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-261-822A-3

Query Match 50.6%; Score 45; DB 1; Length 1321;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPA 13
Db 939 HLPNNKSGYWDPS 951
```

RESULT 15
PCT-US95-07744A-3
; Sequence 3, Application PC/TUS9507744A
; GENERAL INFORMATION:
; APPLICANT: Trustees of The University of Pennsylvania
; TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
; TITLE OF INVENTION: and Pathogens
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07744A
; FILING DATE: 15-JUNE-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/261,822
; FILING DATE: June 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Beardell, Lori Y.
; REGISTRATION NUMBER: 34,293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1321 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; PCT-US95-07744A-3

Query Match 50.6%; Score 45; DB 5; Length 1321;
Best Local Similarity 61.5%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HLFNKSPPHDPDA 13
||| ||| : |||
Db 939 HLFNKSPPHDPDA 951

RESULT 16
US-09-252-991A-32717
; Sequence 32717, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32717
; LENGTH: 372
; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32717

Query Match 50.0%; Score 44.5; DB 4; Length 372;
Best Local Similarity 56.2%; Pred. No. 43;
Matches 9; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

Qy 3 PGNKSPH---RDPAPR 15
||| : ||| |||
Db 216 PGEDPFRPRGPAPR 231

RESULT 17
US-09-252-991A-23226
; Sequence 23226, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23226
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23226

Query Match 49.4%; Score 44; DB 4; Length 372;
Best Local Similarity 42.9%; Pred. No. 51;
Matches 9; Conservative 4; Mismatches 2; Indels 6; Gaps 1;

Qy 1 HLPG-----NKSPHRDPAPR 15
||| : ||| : |||
Db 141 HLPGADRRHLRPHORPAPR 161

RESULT 18
US-09-252-991A-27502
; Sequence 27502, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27502
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27502

Query Match 49.4%; Score 44; DB 4; Length 441;
Best Local Similarity 56.2%; Pred. No. 61;
Matches 9; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

Qy 4 GNKSPHRD----PAPR 15
| : ||| |||
Db 76 GTRRPHRDLEAPAPR 91

Wed Mar 3 08:19:50 2004

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; MOLECULE TYPE: protein
; US-07-999-280A-22

Query Match          49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches              7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGKNSPHRDPA 14
DB      202 PASASPHQPPAP 213

RESULT 21
US-07-999-280A-24
; Sequence 24, Application US/07999280A
; Patent No. 5573930
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.
; APPLICANT: NOBLE, JANELLE A.
; APPLICANT: MARTIN, GEORGE A.
; APPLICANT: KAWASAKI, ERNEST S.
; APPLICANT: COYNE, MAZIE YEE
; APPLICANT: HALENBECK, ROBERT F.
; APPLICANT: KOTH, KIRSTON E.
; TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/999,280A
; FILING DATE: 28-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0681.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-999-280A-24

Query Match          49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches              7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGKNSPHRDPA 14
DB      202 PASASPHQPPAP 213

RESULT 22
US-08-426-279-22
; Sequence 22, Application US/08426279
; Patent No. 5672343
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.

```

APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,279
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-426-279-22

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKNSPHRDPA 14
| : ||| : |||
Db 202 PASASPHQPPAP 213

RESULT 23
US-08-426-279-24
; Sequence 24, Application US/08426279
; Patent No. 5672343
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.
; APPLICANT: NOBLE, JANELLE A.
; APPLICANT: MARTIN, GEORGE A.
; APPLICANT: KAWASAKI, ERNEST S.
; APPLICANT: COYNE, MAZIE YEE
; APPLICANT: HALENBECK, ROBERT F.
; APPLICANT: KOTHS, KIRSTON E.
; TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,279
FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-426-279-24

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKNSPHRDPA 14
| : ||| : |||
Db 202 PASASPHQPPAP 213

RESULT 24
US-08-401-013-22
; Sequence 22, Application US/08401013
; Patent No. 5681719
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.
; APPLICANT: NOBLE, JANELLE A.
; APPLICANT: MARTIN, GEORGE A.
; APPLICANT: KAWASAKI, ERNEST S.
; APPLICANT: COYNE, MAZIE YEE
; APPLICANT: HALENBECK, ROBERT F.
; APPLICANT: KOTHS, KIRSTON E.
; TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/401,013
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/999,280
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0681.007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-013-22

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKNSPHRD PAP 14
Db 202 PASASPHQPPAP 213

RESULT 25

US-08-401-013-24
Sequence 24, Application US/08401013

Patent No. 5681719
GENERAL INFORMATION:

APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHIS, KIRSTON E.

TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.

ZIP: 94662-8097

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/401,013
FILING DATE: 08-MAR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/999,280

FILING DATE: 28-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: McGarrigle Jr., Philip L.

REGISTRATION NUMBER: 31,395

REFERENCE/DOCKET NUMBER: 0681.007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2718

TELEFAX: (510) 655-3542

TELEX: n/a

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 552 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-401-013-24

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKNSPHRD PAP 14
Db 202 PASASPHQPPAP 213

RESULT 26

US-08-426-570-22

Sequence 22, Application US/08426570
Patent No. 6103224

GENERAL INFORMATION:

APPLICANT: LADNER, MARTHA B.

APPLICANT: NOBLE, JANELLE A.

APPLICANT: MARTIN, GEORGE A.

APPLICANT: KAWASAKI, ERNEST S.

APPLICANT: COYNE, MAZIE YEE

APPLICANT: HALENBECK, ROBERT F.

APPLICANT: KOTHIS, KIRSTON E.

TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: Intellectual Property - R440, P.O. Box 8097

CITY: Emeryville

STATE: California

COUNTRY: U.S.A.

ZIP: 94662-8097

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,570

FILING DATE: 21-APR-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: McGarrigle Jr., Philip L.

REGISTRATION NUMBER: 31,395

REFERENCE/DOCKET NUMBER: 0681.012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (510) 601-2718

TELEFAX: (510) 655-3542

TELEX: n/a

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 552 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-426-570-22

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKNSPHRD PAP 14

Db 202 PASASPHQPPAP 213

RESULT 27

US-08-426-570-24

Sequence 24, Application US/08426570

Patent No. 6103224

GENERAL INFORMATION:

APPLICANT: LADNER, MARTHA B.

APPLICANT: NOBLE, JANELLE A.

APPLICANT: MARTIN, GEORGE A.

APPLICANT: KAWASAKI, ERNEST S.

APPLICANT: COYNE, MAZIE YEE

APPLICANT: HALENBECK, ROBERT F.

APPLICANT: KOTHIS, KIRSTON E.

TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHIRON CORPORATION

STREET: Intellectual Property - R440, P.O. Box 8097

Wed Mar 3 08:19:50 2004

```
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,570
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0681.012
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-426-570-24

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : |||: |||
Db 202 PASASPHQPPAP 213

RESULT 28
US-08-425-876-22
; Sequence 22, Application US/08425876
; Patent No. 6117422
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.
; APPLICANT: NOBLE, JANELLE A.
; APPLICANT: MARTIN, GEORGE A.
; APPLICANT: KAWASAKI, ERNEST S.
; APPLICANT: COYNE, MAZIE YEE
; APPLICANT: HALENBECK, ROBERT F.
; APPLICANT: KOTHS, KIRSTON E.
; TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,876
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0681.011
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-876-24

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : |||: |||
Db 202 PASASPHQPPAP 213

RESULT 28
US-08-425-876-22
; Sequence 22, Application US/08425876
; Patent No. 6117422
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.
; APPLICANT: NOBLE, JANELLE A.
; APPLICANT: MARTIN, GEORGE A.
; APPLICANT: KAWASAKI, ERNEST S.
; APPLICANT: COYNE, MAZIE YEE
; APPLICANT: HALENBECK, ROBERT F.
; APPLICANT: KOTHS, KIRSTON E.
; TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,876
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0681.011
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-876-24

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : |||: |||
Db 202 PASASPHQPPAP 213

TELECOMMUNICATION INFORMATION:
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; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-876-22

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : |||: |||
Db 202 PASASPHQPPAP 213

RESULT 29
US-08-425-876-24
; Sequence 24, Application US/08425876
; Patent No. 6117422
; GENERAL INFORMATION:
; APPLICANT: LADNER, MARTHA B.
; APPLICANT: NOBLE, JANELLE A.
; APPLICANT: MARTIN, GEORGE A.
; APPLICANT: KAWASAKI, ERNEST S.
; APPLICANT: COYNE, MAZIE YEE
; APPLICANT: HALENBECK, ROBERT F.
; APPLICANT: KOTHS, KIRSTON E.
; TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHIRON CORPORATION
; STREET: Intellectual Property - R440, P.O. Box 8097
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,876
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McGarrigle Jr., Philip L.
; REGISTRATION NUMBER: 31,395
; REFERENCE/DOCKET NUMBER: 0681.011
; TELEPHONE: (510) 601-2718
; TELEFAX: (510) 655-3542
; TELEX: n/a
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 552 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-425-876-24

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : |||: |||
Db 202 PASASPHQPPAP 213

TELECOMMUNICATION INFORMATION:
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FILING DATE: 09-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-632-22

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : ||| : |||
Db 202 PASASPHQPPAP 213

RESULT 33
US-08-401-632-24
Sequence 24, Application US/08401632
Patent No. 6204020
GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENBECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,632
FILING DATE: 09-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-632-24

us-10-060-765-8.rai

Query Match 49.4%; Score 44; DB 3; Length 552;
Best Local Similarity 58.3%; Pred. No. 77;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
| : ||| : |||
Db 202 PASASPHQPPAP 213

RESULT 34
US-09-252-991A-26118
Sequence 26118, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26118
LENGTH: 969
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26118

Query Match 49.4%; Score 44; DB 4; Length 969;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 15
| : ||| : |||
Db 4 PASSRPSRDPSPR 16

RESULT 35
US-09-252-991A-22814
Sequence 22814, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22814
LENGTH: 172
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22814

Query Match 48.3%; Score 43; DB 4; Length 172;
Best Local Similarity 64.7%; Pred. No. 31;
Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

QY 1 HLPKNSP-HR-DPAPR 15
| : ||| : |||
Db 78 HLPKNSP-HR-DPAPR 94

RESULT 36
US-09-252-991A-22135

Wed Mar 3 08:19:50 2004

us-10-060-765-8-rai

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/123,343A

FILING DATE: 17-SEP-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/004,957

FILING DATE: 15-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: MIT-5907A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 61861-9540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 410 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-123-343A-5

Query Match 48.3%; Score 43; DB 1; Length 410;

Best Local Similarity 63.6%; Pred. No. 79;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GNKSPHRDPAP 14

DB 24 GNSSPHNP 34

RESULT 39

US-08-123-343A-7

Sequence 7, Application US/08123343A

Patent No. 5593879

GENERAL INFORMATION:

APPLICANT: Steller, Hermann

APPLICANT: Abrams, John M.

APPLICANT: Grether, Megan E.

APPLICANT: White, Kristin

TITLE OF INVENTION: Cell Death Genes of Drosophila

TITLE OF INVENTION: Melanogaster and Vertebrate Analogs

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/123,343A

FILING DATE: 17-SEP-1993

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/004,957

Sequence 22135, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22135

LENGTH: 247

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22135

Query Match 48.3%; Score 43; DB 4; Length 247;

Best Local Similarity 61.5%; Pred. No. 46;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAP 14

DB 65 LPGLRRPRRRPAP 77

RESULT 37

US-09-252-991A-26571

Sequence 26571, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26571

LENGTH: 356

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26571

Query Match 48.3%; Score 43; DB 4; Length 356;

Best Local Similarity 53.3%; Pred. No. 68;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAP 15

DB 128 HPGLRRSHRDPAP 142

RESULT 38

US-08-123-343A-5

Sequence 5, Application US/08123343A

Patent No. 5593879

GENERAL INFORMATION:

APPLICANT: Steller, Hermann

APPLICANT: Abrams, John M.

APPLICANT: Grether, Megan E.

APPLICANT: White, Kristin

TITLE OF INVENTION: Cell Death Genes of Drosophila

TITLE OF INVENTION: Melanogaster and Vertebrate Analogs

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5907A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 61861-9540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-123-343A-7

Query Match 48.3%; Score 43; DB 1; Length 410;
Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 24 GNSSPHNPLP 34

RESULT 40
US-09-431-573-4
; Sequence 4, Application US/09431573
; Patent No. 6235524
; GENERAL INFORMATION:
; APPLICANT: STELLER, HERMAN
; APPLICANT: AGAPITE, JULIE
; APPLICANT: MC CALL, KIMBERLY
; APPLICANT: BERGMANN, ANDREAS
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING AGENTS THAT
; TITLE OF INVENTION: INHIBIT MARK MEDIATED ANTI-APOPTOTIC SIGNALS
; FILE REFERENCE: MIT-04019
; CURRENT APPLICATION NUMBER: US/09/431,573
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,108
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-431-573-4

Query Match 48.3%; Score 43; DB 3; Length 410;
Best Local Similarity 63.6%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GNKSPHRDPAP 14
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Db 24 GNSSPHNPLP 34

Search completed: March 2, 2004, 16:09:02
Job time : 3.6875 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2004, 16:07:28 ; Search time 5.4 Seconds
(without alignments)
625.639 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRYLYTDDAQQTAAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	13 US-10-060-765-7	Sequence 7, Appl
2	86	100.0	136	9 US-09-901-938-33	Sequence 33, Appl
3	86	100.0	136	14 US-10-379-334-33	Sequence 33, Appl
4	86	100.0	208	9 US-09-755-695-2	Sequence 2, Appl
5	86	100.0	208	14 US-10-227-884-78	Sequence 78, Appl
6	86	100.0	208	14 US-10-230-163-78	Sequence 78, Appl
7	86	100.0	208	14 US-10-230-338-78	Sequence 78, Appl
8	86	100.0	208	14 US-10-218-631-78	Sequence 78, Appl
9	86	100.0	208	14 US-10-230-414-78	Sequence 78, Appl
10	86	100.0	208	14 US-10-216-159A-78	Sequence 78, Appl
11	86	100.0	208	14 US-10-218-849-78	Sequence 78, Appl
12	86	100.0	208	14 US-10-227-873-78	Sequence 78, Appl
13	86	100.0	208	14 US-10-227-883-78	Sequence 78, Appl
14	86	100.0	208	14 US-10-219-076-78	Sequence 78, Appl
15	86	100.0	208	14 US-10-230-434-78	Sequence 78, Appl

16	86	100.0	208	14	US-10-219-003-78	Sequence 78, Appl
17	86	100.0	208	14	US-10-219-075-78	Sequence 78, Appl
18	86	100.0	208	14	US-10-219-464-78	Sequence 78, Appl
19	86	100.0	208	14	US-10-219-466-78	Sequence 78, Appl
20	86	100.0	208	14	US-10-219-479-78	Sequence 78, Appl
21	86	100.0	208	14	US-10-219-481-78	Sequence 78, Appl
22	86	100.0	208	14	US-10-230-260-78	Sequence 78, Appl
23	86	100.0	208	14	US-10-232-231-78	Sequence 78, Appl
24	86	100.0	208	14	US-10-232-233-78	Sequence 78, Appl
25	86	100.0	208	14	US-10-216-165-78	Sequence 78, Appl
26	86	100.0	208	14	US-10-218-956-78	Sequence 78, Appl
27	86	100.0	208	14	US-10-219-468-78	Sequence 78, Appl
28	86	100.0	208	14	US-10-219-478-78	Sequence 78, Appl
29	86	100.0	208	14	US-10-219-536-78	Sequence 78, Appl
30	86	100.0	208	14	US-10-233-205-78	Sequence 78, Appl
31	86	100.0	208	14	US-10-219-072-78	Sequence 78, Appl
32	86	100.0	208	14	US-10-219-470-78	Sequence 78, Appl
33	86	100.0	208	14	US-10-219-474-78	Sequence 78, Appl
34	86	100.0	208	14	US-10-219-524-78	Sequence 78, Appl
35	86	100.0	208	14	US-10-219-528-78	Sequence 78, Appl
36	86	100.0	208	14	US-10-227-880-78	Sequence 78, Appl
37	86	100.0	208	14	US-10-227-881-78	Sequence 78, Appl
38	86	100.0	208	14	US-10-227-882-78	Sequence 78, Appl
39	86	100.0	208	14	US-10-230-436-78	Sequence 78, Appl
40	86	100.0	208	14	US-10-232-223-78	Sequence 78, Appl
41	86	100.0	208	14	US-10-232-225-78	Sequence 78, Appl
42	86	100.0	208	14	US-10-232-227-78	Sequence 78, Appl
43	86	100.0	208	14	US-10-232-229-78	Sequence 78, Appl
44	86	100.0	208	14	US-10-232-234-78	Sequence 78, Appl
45	86	100.0	208	14	US-10-219-060-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1

US-10-060-765-7
; Sequence 7, Application US/10060765
; Publication No. US20020164713A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020164713A1uyuki
; APPLICANT: Kavanagh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/060,765
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-765-7

Query Match 100.0%; Score 86; DB 13; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTAAH 16

DB 1 RQRYLYTDDAQQTAAH 16

RESULT 2

US-09-901-938-33
; Sequence 33, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECOS, Michael
; APPLICANT: WHITE, Kenneth

```
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-901-938-33
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Query Match 100.0%; Score 86; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RQRYLYTDDAQTEAH 16
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Db 7 RQRYLYTDDAQTEAH 22
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RESULT 3
US-10-379-334-33
; Sequence 33, Application US/10379334
; Publication No. US20030181379A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/10/379,334
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US/09/901,938
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-379-334-33
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Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 7 RQRYLYTDDAQTEAH 22
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RESULT 4
US-09-755-695-2
; Sequence 2, Application US/09755695
; Patent No. US20020081663A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
; FILE REFERENCE: 00-03
; CURRENT APPLICATION NUMBER: US/09/755,695
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/174,526
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-695-2
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Query Match 100.0%; Score 86; DB 9; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 RQRYLYTDDAQTEAH 16
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Db 44 RQRYLYTDDAQTEAH 59
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RESULT 5
US-10-227-884-78
; Sequence 78, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
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7	PRIOR APPLICATION NUMBER: 60/108801	
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7	PRIOR APPLICATION NUMBER: 60/108849	
7	PRIOR FILING DATE: 1998-11-18	
7	PRIOR APPLICATION NUMBER: 60/112422	
7	PRIOR FILING DATE: 1998-12-15	
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7	PRIOR APPLICATION NUMBER: 60/113605	
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7	PRIOR APPLICATION NUMBER: 60/113621	
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7	PRIOR APPLICATION NUMBER: 60/119549	
7	PRIOR FILING DATE: 1999-02-10	
7	PRIOR APPLICATION NUMBER: 60/123618	
7	PRIOR FILING DATE: 1999-03-10	
7	PRIOR APPLICATION NUMBER: 60/125259	
7	PRIOR FILING DATE: 1999-03-19	
7	PRIOR APPLICATION NUMBER: 60/125775	
7	PRIOR FILING DATE: 1999-03-23	
7	PRIOR APPLICATION NUMBER: 60/126773	
7	PRIOR FILING DATE: 1999-03-29	
7	PRIOR APPLICATION NUMBER: 60/127887	
7	PRIOR FILING DATE: 1999-04-05	
7	PRIOR APPLICATION NUMBER: 60/130232	
7	PRIOR FILING DATE: 1999-04-21	
7	PRIOR APPLICATION NUMBER: 60/131291	
7	PRIOR FILING DATE: 1999-04-27	
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7	PRIOR FILING DATE: 1999-04-26	
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7	PRIOR FILING DATE: 1999-06-22	
7	PRIOR APPLICATION NUMBER: 60/141037	
7	PRIOR FILING DATE: 1999-06-23	
7	PRIOR APPLICATION NUMBER: 60/144758	
7	PRIOR FILING DATE: 1999-07-20	
7	PRIOR APPLICATION NUMBER: 60/145698	
7	PRIOR FILING DATE: 1999-07-26	
7	PRIOR APPLICATION NUMBER: 60/146222	
7	PRIOR FILING DATE: 1999-07-28	
7	PRIOR APPLICATION NUMBER: 60/146963	
7	PRIOR FILING DATE: 1999-08-03	
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7	PRIOR FILING DATE: 1999-08-17	
7	PRIOR APPLICATION NUMBER: 60/149638	
7	PRIOR FILING DATE: 1999-08-17	
7	PRIOR APPLICATION NUMBER: 60/151733	
7	PRIOR FILING DATE: 1999-08-31	
7	PRIOR APPLICATION NUMBER: 60/164418	
7	PRIOR FILING DATE: 1999-11-09	
7	PRIOR APPLICATION NUMBER: 60/166361	
7	PRIOR FILING DATE: 1999-11-16	
7	PRIOR APPLICATION NUMBER: 60/169445	
7	PRIOR FILING DATE: 1999-12-07	
7	PRIOR APPLICATION NUMBER: 60/169495	
7	PRIOR FILING DATE: 1999-12-07	
7	PRIOR APPLICATION NUMBER: 60/169835	

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Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RORVLYTDDAQOTEAH 16
Db      44 RORVLYTDDAQOTEAH 59

RESULT 6
US-10-230-163-78
; Sequence 78, Application US/10230163
; Publication No. US2003003635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
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; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
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; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
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; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
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; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
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; PRIOR APPLICATION NUMBER: 60/101738
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; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
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; PRIOR FILING DATE: 1998-11-18
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; PRIOR FILING DATE: 1998-12-15
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PRIOR APPLICATION NUMBER: 60/113296
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PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
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PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
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PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-14
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PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
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PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
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PRIOR APPLICATION NUMBER: 60/146222
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PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
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PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
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PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
| | | | | | | | | | | | | | | | | | | | | |
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 7
US-10-230-338-78
Sequence 78, Application US/10230338
Publication No. US20030044934A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530P1C92
CURRENT APPLICATION NUMBER: US/10/230,338
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 78
LENGTH: 208
TYPE: PRT
ORGANISM: Homo Sapien
US-10-230-338-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
| | | | | | | | | | | | | | | | | | | | | |
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 8
US-10-218-631-78
Sequence 78, Application US/10218631
Publication No. US20030045687A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria

```
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3530P1C14
/ CURRENT APPLICATION NUMBER: US/10/216,631
/ CURRENT FILING DATE: 2002-08-12
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 78
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-218-631-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQOQTEAH 16
Db 44 RORYLYTDDAQOQTEAH 59

RESULT 9
US-10-230-414-78
/ Sequence 78, Application US/10230414
/ Publication No. US20030050448A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3530P1C98
/ CURRENT APPLICATION NUMBER: US/10/230,414
/ CURRENT FILING DATE: 2002-08-28
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
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/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 78
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-230-414-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQOQTEAH 16
Db 44 RORYLYTDDAQOQTEAH 59

RESULT 10
US-10-216-159A-78
/ Sequence 78, Application US/10216159A
/ Publication No. US20030069397A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3530P1C6
/ CURRENT APPLICATION NUMBER: US/10/216,159A
/ CURRENT FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
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; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTFAH 16
Db      44 RQRYLYTDDAQQTFAH 59

RESULT 11
US-10-218-849-78
; Sequence 78, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTFAH 16
Db      44 RQRYLYTDDAQQTFAH 59

RESULT 12
US-10-227-873-78
; Sequence 78, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
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; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
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; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
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1 PRIOR APPLICATION NUMBER: 60/099812
2 PRIOR FILING DATE: 1998-09-10
3 PRIOR APPLICATION NUMBER: 60/099816
4 PRIOR FILING DATE: 1998-09-10
5 PRIOR APPLICATION NUMBER: 60/100038
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7 PRIOR APPLICATION NUMBER: 60/100385
8 PRIOR FILING DATE: 1998-09-15
9 PRIOR APPLICATION NUMBER: 60/100390
10 PRIOR FILING DATE: 1998-09-15
11 PRIOR APPLICATION NUMBER: 60/100627
12 PRIOR FILING DATE: 1998-09-16
13 PRIOR APPLICATION NUMBER: 60/100848
14 PRIOR FILING DATE: 1998-09-18
15 PRIOR APPLICATION NUMBER: 60/100919
16 PRIOR FILING DATE: 1998-09-17
17 PRIOR APPLICATION NUMBER: 60/101477
18 PRIOR FILING DATE: 1998-09-23
19 PRIOR APPLICATION NUMBER: 60/101738
20 PRIOR FILING DATE: 1998-09-24
21 PRIOR APPLICATION NUMBER: 60/101741
22 PRIOR FILING DATE: 1998-09-24
23 PRIOR APPLICATION NUMBER: 60/101786
24 PRIOR FILING DATE: 1998-09-25
25 PRIOR APPLICATION NUMBER: 60/101916
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27 PRIOR APPLICATION NUMBER: 60/101922
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29 PRIOR APPLICATION NUMBER: 60/106178
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33 PRIOR APPLICATION NUMBER: 60/106454
34 PRIOR FILING DATE: 1998-10-30
35 PRIOR APPLICATION NUMBER: 60/106905
36 PRIOR FILING DATE: 1998-11-03
37 PRIOR APPLICATION NUMBER: 60/108787
38 PRIOR FILING DATE: 1998-11-17
39 PRIOR APPLICATION NUMBER: 60/108801
40 PRIOR FILING DATE: 1998-11-17
41 PRIOR APPLICATION NUMBER: 60/108849
42 PRIOR FILING DATE: 1998-11-18
43 PRIOR APPLICATION NUMBER: 60/112422
44 PRIOR FILING DATE: 1998-12-15
45 PRIOR APPLICATION NUMBER: 60/113296
46 PRIOR FILING DATE: 1998-12-22
47 PRIOR APPLICATION NUMBER: 60/113605
48 PRIOR FILING DATE: 1998-12-23
49 PRIOR APPLICATION NUMBER: 60/113621
50 PRIOR FILING DATE: 1998-12-23
51 PRIOR APPLICATION NUMBER: 60/115558
52 PRIOR FILING DATE: 1999-01-12
53 PRIOR APPLICATION NUMBER: 60/115565
54 PRIOR FILING DATE: 1999-01-12
55 PRIOR APPLICATION NUMBER: 60/115733
56 PRIOR FILING DATE: 1999-01-12
57 PRIOR APPLICATION NUMBER: 60/119549
58 PRIOR FILING DATE: 1999-02-10
59 PRIOR APPLICATION NUMBER: 60/123618
60 PRIOR FILING DATE: 1999-03-10
61 PRIOR APPLICATION NUMBER: 60/125259
62 PRIOR FILING DATE: 1999-03-19
63 PRIOR APPLICATION NUMBER: 60/125775
64 PRIOR FILING DATE: 1999-03-23
65 PRIOR APPLICATION NUMBER: 60/126773
66 PRIOR FILING DATE: 1999-03-29
67 PRIOR APPLICATION NUMBER: 60/127887
68 PRIOR FILING DATE: 1999-04-05
69 PRIOR APPLICATION NUMBER: 60/130232
70 PRIOR FILING DATE: 1999-04-21
71 PRIOR APPLICATION NUMBER: 60/131022
72 PRIOR FILING DATE: 1999-04-26
73 PRIOR APPLICATION NUMBER: 60/131270

1 PRIOR FILING DATE: 1999-04-27
2 PRIOR APPLICATION NUMBER: 60/131291
3 PRIOR FILING DATE: 1999-04-27
4 PRIOR APPLICATION NUMBER: 60/131445
5 PRIOR FILING DATE: 1999-04-28
6 PRIOR APPLICATION NUMBER: 60/134287
7 PRIOR FILING DATE: 1999-05-14
8 PRIOR APPLICATION NUMBER: 60/140650
9 PRIOR FILING DATE: 1999-06-22
10 PRIOR APPLICATION NUMBER: 60/140723
11 PRIOR FILING DATE: 1999-06-22
12 PRIOR APPLICATION NUMBER: 60/141037
13 PRIOR FILING DATE: 1999-06-23
14 PRIOR APPLICATION NUMBER: 60/144758
15 PRIOR FILING DATE: 1999-07-20
16 PRIOR APPLICATION NUMBER: 60/145698
17 PRIOR FILING DATE: 1999-07-26
18 PRIOR APPLICATION NUMBER: 60/146222
19 PRIOR FILING DATE: 1999-07-28
20 PRIOR APPLICATION NUMBER: 60/146963
21 PRIOR FILING DATE: 1999-08-03
22 PRIOR APPLICATION NUMBER: 60/149320
23 PRIOR FILING DATE: 1999-08-17
24 PRIOR APPLICATION NUMBER: 60/149638
25 PRIOR FILING DATE: 1999-08-17
26 PRIOR APPLICATION NUMBER: 60/151733
27 PRIOR FILING DATE: 1999-08-31
28 PRIOR APPLICATION NUMBER: 60/164418
29 PRIOR FILING DATE: 1999-11-09
30 PRIOR APPLICATION NUMBER: 60/166361
31 PRIOR FILING DATE: 1999-11-16
32 PRIOR APPLICATION NUMBER: 60/169445
33 PRIOR FILING DATE: 1999-12-07
34 PRIOR APPLICATION NUMBER: 60/169495
35 PRIOR FILING DATE: 1999-12-07
36 PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
DB 44 RQRYLYTDDAQOQTEAH 59

RESULT 13

US-10-227-883-78
Sequence 78, Application US/10227883
Publication No. US20030073817A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe P.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PLC78
CURRENT APPLICATION NUMBER: US/10/227,883
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17

1	PRIOR FILING DATE: 1998-09-15	60/100390
2	PRIOR APPLICATION NUMBER: 60/100390	
3	PRIOR FILING DATE: 1998-09-15	60/100627
4	PRIOR APPLICATION NUMBER: 60/100627	
5	PRIOR FILING DATE: 1998-09-16	60/100848
6	PRIOR APPLICATION NUMBER: 60/100848	
7	PRIOR FILING DATE: 1998-09-18	60/100919
8	PRIOR APPLICATION NUMBER: 60/100919	
9	PRIOR FILING DATE: 1998-09-17	60/101477
10	PRIOR APPLICATION NUMBER: 60/101477	
11	PRIOR FILING DATE: 1998-09-23	60/101738
12	PRIOR APPLICATION NUMBER: 60/101738	
13	PRIOR FILING DATE: 1998-09-24	60/101741
14	PRIOR APPLICATION NUMBER: 60/101741	
15	PRIOR FILING DATE: 1998-09-24	60/101786
16	PRIOR APPLICATION NUMBER: 60/101786	
17	PRIOR FILING DATE: 1998-09-25	60/101916
18	PRIOR APPLICATION NUMBER: 60/101916	
19	PRIOR FILING DATE: 1998-09-24	60/101922
20	PRIOR APPLICATION NUMBER: 60/101922	
21	PRIOR FILING DATE: 1998-09-24	60/106178
22	PRIOR APPLICATION NUMBER: 60/106178	
23	PRIOR FILING DATE: 1998-10-28	60/106248
24	PRIOR APPLICATION NUMBER: 60/106248	
25	PRIOR FILING DATE: 1998-10-29	60/106464
26	PRIOR APPLICATION NUMBER: 60/106464	
27	PRIOR FILING DATE: 1998-10-30	60/106905
28	PRIOR APPLICATION NUMBER: 60/106905	
29	PRIOR FILING DATE: 1998-11-03	60/108787
30	PRIOR APPLICATION NUMBER: 60/108787	
31	PRIOR FILING DATE: 1998-11-17	60/108801
32	PRIOR APPLICATION NUMBER: 60/108801	
33	PRIOR FILING DATE: 1998-11-17	60/108849
34	PRIOR APPLICATION NUMBER: 60/108849	
35	PRIOR FILING DATE: 1998-11-18	60/112422
36	PRIOR APPLICATION NUMBER: 60/112422	
37	PRIOR FILING DATE: 1998-12-15	60/113296
38	PRIOR APPLICATION NUMBER: 60/113296	
39	PRIOR FILING DATE: 1998-12-22	60/113605
40	PRIOR APPLICATION NUMBER: 60/113605	
41	PRIOR FILING DATE: 1998-12-23	60/113621
42	PRIOR APPLICATION NUMBER: 60/113621	
43	PRIOR FILING DATE: 1998-12-23	60/115558
44	PRIOR APPLICATION NUMBER: 60/115558	
45	PRIOR FILING DATE: 1999-01-12	60/115565
46	PRIOR APPLICATION NUMBER: 60/115565	
47	PRIOR FILING DATE: 1999-01-12	60/115733
48	PRIOR APPLICATION NUMBER: 60/115733	
49	PRIOR FILING DATE: 1999-01-12	60/119549
50	PRIOR APPLICATION NUMBER: 60/119549	
51	PRIOR FILING DATE: 1999-02-10	60/123618
52	PRIOR APPLICATION NUMBER: 60/123618	
53	PRIOR FILING DATE: 1999-03-10	60/125259
54	PRIOR APPLICATION NUMBER: 60/125259	
55	PRIOR FILING DATE: 1999-03-19	60/125775
56	PRIOR APPLICATION NUMBER: 60/125775	
57	PRIOR FILING DATE: 1999-03-23	60/126773
58	PRIOR APPLICATION NUMBER: 60/126773	
59	PRIOR FILING DATE: 1999-03-29	60/127887
60	PRIOR APPLICATION NUMBER: 60/127887	
61	PRIOR FILING DATE: 1999-04-05	60/130232
62	PRIOR APPLICATION NUMBER: 60/130232	
63	PRIOR FILING DATE: 1999-04-21	60/131022
64	PRIOR APPLICATION NUMBER: 60/131022	
65	PRIOR FILING DATE: 1999-04-26	60/131270
66	PRIOR APPLICATION NUMBER: 60/131270	
67	PRIOR FILING DATE: 1999-04-27	60/131291
68	PRIOR APPLICATION NUMBER: 60/131291	
69	PRIOR FILING DATE: 1999-04-27	60/131445
70	PRIOR APPLICATION NUMBER: 60/131445	
71	PRIOR FILING DATE: 1999-04-28	60/134287
72	PRIOR APPLICATION NUMBER: 60/134287	
73	PRIOR FILING DATE: 1999-05-14	60/134877
74	PRIOR APPLICATION NUMBER: 60/134877	

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; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
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Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RQRYLYTDDAQQTEAH 16
      |||||
Db      44 RQRYLYTDDAQQTEAH 59
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RESULT 14

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US-10-219-076-78
; Sequence 78, Application US/10219076
; Publication No. US20030078379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC62
; CURRENT APPLICATION NUMBER: US/10/219,076
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-076-78
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Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      1 RQRYLYTDDAQQTEAH 16
      |||||
Db      44 RQRYLYTDDAQQTEAH 59
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RESULT 15

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US-10-230-434-78
; Sequence 78, Application US/10230434
; Publication No. US20030078380A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC82
; CURRENT APPLICATION NUMBER: US/10/230,434
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
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1	PRIOR FILING DATE: 1998-10-28	
2	PRIOR APPLICATION NUMBER: 60/106248	
3	PRIOR FILING DATE: 1998-10-29	
4	PRIOR APPLICATION NUMBER: 60/106464	
5	PRIOR FILING DATE: 1998-10-30	
6	PRIOR APPLICATION NUMBER: 60/106905	
7	PRIOR FILING DATE: 1998-11-03	
8	PRIOR APPLICATION NUMBER: 60/108787	
9	PRIOR FILING DATE: 1998-11-17	
10	PRIOR APPLICATION NUMBER: 60/108801	
11	PRIOR FILING DATE: 1998-11-17	
12	PRIOR APPLICATION NUMBER: 60/108849	
13	PRIOR FILING DATE: 1998-11-18	
14	PRIOR APPLICATION NUMBER: 60/112422	
15	PRIOR FILING DATE: 1998-12-15	
16	PRIOR APPLICATION NUMBER: 60/113296	
17	PRIOR FILING DATE: 1998-12-22	
18	PRIOR APPLICATION NUMBER: 60/113605	
19	PRIOR FILING DATE: 1998-12-23	
20	PRIOR APPLICATION NUMBER: 60/113621	
21	PRIOR FILING DATE: 1998-12-23	
22	PRIOR APPLICATION NUMBER: 60/115558	
23	PRIOR FILING DATE: 1999-01-12	
24	PRIOR APPLICATION NUMBER: 60/115565	
25	PRIOR FILING DATE: 1999-01-12	
26	PRIOR APPLICATION NUMBER: 60/115733	
27	PRIOR FILING DATE: 1999-01-12	
28	PRIOR APPLICATION NUMBER: 60/119549	
29	PRIOR FILING DATE: 1999-02-10	
30	PRIOR APPLICATION NUMBER: 60/123618	
31	PRIOR FILING DATE: 1999-03-10	
32	PRIOR APPLICATION NUMBER: 60/125259	
33	PRIOR FILING DATE: 1999-03-19	
34	PRIOR APPLICATION NUMBER: 60/125775	
35	PRIOR FILING DATE: 1999-03-23	
36	PRIOR APPLICATION NUMBER: 60/126773	
37	PRIOR FILING DATE: 1999-03-29	
38	PRIOR APPLICATION NUMBER: 60/127887	
39	PRIOR FILING DATE: 1999-04-05	
40	PRIOR APPLICATION NUMBER: 60/130232	
41	PRIOR FILING DATE: 1999-04-21	
42	PRIOR APPLICATION NUMBER: 60/131022	
43	PRIOR FILING DATE: 1999-04-26	
44	PRIOR APPLICATION NUMBER: 60/131270	
45	PRIOR FILING DATE: 1999-04-27	
46	PRIOR APPLICATION NUMBER: 60/131291	
47	PRIOR FILING DATE: 1999-04-27	
48	PRIOR APPLICATION NUMBER: 60/131445	
49	PRIOR FILING DATE: 1999-04-28	
50	PRIOR APPLICATION NUMBER: 60/134287	
51	PRIOR FILING DATE: 1999-05-14	
52	PRIOR APPLICATION NUMBER: 60/140650	
53	PRIOR FILING DATE: 1999-06-22	
54	PRIOR APPLICATION NUMBER: 60/140723	
55	PRIOR FILING DATE: 1999-06-22	
56	PRIOR APPLICATION NUMBER: 60/141037	
57	PRIOR FILING DATE: 1999-06-23	
58	PRIOR APPLICATION NUMBER: 60/144758	
59	PRIOR FILING DATE: 1999-07-20	
60	PRIOR APPLICATION NUMBER: 60/145698	
61	PRIOR FILING DATE: 1999-07-26	
62	PRIOR APPLICATION NUMBER: 60/146222	
63	PRIOR FILING DATE: 1999-07-28	
64	PRIOR APPLICATION NUMBER: 60/146963	
65	PRIOR FILING DATE: 1999-08-03	
66	PRIOR APPLICATION NUMBER: 60/149320	
67	PRIOR FILING DATE: 1999-08-17	
68	PRIOR APPLICATION NUMBER: 60/149638	
69	PRIOR FILING DATE: 1999-08-17	
70	PRIOR APPLICATION NUMBER: 60/151733	
71	PRIOR FILING DATE: 1999-08-31	
72	PRIOR APPLICATION NUMBER: 60/164418	
73	PRIOR FILING DATE: 1999-11-09	

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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
; PRIOR FILING DATE: 1999-12-07

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 RQRYLYTDDAQQTQEAH 16
Db      44 RQRYLYTDDAQQTQEAH 59

RESULT 16
US-10-219-003-78
; Sequence 78, Application US/10219003
; Publication No. US20030088063A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
; FILE REFERENCE: P5330P1C12
; CURRENT APPLICATION NUMBER: US/10/219,003
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-09-25
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; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
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; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
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PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
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PRIOR APPLICATION NUMBER: 60/113621
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PRIOR APPLICATION NUMBER: 60/119549
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PRIOR APPLICATION NUMBER: 60/123618
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PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887
PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022
PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037
PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: 60/146222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: 60/146963
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/149320
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
|||
Db 44 RQRYLYTDDAQOTEAH 59

RESULT 17

US-10-219-075-78
; Sequence 78, Application US/10219075
; Publication No. US20030088064A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC61
; CURRENT APPLICATION NUMBER: US/10/219,075
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-075-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
|||
Db 44 RQRYLYTDDAQOTEAH 59

RESULT 18

US-10-219-464-78
; Sequence 78, Application US/10219464
; Publication No. US20030088065A1
; GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC57
; CURRENT APPLICATION NUMBER: US/10/219,464
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-464-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQRYLYTDDAQQTEAH 16
Db      44 RQRYLYTDDAQQTEAH 59

RESULT 19
US-10-219-466-78
; Sequence 78, Application US/10219466
; Publication No. US2003008066A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC47
; CURRENT APPLICATION NUMBER: US/10/219,466
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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-466-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RQRYLYTDDAQQTEAH 16
Db      44 RQRYLYTDDAQQTEAH 59

RESULT 20
US-10-219-479-78
; Sequence 78, Application US/10219479
; Publication No. US2003008067A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC33
; CURRENT APPLICATION NUMBER: US/10/219,479
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
```

;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 246
;; SEQ ID NO 78
;; LENGTH: 208
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-219-479-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 21
US-10-219-481-78
; Sequence 78, Application US/10219481
; Publication No. US20030088068A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C28
; CURRENT APPLICATION NUMBER: US/10/219,481
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-481-78

Query Match 100.0%; Score 86; DB 14; Length 208;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQOQTEAH 16
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 22
US-10-230-260-78
; Sequence 78, Application US/10230260
; Publication No. US20030088070A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C83
; CURRENT APPLICATION NUMBER: US/10/230,260
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-260-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 23
US-10-232-231-78
; Sequence 78, Application US/10232231
; Publication No. US20030088071A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

```

; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC104
; CURRENT APPLICATION NUMBER: US/10/232,231
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-231-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTAAH 16
        |||||
Db      44 RQRYLYTDDAQQTAAH 59

RESULT 24
US-10-232-233-78
; Sequence 78, Application US/10232233
; Publication No. US20030088072A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC108
; CURRENT APPLICATION NUMBER: US/10/232,233
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480

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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-233-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTAAH 16
        |||||
Db      44 RQRYLYTDDAQQTAAH 59

RESULT 25
US-10-216-165-78
; Sequence 78, Application US/10216165
; Publication No. US20030092886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC7
; CURRENT APPLICATION NUMBER: US/10/216,165
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-165-78
  Query Match      100.0%; Score 86; DB 14; Length 208;
  Best Local Similarity 100.0%; Pred.No. 8.3e-07;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQTEAH 16
        |||||
Db      44 RQRYLYTDDAQTEAH 59

RESULT 26
US-10-218-956-78
; Sequence 78, Application US/10218956
; Publication No. US20030092887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC15
; CURRENT APPLICATION NUMBER: US/10/218,956
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
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; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445

; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORYLYTDDAQOTEAH 16
| | | | | | | | | | | | | | | |
Db 44 RORYLYTDDAQOTEAH 59

RESULT 27
US-10-219-468-78
; Sequence 78, Application US/10219468
; Publication No. US20030092888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C34
; CURRENT APPLICATION NUMBER: US/10/219,468
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-468-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORYLYTDDAQOTEAH 16
| | | | | | | | | | | | | | | |
Db 44 RORYLYTDDAQOTEAH 59

RESULT 28

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/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEI
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3530PIC67
/ CURRENT APPLICATION NUMBER: US/10/219,536
/ CURRENT FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ REMAINING PRIOR Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 78
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-219-536-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTQEAH 16
Db 44 RQRYLYTDDAQQTQEAH 59
|||||
|||||

RESULT 30
US-10-233-205-78
/ Sequence 78, Application US/10233205
/ Publication No. US2003009362A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEI
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3530PIC115
/ CURRENT APPLICATION NUMBER: US/10/233,205
/ CURRENT FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31

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; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-233-205-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTAAH 16
      |||||
Db      44 RQRYLYTDDAQQTAAH 59

RESULT 31
US-10-219-072-78
; Sequence 78, Application US/10219072
; Publication No. US2003009659A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC45
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/10/219,072
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-072-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTAAH 16
      |||||
Db      44 RQRYLYTDDAQQTAAH 59

RESULT 32
US-10-219-470-78
; Sequence 78, Application US/10219470
; Publication No. US2003009660A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC59
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US/10/219,470
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-470-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQQTAAH 16
      |||||
Db      44 RQRYLYTDDAQQTAAH 59

RESULT 33
US-10-219-474-78
; Sequence 78, Application US/10219474
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/ Publication No. US20030096961A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3530PIC36
/ CURRENT APPLICATION NUMBER: US/10/219,474
/ CURRENT FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 78
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-219-474-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQQTAAH 16
Db 44 RORYLYTDDAQQTAAH 59

RESULT 34
US-10-219-524-78
/ Sequence 78, Application US/10219524
/ Publication No. US20030096962A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3530PIC36
/ CURRENT APPLICATION NUMBER: US/10/219,528
/ CURRENT FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
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/ FILE REFERENCE: P3530PIC37
/ CURRENT APPLICATION NUMBER: US/10/219,524
/ CURRENT FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
/ PRIOR APPLICATION NUMBER: 60/078910
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: 60/079294
/ PRIOR FILING DATE: 1998-03-25
/ PRIOR APPLICATION NUMBER: 60/079656
/ PRIOR FILING DATE: 1998-03-26
/ PRIOR APPLICATION NUMBER: 60/079728
/ PRIOR FILING DATE: 1998-03-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 246
/ SEQ ID NO 78
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Homo Sapien
/ US-10-219-524-78

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQQTAAH 16
Db 44 RORYLYTDDAQQTAAH 59

RESULT 35
US-10-219-528-78
/ Sequence 78, Application US/10219528
/ Publication No. US20030096963A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3530PIC38
/ CURRENT APPLICATION NUMBER: US/10/219,528
/ CURRENT FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/062287
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/063549
/ PRIOR FILING DATE: 1997-10-28
/ PRIOR APPLICATION NUMBER: 60/064103
/ PRIOR FILING DATE: 1997-10-31
/ PRIOR APPLICATION NUMBER: 60/069873
/ PRIOR FILING DATE: 1997-12-17
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1	PRIOR FILING DATE: 1998-09-18
2	PRIOR APPLICATION NUMBER: 60/100919
3	PRIOR FILING DATE: 1998-09-17
4	PRIOR APPLICATION NUMBER: 60/101477
5	PRIOR FILING DATE: 1998-09-23
6	PRIOR APPLICATION NUMBER: 60/101738
7	PRIOR FILING DATE: 1998-09-24
8	PRIOR APPLICATION NUMBER: 60/101741
9	PRIOR FILING DATE: 1998-09-24
10	PRIOR APPLICATION NUMBER: 60/101786
11	PRIOR FILING DATE: 1998-09-25
12	PRIOR APPLICATION NUMBER: 60/101916
13	PRIOR FILING DATE: 1998-09-24
14	PRIOR APPLICATION NUMBER: 60/101922
15	PRIOR FILING DATE: 1998-09-24
16	PRIOR APPLICATION NUMBER: 60/106178
17	PRIOR FILING DATE: 1998-10-28
18	PRIOR APPLICATION NUMBER: 60/106248
19	PRIOR FILING DATE: 1998-10-29
20	PRIOR APPLICATION NUMBER: 60/106464
21	PRIOR FILING DATE: 1998-10-30
22	PRIOR APPLICATION NUMBER: 60/106905
23	PRIOR FILING DATE: 1998-11-03
24	PRIOR APPLICATION NUMBER: 60/108787
25	PRIOR FILING DATE: 1998-11-17
26	PRIOR APPLICATION NUMBER: 60/108801
27	PRIOR FILING DATE: 1998-11-17
28	PRIOR APPLICATION NUMBER: 60/108849
29	PRIOR FILING DATE: 1998-11-18
30	PRIOR APPLICATION NUMBER: 60/112422
31	PRIOR FILING DATE: 1998-12-15
32	PRIOR APPLICATION NUMBER: 60/113296
33	PRIOR FILING DATE: 1998-12-22
34	PRIOR APPLICATION NUMBER: 60/113605
35	PRIOR FILING DATE: 1998-12-23
36	PRIOR APPLICATION NUMBER: 60/113621
37	PRIOR FILING DATE: 1998-12-23
38	PRIOR APPLICATION NUMBER: 60/115558
39	PRIOR FILING DATE: 1999-01-12
40	PRIOR APPLICATION NUMBER: 60/115565
41	PRIOR FILING DATE: 1999-01-12
42	PRIOR APPLICATION NUMBER: 60/115733
43	PRIOR FILING DATE: 1999-01-12
44	PRIOR APPLICATION NUMBER: 60/119549
45	PRIOR FILING DATE: 1999-02-10
46	PRIOR APPLICATION NUMBER: 60/123618
47	PRIOR FILING DATE: 1999-03-10
48	PRIOR APPLICATION NUMBER: 60/125259
49	PRIOR FILING DATE: 1999-03-19
50	PRIOR APPLICATION NUMBER: 60/125775
51	PRIOR FILING DATE: 1999-03-23
52	PRIOR APPLICATION NUMBER: 60/126773
53	PRIOR FILING DATE: 1999-03-29
54	PRIOR APPLICATION NUMBER: 60/127887
55	PRIOR FILING DATE: 1999-04-05
56	PRIOR APPLICATION NUMBER: 60/130232
57	PRIOR FILING DATE: 1999-04-21
58	PRIOR APPLICATION NUMBER: 60/131022
59	PRIOR FILING DATE: 1999-04-26
60	PRIOR APPLICATION NUMBER: 60/131270
61	PRIOR FILING DATE: 1999-04-27
62	PRIOR APPLICATION NUMBER: 60/131291
63	PRIOR FILING DATE: 1999-04-27
64	PRIOR APPLICATION NUMBER: 60/131445
65	PRIOR FILING DATE: 1999-04-28
66	PRIOR APPLICATION NUMBER: 60/134287
67	PRIOR FILING DATE: 1999-05-14
68	PRIOR APPLICATION NUMBER: 60/140650
69	PRIOR FILING DATE: 1999-06-22
70	PRIOR APPLICATION NUMBER: 60/140723
71	PRIOR FILING DATE: 1999-06-22
72	PRIOR APPLICATION NUMBER: 60/141037
73	PRIOR FILING DATE: 1999-06-23

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; PRIOR APPLICATION NUMBER: 60/144758
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; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151713
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match          100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQQTEAH 16
Db 44 RORYLYTDDAQQTEAH 59

RESULT 36
US-10-227-880-78
; Sequence 78, Application US/10227880
; Publication No. US20030096964A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Garney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C74
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
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; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24

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; PRIOR APPLICATION NUMBER: 60/101741
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; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
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; PRIOR FILING DATE: 1998-09-24
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; PRIOR APPLICATION NUMBER: 60/108787
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; PRIOR FILING DATE: 1999-01-12
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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
DB 44 RQRYLYTDDAQOQTEAH 59

RESULT 37

US-10-227-881-78
; Sequence 78, Application US/10227881
; Publication No. US2003009695A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC80
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR APPLICATION NUMBER: 60/064103
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; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22

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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/083323
; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
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; PRIOR APPLICATION NUMBER: 60/131022
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; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
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; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
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;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
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;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 86; DB 14; Length 208;

Best Local Similarity 100.0%; Pred. No. 8.3e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTGAH 16

DB 44 RQRYLYTDDAQTGAH 59

RESULT 38

US-10-227-882-78

;; Sequence 78, Application US/10227882

;; Publication No. US2003009696A1

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Gerritsen, Mary

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Grimaldi, J. Christopher

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Smith, Victoria

;; APPLICANT: Stephan, Jean-Philippe F.

;; APPLICANT: Watanabe, Colin L.

;; APPLICANT: Wood, William I.

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME

;; FILE REFERENCE: P3530P1C81

;; CURRENT APPLICATION NUMBER: US/10/227,882

;; CURRENT FILING DATE: 2002-08-26

;; PRIOR APPLICATION NUMBER: 10/119,480

;; PRIOR FILING DATE: 2002-04-09

;; PRIOR APPLICATION NUMBER: 60/059113

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/062287

;; PRIOR FILING DATE: 1997-10-17

;; PRIOR APPLICATION NUMBER: 60/063549

;; PRIOR FILING DATE: 1997-10-28

;; PRIOR APPLICATION NUMBER: 60/064103

;; PRIOR FILING DATE: 1997-10-31

;; PRIOR APPLICATION NUMBER: 60/069873

;; PRIOR FILING DATE: 1997-12-17

;; PRIOR APPLICATION NUMBER: 60/078910

;; PRIOR FILING DATE: 1998-03-20

;; PRIOR APPLICATION NUMBER: 60/079294

;; PRIOR FILING DATE: 1998-03-25

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;; PRIOR APPLICATION NUMBER: 60/099598
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099811
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099812
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099816
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100038
;; PRIOR FILING DATE: 1998-09-11
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;; PRIOR APPLICATION NUMBER: 60/100390
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;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: 60/100848
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100919
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101786
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;; PRIOR APPLICATION NUMBER: 60/101916
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;; PRIOR APPLICATION NUMBER: 60/101922
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;; PRIOR APPLICATION NUMBER: 60/106178
;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/106248
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 60/106464
;; PRIOR FILING DATE: 1998-10-30

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; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495

; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQOTEAH 16
      |||||
Db      44 RQRYLYTDDAQOTEAH 59
      |||||

RESULT 39
US-10-230-436-78
; Sequence 78, Application US/10230436
; Publication No. US20030096967A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC97
; CURRENT APPLICATION NUMBER: US/10/230,436
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-230-436-78

Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RQRYLYTDDAQOTEAH 16
      |||||
Db      44 RQRYLYTDDAQOTEAH 59
      |||||

RESULT 40
US-10-232-223-78
; Sequence 78, Application US/10232223
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; Publication No. US20030096968A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC102
; CURRENT APPLICATION NUMBER: US/10/232,223
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-223-78
```

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Query Match      100.0%; Score 86; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 8.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RQRYLYTDDAQOQTEAH 16
Db      44 RQRYLYTDDAQOQTEAH 59
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Search completed: March 2, 2004, 16:19:58
Job time : 6.4 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2004, 15:50:07 ; Search time 9.6 Seconds
(without alignments)
470.913 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRVLYTDDAQQTEAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	86	100.0	16	4 AAB68418	Aab68418 Epitope-b
2	86	100.0	124	5 AAB81312	Aab81312 Human FGF
3	86	100.0	153	4 AAB73069	Aab73069 Human fib
4	86	100.0	181	4 AAU00965	Aau00965 Human fib
5	86	100.0	208	4 AAE05078	Aae05078 Human fib
6	86	100.0	208	5 AAU83630	Aau83630 Human fib
7	86	100.0	208	5 ABG32358	Abg32358 Human fib
8	86	100.0	208	5 AAE17601	Aae17601 Human ext
9	86	100.0	208	6 ABU80777	Abu80777 Human PRO
10	86	100.0	208	6 ABO33743	Abc33743 Novel hum
11	86	100.0	208	6 ABU82086	Abu82086 Novel hum
12	86	100.0	208	6 ABP96156	Abp96156 Human fib
13	86	100.0	208	6 ABJ72266	Abj72266 Human PRO
14	86	100.0	208	6 ABJ72394	Abj72394 Human PRO
15	86	100.0	208	6 ABO34289	Abc34289 Human sec
16	86	100.0	208	7 ADA37038	Ada37038 Human fib
17	86	100.0	208	7 ABJ72096	Abj72096 Human mem
18	86	100.0	208	7 ADB83568	Adb83568 Novel hum
19	86	100.0	208	7 ADB80674	Adb80674 Novel hum
20	86	100.0	208	7 ADB73215	Adb73215 Novel hum
21	86	100.0	208	7 ADB78297	Adb78297 Novel hum
22	86	100.0	208	7 ADB84945	Adb84945 Human PRO
23	86	100.0	208	7 ADB78051	Adb78051 Novel hum
24	86	100.0	208	7 ADB87117	Adb87117 Human PRO
25	86	100.0	208	7 ADB84699	Adb84699 Human PRO

26	86	100.0	208	7 ADB83814	Adb83814 Novel hum
27	86	100.0	208	7 ADB72969	Adb72969 Novel hum
28	86	100.0	208	7 ADC36807	Adc36807 Human PRO
29	86	100.0	208	7 ADC21797	Adc21797 Human PRO
30	86	100.0	208	7 ADC49828	Adc49828 Novel hum
31	86	100.0	208	7 ADC49027	Adc49027 Novel hum
32	86	100.0	208	7 ADC49544	Adc49544 Novel hum
33	86	100.0	208	7 ADC47405	Adc47405 Novel hum
34	86	100.0	208	7 ADC47150	Adc47150 Novel hum
35	86	100.0	208	7 ADC78025	Adc78025 Novel hum
36	86	100.0	208	7 ADC08260	Adc08260 Novel hum
37	86	100.0	208	7 ADC77779	Adc77779 Novel hum
38	86	100.0	208	7 ADD50742	Add50742 Novel hum
39	86	100.0	208	7 ADD50988	Add50988 Human PRO
40	86	100.0	208	7 ADD50469	Add50469 Human PRO
41	86	100.0	208	7 ADD50223	Add50223 Human PRO
42	86	100.0	208	7 ADD51234	Add51234 Novel hum
43	86	100.0	208	8 ADC48781	Adc48781 Novel hum
44	86	100.0	208	8 ADE20952	Ade20952 Novel hum
45	86	100.0	208	8 ADE05796	Ade05796 Human PRO

ALIGNMENTS

RESULT 1

AAB68418

ID AAB68418 standard; peptide; 16 AA.

XX

AC AAB68418;

XX 23-JUL-2001 (first entry)

XX Epitope-bearing portion of human fibroblast growth factor-21 (FGF-21).

XX Fibroblast growth factor-21; FGF-21; cell growth; cell differentiation;

KW hepatic cell; cirrhosis; infertility; impotence; testicular cancer;

KW leukemia; lymphoma; autoimmune disease; thymus proliferative disorder.

XX Homo sapiens.

OS

XX WO200136640-A2.

XX 25-MAY-2001.

XX 16-NOV-2000; 2000WO-US031745.

XX 18-NOV-1999; 99US-0166540P.

XX 11-MAY-2000; 2000US-0203633P.

XX (CHIR) CHIRON CORP.

XX (KYOU) UNIV KYOTO.

XX Itch N, Kavanaugh WM;

XX WPI; 2001-343823/36.

XX New nucleic acid molecule useful for treating disease, e.g. infertility,

XX impotence, or testicular cancer.

XX Claim 17; Page 39; 61pp; English.

XX The present sequence represents an epitope-bearing portion of human fibroblast growth factor-21 (FGF-21). FGF proteins regulate growth and differentiation of a variety of cell types. FGF-21 nucleic acids and polypeptides are useful for treating diseases and disorders characterised by inadequate numbers of hepatic cells, preferably cirrhosis of the liver. They may also be used in the treatment of infertility, impotence, and testicular cancer, as well as leukemia, lymphoma, autoimmune disease, or proliferative disorders of the thymus

XX Sequence 16 AA;

SQ

Query Match		100.0%;	Score 86;	DB 4;	Length 16;														
Best Local Similarity		100.0%;	Pred. No. 2.4e-08;																
Matches 16;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;														
QY	1	RQRYLYTDDAQQTAAH	16																
Db	1	RQRYLYTDDAQQTAAH	16																
RESULT 2																			
ABB81312																			
ID	ABB81312	standard; protein; 124 AA.																	
AC	XX																		
DT	XX																		
DE	XX	21-AUG-2002 (first entry)																	
KW	XX	Human FGF21 core structure amino acid sequence.																	
KW	XX	Fibroblast growth factor 9; FGF-9; cytostatic; vulnery; osteopathic;																	
KW	XX	antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder;																	
KW	XX	fibroblast growth factor receptor; cancer; bone fracture healing;																	
KW	XX	bone growth; wound healing; achondroplasia; hypochondroplasia;																	
KW	XX	osteoporosis; cartilage defect; multiple myeloma.																	
OS	XX	Homo sapiens.																	
PN	XX	WO200236732-A2.																	
PD	XX	10-MAY-2002.																	
PF	XX	18-OCT-2001; 2001WO-IL000962.																	
PR	XX	31-OCT-2000; 2000IL-00139380.																	
PA	XX	(PROC-) PROCHON BIOTECH LTD.																	
PI	XX	Bogin O, Adar R, Yayon A;																	
DR	XX	WPI; 2002-479754/51.																	
PT	XX	New variants of fibroblast growth factor, useful for treating skeletal																	
PT	XX	disorders including osteoporosis, malignancies and to enhance wound and																	
PT	XX	fracture healing.																	
PS	XX	Disclosure; Fig 1; 74pp; English.																	
CC	XX	The present invention describes an active variant (I) of a fibroblast																	
CC	XX	growth factor (FGF) having at least one mutation in the beta-8-beta-9																	
CC	XX	loop, having enhanced specificity for one receptor subtype compared to																	
CC	XX	the corresponding wild type FGF, by decreasing the biological activity																	
CC	XX	mediated by at least one receptor subtype while retaining the activity																	
CC	XX	mediated through another receptor subtype. (I) has cytostatic, vulnerary,																	
CC	XX	osteopathic and antiarthritic activities. (I) can be used as a regulator																	
CC	XX	of vasculogenesis or angiogenesis. (I) is useful for preparing a																	
CC	XX	medicament and for treating a disease or disorder related to normal or																	
CC	XX	abnormal FGF receptors (FGFRs), especially skeletal disorders, cancer, to																	
CC	XX	enhance bone fracture healing or bone growth processes and wound healing																	
CC	XX	processes. (I) is useful in detection and treatment of various FGFR																	
CC	XX	related disorders including skeletal disorders e.g. achondroplasia,																	
CC	XX	hypochondroplasia, and osteoporosis, and cartilage defects, multiple																	
CC	XX	myeloma, epithelial cancers such as transitional cell carcinoma of the																	
CC	XX	bladder and cervical carcinoma. The novel mutants are useful in high																	
CC	XX	expression systems suitable for pharmaceutical production, targeting of																	
CC	XX	drugs or other agents to tissues and cells having specific FGFR subtypes,																	
CC	XX	and serve as template for the formation of improved agonists and																	
CC	XX	antagonists of FGFRs in various disorders such as skeletal disorders and																	
CC	XX	cancer. The present sequence represents a FGF core structure amino acid																	
CC	XX	sequence which is given in the exemplification of the present invention																	
SQ	XX	Sequence 124 AA;																	
Query Match																			
Best Local Similarity 100.0%; Score 86; DB 5; Length 124;																			
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																			
QY	1	RQRYLYTDDAQQTAAH	16																
Db	1	RQRYLYTDDAQQTAAH	16																
RESULT 3																			
AAB73069																			
ID	AAB73069	standard; protein; 153 AA.																	
AC	XX																		
DT	XX																		
DE	XX	17-MAY-2001 (first entry)																	
KW	XX	Human fibroblast growth factor 19 homologue FGF19X.																	
KW	XX	Human; fibroblast growth factor 19; FGF19X; embryonic development;																	
KW	XX	proliferative disorder; cancer; restenosis; psoriasis;																	
KW	XX	rheumatoid arthritis; Dupuytren's contracture.																	
OS	XX	Homo sapiens.																	
PN	XX	WO200118209-A1.																	
PD	XX	15-MAR-2001.																	
PF	XX	08-SEP-2000; 2000WO-US024863.																	
PR	XX	10-SEP-1999; 99US-0153303P.																	
PR	XX	03-APR-2000; 2000US-0194246P.																	
PR	XX	19-JUL-2000; 2000US-00619251.																	
PA	XX	(CURA-) CURAGEN CORP.																	
PI	XX	Shimkets RA, Vernet C, Burgess C, Fernandes E, Taupier R;																	
PI	XX	Quinn KE, Spyteck KA, Rastelli L, Herrmann JL;																	
DR	XX	WPI; 2001-218559/22.																	
DR	XX	N-PSDB; AAF76715.																	
PT	XX	Fibroblast growth factor-19X polypeptides and polynucleotides useful for																	
PT	XX	diagnosis, prevention, treatment of proliferative, differentiative,																	
PT	XX	tumorigenic disorders such as tumor, psoriasis, rheumatoid arthritis.																	
PS	XX	Claim 11; Page 7; 97pp; English.																	
CC	XX	The present invention describes the protein and coding sequences of the																	
CC	XX	human fibroblast growth factor (FGF) 19 homologue FGF19X, the former of																	
CC	XX	which is shown here. The sequences can be used in the prognosis and																	
CC	XX	treatment of proliferative diseases such as cancer, restenosis,																	
CC	XX	psoriasis, rheumatoid arthritis and Dupuytren's contracture, as well as																	
CC	XX	to stimulate cell growth for treating neurological disorders such as																	
CC	XX	Alzheimer's disease																	
SQ	XX	Sequence 153 AA;																	
Query Match																			
Best Local Similarity 100.0%; Score 86; DB 4; Length 153;																			
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;																			
QY	1	RQRYLYTDDAQQTAAH	16																
Db	45	RQRYLYTDDAQQTAAH	60																
RESULT 4																			
AAU00965																			
ID	AAU00965	standard; protein; 181 AA.																	
AC	XX																		
XX	XX	AAU00965;																	
XX	XX																		

DT 24-MAY-2001 (first entry)
 XX Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.
 DE
 XX Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;
 KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;
 KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;
 KW neurodegenerative disease; haematopoietic cell reconstruction; cachexia;
 KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;
 KW multiple sclerosis; short stature; delayed maturation; excessive growth;
 KW acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;
 KW androgen target organ abnormality; respiratory distress syndrome; stroke;
 KW cancer; atherosclerosis; hypercholesterolaemia; osteoporosis; baldness;
 KW osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;
 KW decreased stamina; decreased cardiac function; immune system dysfunction;
 KW Parkinson's disease; Alzheimer's disease; decreased cognitive function;
 KW senile dementia; human.
 XX Homo sapiens.
 OS
 XX WO200118172-A2.
 PN
 XX 15-MAR-2001.
 PD
 XX
 XX 05-SEP-2000; 2000WO-US024373.
 PF
 XX
 XX 07-SEP-1999; 99US-00391861.
 PR
 XX 23-AUG-2000; 2000US-00644052.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Thomason AR, Liu B;
 PI
 XX WPI; 2001-226743/23.
 DR
 XX Novel isolated fibroblast growth factor-like polypeptide useful for
 PT treating, preventing or ameliorating cirrhosis, inflammatory bowel
 PT disease, mucositis, Crohn's disease, diabetes, obesity, stroke and
 PT osteoporosis.
 XX
 PS Claim 14; Page 116-117; 138pp; English.
 XX
 CC The sequence represents a fragment of a fibroblast growth factor-like
 CC (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid
 CC play a role in modulating body growth, maturation or life-span. They are
 CC also useful for treating, preventing or ameliorating disorders such as
 CC cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease,
 CC diabetes, obesity, gastrointestinal abnormalities, neurodegenerative
 CC diseases, damage to renal tubules as a result of acute tubular necrosis,
 CC haematopoietic cell reconstruction following chemotherapy, wasting
 CC syndromes (e.g., cancer associated cachexia), damage to the corneal
 CC epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short
 CC stature, delayed maturation, excessive growth (e.g. acromegaly),
 CC premature maturation, alopecia, abnormalities of androgen target organs,
 CC bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours
 CC of the eye or other tissues, atherosclerosis, hypercholesterolemia,
 CC stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,
 CC baldness, wrinkles, increased fatigue, decreased stamina, decreased
 CC cardiac function, immune system dysfunction, cancer, Parkinson's disease,
 CC senile dementia, Alzheimer's disease, and decreased cognitive function
 XX
 SQ Sequence 181 AA;
 Query Match 100.0%; Score 86; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 3.8e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RORYLYTDDAQQTFAH 16
 Db |||||
 17 RORYLYTDDAQQTFAH 32
 RESULT 5

AAE05078
 ID AAE05078 standard; protein; 208 AA.
 AC AAE05078;
 XX
 DT 18-SEP-2001 (first entry)
 XX Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
 DE
 XX Human; fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;
 KW proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis;
 KW chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture;
 KW bone formation; diabetes mellitus; neural cell development; angiogenesis;
 KW amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer;
 KW congenital disorder; wound healing; cardiac function; glomerulonephritis;
 KW surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
 KW hypertension; cytostatic; vasotropic; therapy.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..27
 FT /label= Signal_peptide
 FT Protein 28..208
 FT /label= Human_mature_zFGF11_protein
 FT Binding-site 44..46
 FT /note= "Heparin binding domain"
 XX WO200149849-A1.
 PN
 XX 12-JUL-2001.
 PD
 XX 05-JAN-2001; 2001WO-US000324.
 PF
 XX 05-JAN-2000; 2000US-00477886.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Conklin DC, Chen Z;
 PI
 XX WPI; 2001-441880/47.
 DR N-PSDB; AAD09151.
 XX Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast
 PT growth factor family, for stimulating proliferation of mesenchymal,
 PT osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
 PT cancer.
 XX
 PS Claim 1; Page 63; 69pp; English.
 XX The present sequence is human fibroblast growth factor (FGF) homologue,
 CC zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
 CC for stimulating proliferation of mesenchymal cells, osteoblastic lineage
 CC cells. zFGF11 is useful for identifying chromosomal disorders associated
 CC with abnormal expression of zFGF11 protein. zFGF11 is also useful for
 CC stimulation, inhibition or proliferation of myocytes, smooth muscle
 CC cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
 CC crest stem cells and neuronal progenitors, pancreatic cells, prostate-
 CC derived cells and endothelial cells and inhibiting chondrosarcomas,
 CC atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
 CC results in bone formation useful for treating bone defects, fractures,
 CC osteoporosis and other deficiencies in bone structure and formation.
 CC zFGF11 is useful for treating disorders associated with diabetes
 CC mellitus, neural cell development or degeneration, amyotrophic lateral
 CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of the
 CC maintenance of neuronal differentiation and congenital disorders of the
 CC nervous system or lack of neuronal development, promoting angiogenesis
 CC and wound healing, for revascularisation in eye, complications related to
 CC poor circulation such as diabetic food ulcers, improving cardiac
 CC function, modulating surfactant production in the lung epithelium, to
 CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
 CC events, particularly in the heart or brain and for inducing skeletal
 CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for

CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
CC are useful for inhibiting disorders associated with kidney epithelium
CC such as glomerulonephritis
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 6
AAU83630
ID AAU83630 standard; protein; 208 AA.

XX AAU83630;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 78.

XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX

PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX

PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CX, Wood WI;
XX WPI; 2002-172001/22.
XX N-PSDB; ABK33574.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT

PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
or liver tumor.
XX
XX Claim 11; Fig 78; 359pp; English.

XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumor, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX

SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOQTEAH 16
Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 7
ABG32358
ID ABG32358 standard; protein; 208 AA.
XX

AC ABG32358;
XX

DT 05-NOV-2002 (first entry)
XX

DE Human fibroblast growth factor (FGF) homologue, zFGF11.
XX

KW Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFR1IIC;
KW osteoblastic lineage cell; diabetes mellitus; neuropathy;
KW neural cell development; amyotrophic lateral sclerosis;
KW cerebrovascular stroke; neuronal differentiation; congenital disorder;
KW nervous system disorder; cardiac function; wound healing.
XX

OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Peptide 1..27 /label= Signal_sequence
FT Protein 28..208 /note= "Mature fibroblast growth factor homologue,
zFGF11. This sequence is specifically claimed in claim 4"

FT US2002081663-A1.
XX
PN 27-JUN-2002.
XX

PD 05-JAN-2001; 2001US-00755695.
XX

PF 05-JAN-2000; 2000US-0174526P.
XX

PR {CONK/} CONKLIN D C.
PA (CHEN/) CHEN Z.
XX

XX Conklin DC, Chen Z;
PI WPI; 2002-626540/67.
XX

DR N-PSDB; ABK91310.
XX Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in
XX treatment of disorders associated with diabetes mellitus, neural cell
PT development or degeneration, amyotrophic lateral sclerosis,
PT cerebrovascular stroke.
XX
XX Claim 4; Fig 1; 35pp; English.
PS
CC The invention relates to an isolated human polypeptide (I) for zFGF11 (a
XX fibroblast growth factor), and the encoding polynucleotide (II). (I) and
CC (II) are used in methods of the invention stimulating proliferation of
CC mesenchymal cells, detecting the presence of zFGF11 in a biological
CC sample, detecting the presence of FGFR11c in a biological sample and
CC stimulating proliferation of osteoblastic lineage cells. The
CC polypeptides, nucleic acid and/or antibodies of the invention may be used
CC in treatment of disorders associated with diabetes mellitus, neural cell
CC development or degeneration, amyotrophic lateral sclerosis,
CC cerebrovascular stroke, neuropathy associated with lack of maintenance of
CC neuronal differentiation, and congenital disorders of the nervous system
CC or lack of neuronal development. Molecules of the invention may also be
CC useful for improving cardiac function and for promoting wound healing of
CC the epidermis. The present sequence represents the amino acid sequence of
CC human zFGF11
XX
SQ Sequence 208 AA;
Query Match 100.0%; Score 86; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 8
ID AAE17601 standard; protein; 208 AA.
XX AAE17601;
AC
XX 22-APR-2002 (first entry)
DT
DE Human extracellular messenger (XMES)-3 protein.
XX
XX Human; extracellular messenger; neurological disorder; epilepsy; XMES-3;
KW Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke;
KW acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic;
KW developmental disorder; anaemia; Cushing's syndrome; endocrine disorder;
KW vascular malformation; cell proliferative disorder; gene therapy; cancer;
KW neuroprotective; trauma; hypopituitarism; hypothyroidism; antihelminthic;
KW hyperthyroidism; gonadal steroid hormone; pancreatic disorder; neotropic;
KW diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial;
KW antiviral; antifungal; parasitic; protozoal; allergy.
XX
XX Homo sapiens.
OS
XX WO200194587-A2.
PN
XX 13-DEC-2001.
PD
XX 06-JUN-2001; 2001WO-US018476.
PF
XX 06-JUN-2000; 2000US-0210233P.
PR
XX 23-JUN-2000; 2000US-0213465P.
PR
XX 14-NOV-2000; 2000US-0249019P.
PR
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Lal P, Yue H, He A, Nguyen DB, Walia N, Gandhi AR, Azimzai Y;
PI Bandman O, Tang YT, Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
PI Policky JL;

XX WPI; 2002-154573/20.
DR N-PSDB; AAD28493.
XX
XX New extracellular messenger polypeptides and polynucleotides encoding
PT them, useful for diagnosing, treating or preventing e.g. neurological,
PT autoimmune, inflammatory, developmental and endocrine disorders.
XX
XX Claim 1; Page 111; 123pp; English.
PS
XX The present invention relates to new extracellular messenger polypeptides
CC and polynucleotides encoding them. XMES is useful in the diagnosis,
CC treatment and prevention of neurological disorders (e.g. epilepsy, (e.g.
CC stroke, or Alzheimer's disease), autoimmune/inflammatory disorders, (e.g.
CC acquired immune deficiency syndrome, AIDS, Addison's disease, or
CC allergies), developmental disorders (e.g. renal tubular acidosis, anaemia
CC or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy,
CC aneurysm or vascular malformation), and cell proliferative disorders
CC (e.g. cancer), and in the assessment of the effects of exogenous
CC compounds on the expression of nucleic acid and amino acid sequences of
CC extracellular messengers. XMES may also be used in the treatment of
CC viral, bacterial, fungal, parasitic, protozoal and helminthic
CC infections, trauma, disorders associated with hypopituitarism,
CC hypothyroidism, hyperthyroidism or gonadal steroid hormones, and
CC pancreatic disorders such as type I or type II diabetes mellitus. The
CC XMES may be used for somatic or germline gene therapy. The present
CC sequence is human XMES-3 protein
XX
SQ Sequence 208 AA;
Query Match 100.0%; Score 86; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 9
ABU80777
ID ABU80777 standard; protein; 208 AA.
XX
XX ABU80777;
AC
XX 23-JUN-2003 (first entry)
DT
XX Human PRO polypeptide #39.
DE
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
KW
XX Homo sapiens.
OS
XX US2003036635-A1.
PN
XX 20-FEB-2003.
PD
XX 28-AUG-2002; 2002US-00230163.
PF
XX 25-JUL-2000; 2000US-0220638P.
PR
XX 01-JUN-2001; 2001WO-US017800.
PR
XX 29-JUN-2001; 2001WO-US021066.
PR
XX 09-APR-2002; 2002US-00119480.
PR
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Desnoyers I, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
PI WPI; 2003-342045/32.
DR N-PSDB; ACA66879.
XX

PT One hundred and twenty two nucleic acids encoding PRO polypeptides.
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX
PS Claim 11; Fig 78; 314pp; English.
XX
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumors. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
XX
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. NO. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORYLYTDDAQOTEAH 16
Db |||||
44 RORYLYTDDAQOTEAH 59

RESULT 10
AB033743
ID AB033743 standard; protein; 208 AA.
XX
AC AB033743;
XX
XX 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX
XX Homo sapiens.
OS
XX US2003045687-A1.
FN
XX
XX PD 06-MAR-2003.
XX
XX PF 12-AUG-2002; 2002US-00218631.
XX
XX PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-512315/48.
DR N-PSDB; ACD68631.
XX
XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
XX Claim 11; Fig 78; 314pp; English.

XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC cells, for stimulating proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
XX SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. NO. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RORYLYTDDAQOTEAH 16
Db |||||
44 RORYLYTDDAQOTEAH 59

RESULT 11
ABU82086
ID ABU82086 standard; protein; 208 AA.
XX
AC ABU82086;
XX
XX 25-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX
XX Homo sapiens.
OS
XX US2003088063-A1.
FN
XX
XX PD 08-MAY-2003.
XX
XX PF 12-AUG-2002; 2002US-00219003.
XX
XX PR 25-JUL-2001; 2000US-0220664P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-393229/37.
 DR N-PSDB; ACA68535.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 PS Claim 11; Fig 78; 314pp; English.
 XX The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX Sequence 208 AA;
 SQ

Query Match 100.0%; Score 86; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RORYLYTDDAQOQTEAH 16
 DB 44 RORYLYTDDAQOQTEAH 59

RESULT 12
 ABP96156
 ID ABP96156 standard; protein; 208 AA.
 XX
 AC ABP96156;
 DT 12-MAY-2003 (first entry)
 XX Human fibroblast growth factor 21 protein SEQ ID NO:2.
 DE Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter;
 XX diabetes; obesity; antidiabetic; anorectic; type 2 diabetes;
 KW type 1 diabetes.
 KW Homo sapiens.
 XX WO2003011213-A2.
 XX 13-FEB-2003.
 PD 22-JUL-2002; 2002WO-US021290.
 XX 30-JUL-2001; 2001US-0308702P.
 XX 10-JAN-2002; 2002US-0347991P.
 XX (ELIL) LILLY & CO ELI.
 XX Glasebrook AL, Hammond LJ, Kharitonov A, Shyanova TL;
 PI N-PSDB; AB379797.
 DR WPI; 2003-248106/24.
 DR N-PSDB; AB379797.
 XX Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or
 PT obesity, by administering composition comprising fibroblast growth factor
 PT -21.
 XX Claim 3; Fig 1; 32pp; English.

CC The present sequence represents human fibroblast growth factor 21 (FGF-
 CC 21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-
 CC qter. The present invention describes a method for treating a mammal
 CC exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for
 CC obesity which comprises administering to the mammal a composition
 CC comprising FGF-21 which has at least 95% amino acid sequence identity to
 CC the 208 amino acid sequence given in ABP96156. Also described: (1)
 CC inducing an increase in glucose uptake in adipocyte cells by
 CC administering FGF-21 to induce an increase in glucose uptake; and (2)
 CC manufacturing a medicament for treating type 1 diabetes, type 2 diabetes
 CC or obesity in a mammal using FGF-21 having 95% amino acid sequence
 CC identity to ABP96156. FGF-21 has antidiabetic and anorectic activities.
 CC The method is useful for treating a mammal exhibiting type 2 or 1
 CC diabetes or for treating a mammal for obesity. The method is preferably
 CC useful for treating humans exhibiting type 1 or type 2 diabetes, and for
 CC treating domestic animals for obesity
 XX Sequence 208 AA;
 SQ

Query Match 100.0%; Score 86; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RORYLYTDDAQOQTEAH 16
 DB 44 RORYLYTDDAQOQTEAH 59

RESULT 13
 ABJ72266
 ID ABJ72266 standard; protein; 208 AA.
 XX
 AC ABJ72266;
 DT 06-NOV-2003 (first entry)
 XX Human PRO10196 protein.
 DE PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
 KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
 KW Homo sapiens.
 XX US2003050448-A1.
 XX 13-MAR-2003.
 PD 28-AUG-2002; 2002US-00230414.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-521818/49.
 XX N-PSDB; ABT44264.
 DR New nucleic acid encoding for a PRO protein, useful for the manufacture
 XX of a medicament for diagnosing or treating tumors or for measuring or
 PT detecting expression of an associated gene.
 PT Claim 11; Fig 78; 315pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding a fully
 CC defined PRO polypeptide. The molecules of the invention may be useful for
 CC stimulating proliferation or gene expression in pericyte cells or the
 CC release of TNF-alpha from human blood. Other possible uses include the
 CC stimulation or inhibition of chondrocyte proliferation or
 CC differentiation, the stimulation of human dermal fibroblast cell

CC proliferation and the detection of the presence of a tumour within a
 CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
 CC of a medicament for diagnosing or treating a tumour within a mammal or
 CC for measuring or detecting the expression of an associated gene, as well
 CC as during gene therapy. The current sequence is that of the human PRO
 CC protein of the invention
 XX

SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOTEAH 16
 Db 44 RQRYLYTDDAQOTEAH 59

RESULT 14
 ABJ72394
 ID ABJ72394 standard; protein; 208 AA.

XX AC ABJ72394;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human PRO10196 protein.

XX KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
 KW tumour necrosis factor; proliferation; differentiation; gene therapy;
 KW dermal fibroblast.

XX OS Homo sapiens.

XX PN US2003027988-A1.

XX PD 06-FEB-2003.

XX PF 26-AUG-2002; 2002US-0027884.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-503301/47.

XX DR N-PSDB; AB744547.

XX New PRO protein encoding nucleic acid, useful for preparing PRO
 PT polypeptides and anti-PRO antibodies for detecting the presence of a
 PT tumor in a mammal.

XX Claim 11; Fig 78; 324pp; English.

XX The invention relates to a novel isolated PRO protein encoding nucleic
 CC acid. The nucleic acid of the invention may be useful for preparing PRO
 CC polypeptides and anti-PRO antibodies for detecting the presence of a
 CC tumour in a mammal. Furthermore, the molecules of the invention may be
 CC useful for stimulating proliferation or gene expression in pericyte
 CC cells, the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, the proliferation or differentiation of chondrocyte cells and for
 CC inhibiting the proliferation of normal human dermal fibroblast cells.
 CC Finally, the molecules may be utilised during gene therapy. The current
 CC sequence is that of the human PRO protein of the invention
 XX

SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RQRYLYTDDAQOTEAH 16
 Db 44 RQRYLYTDDAQOTEAH 59

RESULT 15

ABO34289
 ID ABO34289 standard; protein; 208 AA.

XX AC ABO34289;

XX DT 19-SEP-2003 (first entry)

XX DE Human secreted/transmembrane polypeptide PRO 10196.

XX KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
 KW human dermal fibroblast stimulation; tumour; tissue typing;
 KW affinity purification.

XX OS Homo sapiens.

XX PN US2003044934-A1.

XX PD 06-MAR-2003.

XX PF 28-AUG-2002; 2002US-00230338.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-492274/46.

XX DR N-PSDB; ACD82214.

XX New transmembrane polypeptides and nucleic acids encoding the
 PT polypeptides, useful in gene therapy, in chromosome identification, as
 PT chromosome markers, or in generating probes.

XX Claim 19; Fig 78; 315pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. Nucleic acids that encode PRO can be used to generate either
 CC transgenic animals or knock-out animals useful in developing and
 CC screening of therapeutically useful reagents. The nucleic acids may also
 CC be used in gene therapy for replacing defective gene, in chromosome
 CC identification, as chromosome markers, or in generating probes to isolate
 CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
 CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
 CC and for detecting the presence of tumour in an mammal. The PRO
 CC polypeptides are useful as molecular markers for protein electrophoresis
 CC and the isolated nucleic acids may be used for recombinantly expressing
 CC those markers. The PRO polypeptides and nucleic acids may also be used in
 CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
 CC PRO and in affinity purification of PRO from recombinant cell culture or
 CC natural sources. The present sequence represents the amino acid sequence
 CC of a human secreted/transmembrane PRO polypeptide

SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOTEAH 16

Db 44 RQRYLYTDDAQOTEAH 59

RESULT 16	1 RORYLYTDDAQTEAH 16
ADA37038	
ID ADA37038 standard; protein; 208 AA.	44 RORYLYTDDAQTEAH 59
XX AC ADA37038;	
XX DT 20-NOV-2003 (first entry)	
XX DE Human fibroblast growth factor 21 SEQ ID NO:1.	
XX KW mortality; morbidity; fibroblast growth factor 21; FGF-21;	
XX KW antiinflammatory; respiratory; antibacterial; immunosuppressive;	
XX KW vasotrophic; haemostatic; nephrotropic; glucose level regulator;	
XX KW glucose uptake stimulator; insulin sensitivity enhancer;	
XX KW systemic inflammatory response syndrome; respiratory distress;	
XX KW acute lung injury; acute respiratory distress syndrome;	
XX KW multiple organ dysfunction syndrome; sepsis;	
XX KW chronic obstructive pulmonary disease; emphysema; chronic bronchitis;	
XX KW pancreatitis; ischaemia; multiple trauma; tissue injury;	
XX KW haemorrhagic shock; immune-mediated organ injury; shock; renal failure.	
XX OS Homo sapiens.	
XX PN WO2003059270-A2.	
XX PD 24-JUL-2003.	
XX PF 08-JAN-2003; 2003WO-US000010.	
XX PR 15-JAN-2002; 2002US-0348890P.	
XX PA (ELIL) LILLY & CO ELI.	
XX PI Heuer JG, Kharitonov A;	
XX DR WPI; 2003-618118/58.	
XX PT Use of fibroblast growth factor 21 for reduction of mortality and	
XX PT morbidity in patients suffering from e.g. systemic inflammatory response	
XX PT syndrome and acute respiratory distress syndrome.	
XX PS Disclosure; Page 15-16; 22pp; English.	
XX CC The present invention describes a method for the reduction of mortality	
XX CC and morbidity in critically ill patients, which involves the	
XX CC administration of fibroblast growth factor 21 (FGF-21) (I). (I) has	
XX CC antiinflammatory, respiratory, antibacterial, immunosuppressive,	
XX CC vasotrophic, haemostatic and nephrotropic activities, and can be used as a	
XX CC glucose level regulator, a glucose uptake stimulator, and an insulin	
XX CC sensitivity enhancer. (I) can be used in the manufacture of a medicament	
XX CC for the reduction of morbidity and mortality in critically ill patients	
XX CC suffering from systemic inflammatory response syndrome (SIRS),	
XX CC respiratory distress, acute lung injury, acute respiratory distress	
XX CC syndrome, multiple organ dysfunction syndrome, sepsis and chronic	
XX CC obstructive pulmonary disease (e.g. emphysema and chronic bronchitis).	
XX CC The SIRS includes pancreatitis, ischaemia, multiple trauma and tissue	
XX CC injury, haemorrhagic shock, immune-mediated organ injury, shock and renal	
XX CC failure. FGF-12 regulates glucose levels in response to nutrient	
XX CC digestion; affects the overall metabolic state and counter-acts negative	
XX CC side effects that occur during the body's stress response to sepsis;	
XX CC reduces morbidity and mortality that occurs in critically ill patients;	
XX CC and stimulates glucose uptake and enhances insulin sensitivity. The	
XX CC present sequence represents the human FGF-21 amino acid sequence, which	
XX CC is given in the exemplification of the present invention.	
XX SQ Sequence 208 AA;	
XX Query Match 100.0%; Score 86; DB 7; Length 208;	
XX Best Local Similarity 100.0%; Pred. No. 4.4e-07;	
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	RESULT 17
DB	ABJ72096
	ID ABJ72096 standard; protein; 208 AA.
	XX AC ABJ72096;
	XX DT 16-OCT-2003 (first entry)
	XX DE Human membrane bound receptor/protein PRO10196 amino acid sequence.
	XX KW Human; PRO; membrane bound protein; membrane bound receptor;
	XX KW cell proliferation; cell migration; cell differentiation;
	XX KW mitogenic factor; survival factor; cytotoxic factor;
	XX KW differentiation factor; neuroptide; hormone; cell receptor;
	XX KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
	XX OS Homo sapiens.
	XX PN US2003065147-A1.
	XX PD 03-APR-2003.
	XX PF 29-AUG-2002; 2002US-00232224.
	XX PR 28-JUL-1999; 99US-0146222P.
	XX PR 24-FEB-2000; 2000WO-US005004.
	XX PR 02-MAR-2000; 2000WO-US005841.
	XX PR 01-JUN-2001; 2001WO-US017800.
	XX PR 29-JUN-2001; 2001WO-US021066.
	XX PR 09-APR-2002; 2002US-00119480.
	XX PA (GETH) GENENTECH INC.
	XX PI Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
	XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
	XX DR WPI; 2003-522018/49.
	XX DR N-PSDB; ABT43920.
	XX PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
	XX PT useful for the manufacture of a medicament for diagnosing or treating
	XX PT tumor.
	XX PS Claim 11; Fig 78; 315pp; English.
	XX CC This invention relates to one hundred and twenty two novel nucleic acids
	XX CC encoding human PRO membrane bound proteins or receptors. Extracellular
	XX CC proteins play important roles in the formation, differentiation and
	XX CC maintenance of multicellular organisms. The fate of many individual cells
	XX CC (for example proliferation, migration or differentiation) is typically
	XX CC governed by information received from other cells and the immediate
	XX CC environment. The information is often transmitted by secreted
	XX CC polypeptides (for example mitogenic factors, survival factors, cytotoxic
	XX CC factors, differentiation factors, neuroptides and hormones) which are
	XX CC received and interpreted by diverse cell receptors or membrane bound
	XX CC proteins. These membrane bound proteins and receptors may be of use as
	XX CC pharmaceutical and diagnostic agents, such as in the blocking of receptor
	XX CC -ligand interactions. The current invention provides the amino acid
	XX CC sequences of novel human membrane bound receptors and proteins, along
	XX CC with the cDNA sequences encoding them. The novel proteins of the
	XX CC invention may have cytostatic activities through the stimulation of
	XX CC chondrocytes. The nucleic acids of the invention may be useful for the
	XX CC manufacture of a medicament for diagnosing or treating a tumour in a
	XX CC mammal. In addition, they may be useful for measuring or detecting the
	XX CC expression of a tumour associated gene. The present sequence is the amino
	XX CC acid sequence of a human PRO protein of the invention
	XX SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
 |||||
 DB 44 RQRYLYTDDAQOTEAH 59

RESULT 18
 ADB83568
 ID ADB83568 standard; protein; 208 AA.
 AC ADB83568;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10196.
 XX human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 XX Homo sapiens.
 XX
 XX US2003073814-A1.
 EN
 XX
 XX 17-APR-2003.
 PD
 XX
 XX 12-AUG-2002; 2002US-00218849.
 PF
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 PR
 XX 29-JUN-2001; 2001WO-US021066.
 PR
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX
 XX WPI; 2003-644806/61.
 DR N-PSDB; ADB83567.
 XX
 XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 PT in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX
 XX Claim 11; Fig 78; 315pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO326, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9946, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,

CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (i) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (ii) encoding (i) is
 CC useful for chromosome and gene mapping or gene therapy. (ii) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
 |||||
 DB 44 RQRYLYTDDAQOTEAH 59

RESULT 19

ADB80674

ID ADB80674 standard; protein; 208 AA.

AC ADB80674;

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.

XX US2003088068-A1.

XX 08-MAY-2003.

XX 13-AUG-2002; 2002US-00219481.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-657982/62.

XX N-PSDB; ADB80673.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.

XX ADB782297;
XX 04-DEC-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO10196.
XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX Homo sapiens.
XX OS
XX RESULT 22
XX ADB84945
XX ID ADB84945 standard; protein; 208 AA.
XX AC ADB84945;
XX DT 04-DEC-2003 (first entry)
XX DE Human PRO polypeptide #39.
XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
XX cancer; lung; colon; breast; TNF-alpha; rectum; liver;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
XX arthritis; sports injury; cytostatic; antiarthritic.
XX OS
XX Homo sapiens.
XX US2003073817-A1.
XX EN
XX 17-APR-2003.
XX PD
XX 26-AUG-2002; 2002US-00227883.
XX PF
XX 01-AUG-2000; 2000US-022425P.
XX PR
XX 01-JUN-2001; 2001WO-US017800.
XX PR
XX 29-JUN-2001; 2001WO-US021066.
XX PR
XX 09-APR-2002; 2002US-00119480.
XX PA
XX (GETH) GENENTECH INC.
XX PI
XX Baker KP, Deanoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI: 2003-765495/72.
XX N-PSDB; ADB782296.
XX DR
XX New isolated PRO polypeptide useful for tissue typing, gene therapy, as
XX molecular weight markers in protein electrophoresis, and for treating
XX arthritis and tumors.
XX Claim 11; Fig 78; 308pp; English.
XX PS
XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX useful for stimulating the proliferation of or gene expression in
XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells. PRO331, PRO357, PRO725, PRO155, PRO1306 or PRO1419 polypeptide
XX are useful for stimulating the release of tumour necrosis factor (TNF)-
XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
XX PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
XX PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
XX PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
XX PRO1887, PRO1328, PRO3431, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
XX stimulating the proliferation of normal human dermal fibroblasts cells.
XX PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
XX PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
XX polypeptides such as PRO6004, PRO4381, PRO7174, PRO5778, PRO4332, etc.,
XX are useful for detecting the presence of tumour in a mammal which
XX involves comparing the level of expression of the above PRO polypeptides
XX in a test sample of cells taken from the mammal, and a control sample of
XX normal cells of the same cell type, where a higher level of expression of
XX the PRO polypeptides in the test sample as compared to the control sample
XX is indicative of the presence of tumour in the mammal. The tumour is lung
XX tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. (I) is useful as molecular weight markers, for tissue
XX typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
XX useful for chromosome and gene mapping or gene therapy. (II) is useful

CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.
XX SQ Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RQRYLYTDDAQQTFAH 16
| | | | | | | | | | | | | | | | | |
Db 44 RQRYLYTDDAQQTFAH 59

RESULT 22
ADB84945
ID ADB84945 standard; protein; 208 AA.

XX AC ADB84945;

XX DT 04-DEC-2003 (first entry)

XX DE Human PRO polypeptide #39.

XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
XX cancer; lung; colon; breast; TNF-alpha; rectum; liver;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
XX arthritis; sports injury; cytostatic; antiarthritic.

XX OS

XX Homo sapiens.

XX US2003073817-A1.

XX EN

XX 17-APR-2003.

XX PD

XX 26-AUG-2002; 2002US-00227883.

XX PF

XX 01-AUG-2000; 2000US-022425P.

XX PR

XX 01-JUN-2001; 2001WO-US017800.

XX PR

XX 29-JUN-2001; 2001WO-US021066.

XX PR

XX 09-APR-2002; 2002US-00119480.

XX PA

XX (GETH) GENENTECH INC.

XX PI

XX Baker KP, Deanoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI: 2003-730024/69.

XX N-PSDB; ADB84944.

XX DR

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX e.g. in gene therapy, disease diagnosis, chromosome identification and
XX tissue typing.

XX Claim 11; Fig 78; 314pp; English.

XX The invention relates to human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the PRO polynucleotides encoding them.
XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
XX diagnostics, biosensors or bioreactors. They are particularly useful for
XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
XX prostate tumour, rectal tumour or liver tumour) in a mammal, for
XX stimulating the release of tumour necrosis factor (TNF)-alpha from human
XX blood, for stimulating the proliferation or differentiation of
XX chondrocyte cells, for stimulating the proliferation of or gene
XX expression in pericyte cells or for stimulating the proliferation of
XX normal human dermal fibroblasts. The PRO nucleic acids are useful as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant

CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.

XX Sequence 208 AA;

SQ Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOQTEAH 16
 Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 23

ADB78051
 ID ADB78051 standard; protein; 208 AA.

XX AC ADB78051;

DT 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.

XX US2003092886-A1.

XX 15-MAY-2003.

XX 09-AUG-2002; 2002US-00216165.

XX 25-JUL-2000; 2000US-0220607P.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-765494/72.

XX N-PSDB; ADB78050.

XX Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as

XX molecular weight markers in protein electrophoresis, for treating

XX arthritis, tumor.

XX Claim 11; Fig 78; 308pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)

XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are

XX useful for stimulating the proliferation of or gene expression in

CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQOQTEAH 16

Db 44 RQRYLYTDDAQOQTEAH 59

RESULT 24

ADB87117

ID ADB87117 standard; protein; 208 AA.

XX AC ADB87117;

XX 04-DEC-2003 (first entry)

XX Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.

XX Homo sapiens.

XX US2003088067-A1.

XX 08-MAY-2003.

XX 13-AUG-2002; 2002US-00219479.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-657981/62.
 DR N-PSDB; ADB87116.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX Claim 11; Fig 78; 314pp; English.
 XX The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAAH 16
 DB 44 RQRYLYTDDAQQTAAH 59
 RESULT 25
 ADB84699
 ID ADB84699 standard; protein; 208 AA.
 XX ADB84699;
 AC ADB84699;
 XX 04-DEC-2003 (first entry)
 DT Human PRO polypeptide #39.
 DE Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 XX cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.
 XX Homo sapiens.
 OS US2003092890-A1.
 XX 15-MAY-2003.
 PD 14-AUG-2002; 2002US-00219536.
 XX

PR 28-JUL-1999; 99US-0146222P.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI WPI; 2003-777259/73.
 XX N-PSDB; ADB84698.
 DR New isolated PRO polypeptides, useful for tissue typing, gene therapy, as
 XX molecular weight markers in protein electrophoresis, and for treating
 XX arthritis and tumors.
 XX Claim 11; Fig 78; 308pp; English.
 XX The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAAH 16
 DB 44 RQRYLYTDDAQQTAAH 59
 RESULT 26
 ADB83814
 ID ADB83814 standard; protein; 208 AA.
 XX ADB83814;
 AC ADB83814;
 XX 04-DEC-2003 (first entry)
 DT Novel human secreted and transmembrane protein PRO10196.
 DE human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 XX antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;

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Best local similarity score: 0.99
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (1). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF) - alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO2144, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1136, PRO1185, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1373, PRO1760, PRO1567, PRO1887, PRO1328, PRO4341, PRO1801, PRO4334, PRO19543, PRO3444, PRO4322, PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of

CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
 |||||
 Db 44 RQRYLYTDDAQOTEAH 59

RESULT 28
 ADC36807
 ID ADC36807 standard; protein; 208 AA.

XX ADC36807;

DT 18-DEC-2003 (first entry)

XX Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.

OS Homo sapiens.

XX US2003088065-A1.

XX 08-MAY-2003.

XX 14-AUG-2002; 2002US-00219464.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;
 PI Grimaldi JC, Garney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX WPI; 2003-657979/62.

XX N-ESDB; ADC36806.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, or for preparing a medicament for treating
 PT cancer.

XX Claim 11; Fig 78; 315pp; English.

XX The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of

CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
 |||||
 Db 44 RQRYLYTDDAQOTEAH 59

RESULT 29

ADC21797

ID ADC21797 standard; protein; 208 AA.

XX ADC21797;

DT 18-DEC-2003 (first entry)

DE Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.

OS Homo sapiens.

XX US2003096969-A1.

XX 22-MAY-2003.

XX 29-AUG-2002; 2002US-00232225.

XX 02-JUN-2000; 2000WO-US015264.

XX 05-JUN-2000; 2000US-0209832P.

XX 20-JUN-2000; 2000US-0212901P.

XX 22-JUN-2000; 2000US-0213807P.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220385P.

XX 25-JUL-2000; 2000US-0220605P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220638P.

XX 25-JUL-2000; 2000US-0220664P.

XX 25-JUL-2000; 2000US-0220666P.

XX 26-JUL-2000; 2000US-0220893P.

XX 01-AUG-2000; 2000US-0222425P.

XX 22-AUG-2000; 2000US-0227133P.

XX 23-AUG-2000; 2000WO-US023522.

XX 24-AUG-2000; 2000WO-US023328.

XX 10-NOV-2000; 2000WO-US030873.

XX 28-NOV-2000; 2000US-0253646P.

XX 01-DEC-2000; 2000WO-US032678.

XX 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI
 XX WPI; 2003-765526/72.
 DR N-PSDB; ADC21796.
 XX
 PT Novel isolated PRO polypeptide useful for tissue typing, as molecular
 PT weight markers in protein electrophoresis, for treating arthritis, tumor.
 XX
 XX Claim 11; Fig 78; 308pp; English.
 XX
 CC The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumors (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAAH 16
 DB 44 RQRYLYTDDAQQTAAH 59
 RESULT 30
 ADC49828
 ID ADC49828 standard; protein; 208 AA.
 XX
 AC ADC49828;
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX Novel human secreted and transmembrane protein PRO10196.
 DE
 XX human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;

KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX Homo sapiens.
 XX US2003088064-A1.
 PN
 XX 08-MAY-2003.
 PD
 XX 14-AUG-2002; 2002US-00219075.
 XX
 XX 25-JUL-2000; 2000US-0220605P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI
 XX WPI; 2003-801154/75.
 DR N-PSDB; ADC49827.
 XX
 CC New secreted and transmembrane PRO polypeptide useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC polypeptide or anti-PRO antibody, e.g. cancer.
 PT
 FT
 FT
 XX Claim 11; SEQ ID NO 78; 314pp; English.
 PS
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1150, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO331, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1804, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAAH 16

Db 44 RQRYLYTDDAQQTTEAH 59
 RESULT 31
 ADC49027
 ID ADC49027 standard; protein; 208 AA.
 XX
 AC ADC49027;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 XX
 KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US200308070-A1.
 XX
 XX 08-MAY-2003.
 XX
 XX 28-AUG-2002; 2002US-00230260.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 XX
 XX 29-JUN-2001; 2001WO-US021066.
 XX
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-801155/75.
 XX
 XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 XX in gene therapy, chromosome identification, tissue typing, or as
 XX hybridization probes in chromosome and gene mapping.
 XX
 XX Claim 11; SEQ ID NO 78; 315pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 XX useful for stimulating the proliferation of or gene expression in
 XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 XX for stimulating the proliferation or differentiation of chondrocyte
 XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 XX are useful for stimulating the release of tumour necrosis factor (TNF)-
 XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080.
 XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 XX PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO4412,
 XX PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 XX PRO1343, PRO1376, PRO1387, PRO1349, PRO1409, PRO1917, PRO1760, PRO1567,
 XX PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 XX stimulating the proliferation of normal human dermal fibroblasts cells.
 XX PRO181, PRO229, PRO7154, or PRO7425 polypeptide are useful for
 XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 XX polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 XX are useful for detecting the presence of tumour in a mammal which
 XX involves comparing the level of expression of the above PRO polypeptides
 XX in a test sample of cells taken from the mammal, and a control sample of

CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4,4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RQRYLYTDDAQQTTEAH 16
 Db 44 RQRYLYTDDAQQTTEAH 59
 RESULT 32
 ADC49544
 ID ADC49544 standard; protein; 208 AA.
 XX
 AC ADC49544;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 XX
 KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation; lung tumour;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US200308071-A1.
 XX
 XX 08-MAY-2003.
 XX
 XX 29-AUG-2002; 2002US-00232231.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 XX
 XX 29-JUN-2001; 2001WO-US021066.
 XX
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-801156/75.
 XX
 XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 XX in gene therapy, chromosome identification, tissue typing, or as
 XX hybridization probes in chromosome and gene mapping.
 XX
 XX Claim 11; SEQ ID NO 78; 315pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 XX useful for stimulating the proliferation of or gene expression in
 XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 XX for stimulating the proliferation or differentiation of chondrocyte
 XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 XX are useful for stimulating the release of tumour necrosis factor (TNF)-
 XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080.
 XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 XX PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO4412,
 XX PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 XX PRO1343, PRO1376, PRO1387, PRO1349, PRO1409, PRO1917, PRO1760, PRO1567,
 XX PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 XX stimulating the proliferation of normal human dermal fibroblasts cells.
 XX PRO181, PRO229, PRO7154, or PRO7425 polypeptide are useful for
 XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 XX polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 XX are useful for detecting the presence of tumour in a mammal which
 XX involves comparing the level of expression of the above PRO polypeptides
 XX in a test sample of cells taken from the mammal, and a control sample of

CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO363, PRO331, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.
XX
SQ Sequence 208 AA;
Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 33
ID ADC47405
XX ADC47405; protein; 208 AA.
XX
XX ADC47405;
XX
DT 18-DEC-2003 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO10196.
XX
XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX
XX Homo sapiens.
XX
XX US2003088072-A1.
XX
XX 08-MAY-2003.
XX
XX 29-AUG-2002; 2002US-00232233.
XX
XX 25-JUL-2000; 2000US-0220605P.
XX
XX

PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
PA (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
PI WPI; 2003-801157/75.
XX N-ESDB; ADC47404.
XX
PT New PRO polypeptide for use as molecular weight markers for protein
PT electrophoresis purposes and for detecting the presence of tumor in a
PT mammal.
XX Claim 11; Fig 78; 314pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.
XX
XX Sequence 208 AA;
Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 34
ID ADC47150
XX ADC47150 standard; protein; 208 AA.
XX
XX ADC47150;
XX
XX 18-DEC-2003 (first entry)
XX
XX

Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.

Homo sapiens.

US2003105288-A1.

05-JUN-2003.

13-AUG-2002; 2002US-00219070.

25-JUL-2000; 2000US-0220666P.

01-JUN-2001; 2001WO-US017800.

29-JUN-2001; 2001WO-US021066.

09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

N-PSDB; ABC47149.

WPI; 2003-801246/75.

New isolated nucleic acid encoding a secreted and transmembrane

polypeptide (PRO), for use in recombinantly producing a PRO polypeptide, as a hybridization probe, and in gene therapy.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO1071, PRO1309, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1274, PRO1412, PRO1025, PRO1181, PRO1186, PRO1192, PRO1244, PRO1340, PRO1338, PRO1286, PRO1330, PRO1347, PRO1273, PRO1279, PRO1340, PRO1567, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322, PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO1714, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (i) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (ii) encoding (i) is useful for chromosome and gene mapping or gene therapy. (ii) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and

CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Indels 0;

QY 1 RORYLYTDDAQTEAH 16

Db 44 RORYLYTDDAQTEAH 59

RESULT 35

ADC78025

ID ADC78025 standard; protein; 208 AA.

XX ADC78025;

XX 01-JAN-2004 (first entry)

DE Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary; antiarthritic; pericyte cell proliferation; pericyte cell differentiation; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour necrosis factor alpha release; (TNF)-alpha release; dermal fibroblast cell proliferation; dermal fibroblast cell differentiation inhibitor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; tissue typing; chromosome mapping; gene mapping; gene therapy.

XX Homo sapiens.

XX US2003096972-A1.

XX 22-MAY-2003.

XX 29-AUG-2002; 2002US-00232234.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;

Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

XX N-PSDB; ADC78024.

XX WPI; 2003-765529/72.

Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as molecular weight markers, for treating arthritis and tumor.

Claim 11; Fig 78; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO1071, PRO1309, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1274, PRO1412, PRO1025, PRO1181, PRO1186, PRO1192, PRO1244, PRO1340, PRO1338, PRO1286, PRO1330, PRO1347, PRO1273, PRO1279, PRO1340, PRO1567, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322, PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for

CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.
XX Sequence 208 AA;
SQ
Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 36
ADD06260
ID ADD06260 standard; protein; 208 AA.
AC ADD06260;
XX
XX 01-JAN-2004 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO10196.
XX human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
KW antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX
XX Homo sapiens.
XX
XX US2003073816-A1.
XX
XX 17-APR-2003.
XX
XX 26-AUG-2002; 2002US-00227873.
XX
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen WE, Goddard A, Godowski PU;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
XX WPI; 2003-644807/61.
XX N-PSDB; ADD06259.
XX
XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful

PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX
XX Claim 11; SEQ ID NO 78; 314pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214,
CC PRO247, PRO326, PRO363, PRO531, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1328, PRO4341, PRO1801, PRO4333, PRO3543, PRO4322,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.
XX Sequence 208 AA;
SQ
Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
RESULT 37
ADC77779
ID ADC77779 standard; protein; 208 AA.
XX
XX ADC77779;
XX
XX 01-JAN-2004 (first entry)
XX
XX Novel human secreted and transmembrane protein PRO10196.
XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.
XX
XX Homo sapiens.
XX OS

XX PN US2003088066-A1.
 XX PD 08-MAY-2003.
 XX PF 13-AUG-2002; 2002US-00219466.
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX PI WPI; 2003-657980/62.
 XX DR N-PSDB; ADC77778.
 XX OS One hundred and twenty two nucleic acids encoding PRO polypeptides,
 XX OS useful in gene therapy, or for preparing a medicament for treating a
 XX OS condition that is responsive to the PRO polypeptide or anti-PRO antibody,
 XX OS e.g. cancer.
 XX PS Claim 11; Fig 78; 314pp; English.
 XX CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO331, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1083, PRO840, PRO1080,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX SQ Sequence 208 AA;
 Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RQRYLYTDDAQQTAEH 16
 |||||
 44 RQRYLYTDDAQQTAEH 59

RESULT 38
 ADD50742
 ID ADD50742 standard; protein; 208 AA.
 XX AC ADD50742;
 XX DT 15-JAN-2004 (first entry)
 XX DE Novel human secreted and transmembrane protein PRO10196.
 XX KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW chondrocyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX OS Homo sapiens.
 XX PN US2003105291-A1.
 XX PD 05-JUN-2003.
 XX PF 26-AUG-2002; 2002US-00227877.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX PI WPI; 2003-829361/77.
 XX DR N-PSDB; ADD50741.
 XX OS New isolated nucleic acid encoding a secreted and transmembrane
 XX OS polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 XX OS as a hybridization probe, and in gene therapy.
 XX PS Claim 11; Fig 78; 308pp; English.
 XX CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO331, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue

CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (III) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQQTAAH 16
 |||||
 Db 44 RQRYLYTDDAQQTAAH 59

RESULT 39

ADD50988
 ID ADD50988 standard; protein; 208 AA.

AC ADD50988;

XX 15-JAN-2004 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 XX antiarthritic; pericyte cell proliferation;
 KW chondrocyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.

XX US2003105290-A1.

XX 05-JUN-2003.

XX 13-AUG-2002; 2002US-00219527.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-829360/77.

XX N-PSDB; ADD50987.

XX New isolated nucleic acid encoding a secreted and transmembrane
 XX polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 XX as a hybridization probe, and in gene therapy.

XX Claim 11; Fig 78; 309pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
 XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 XX useful for stimulating the proliferation of or gene expression in
 XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 XX for stimulating the proliferation or differentiation of chondrocyte
 XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 XX are useful for stimulating the release of tumour necrosis factor (TNF)-
 XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,

CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1285, PRO1330, PRO1387, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (III) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 86; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RQRYLYTDDAQQTAAH 16
 |||||
 Db 44 RQRYLYTDDAQQTAAH 59

RESULT 40

ADD50469

ID ADD50469 standard; protein; 208 AA.

XX AC ADD50469;

XX 15-JAN-2004 (first entry)

XX Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 XX cancer; lung; colon; breast; prostate; rectum; liver;
 XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 XX arthritis; sports injury; cytostatic; antiarthritic.

XX Homo sapiens.

XX US2003096971-A1.

XX 22-MAY-2003.

XX 29-AUG-2002; 2002US-00232229.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX WPI; 2003-765528/72.

DR N-PSDB; ADD50468.
XX
XX Novel isolated PRO polypeptide useful for tissue typing, as molecular
PT weight markers in protein electrophoresis, for treating arthritis, tumor.
PT
XX Claim 11; Fig 78; 308pp; English.
PS
XX
XX The invention relates to human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
CC diagnostics, biosensors or bioreactors. They are particularly useful for
CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
CC blood, for stimulating the proliferation or differentiation of
CC chondrocyte cells, for stimulating the proliferation of or gene
CC expression in pericyte cells or for stimulating the proliferation of
CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
CC technology, in generating transgenic animals or knock-out animals which
CC may be used in the development and screening of therapeutically useful
CC reagents, in gene therapy, in chromosome identification, as chromosome
CC markers and in generating probes. The PRO polypeptides, or anti-PRO
CC antibodies, are useful for preparing a medicament for treating a
CC condition which is responsive to the PRO polypeptides or anti-PRO
CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
CC differentiation of chondrocytes. The PRO polypeptides are useful as
CC molecular markers for protein electrophoresis, and in tissue typing. This
CC sequence represents a human PRO polypeptide of the invention.
XX
SQ Sequence 208 AA;
Query Match 100.0%; Score 86; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQTAAH 16
Db 44 RQRYLYTDDAQQTAAH 59
Search completed: March 2, 2004, 16:04:51
Job time : 10.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:51:42 ; Search time 6.66667 Seconds
(without alignments)
757.244 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRYLYTDDAQQTAAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SP TREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	209	4 Q8N683	Q8N683 homo sapien
2	75	87.2	208	11 Q8V180	Q8V180 rattus norv
3	46	53.5	349	10 Q64469	Q64469 arabidopsis
4	43	50.0	233	12 Q65610	Q65610 kairi virus
5	43	50.0	1916	5 Q8IBCI	Q8IBCI plasmodium
6	43	50.0	2225	5 Q45881	Q45881 caenorhabdi
7	41	47.7	93	2 P71428	P71428 lactobacill
8	41	47.7	243	10 Q7XAQ1	Q7XAQ1 houttuynia
9	41	47.7	349	10 Q64468	Q64468 arabidopsis
10	41	47.7	355	10 Q9FSS1	Q9FSS1 oryza sativ
11	41	47.7	355	10 Q7XMQ2	Q7XMQ2 oryza sativ
12	41	47.7	385	2 Q48525	Q48525 lactobacill
13	41	47.7	1031	16 Q8G5K2	Q8G5K2 bifidobacte
14	40	46.5	174	2 Q9EYX7	Q9EYX7 klebsiella
15	40	46.5	332	5 Q9XUN3	Q9XUN3 caenorhabdi
16	40	46.5	403	16 Q67110	Q67110 aquifex aeo

17	40	46.5	506	2 Q8L341	Q8L341 vibrio chol
18	40	46.5	518	5 Q8T0C8	Q8T0C8 drosophila
19	40	46.5	529	2 Q9F237	Q9F237 bacillus fi
20	40	46.5	529	2 Q9RA62	Q9RA62 thermus cal
21	40	46.5	566	3 Q06696	Q06696 saccharomyc
22	40	46.5	775	12 P89057	P89057 rotavirus s
23	40	46.5	819	11 Q8CEB4	Q8CEB4 mus musculu
24	40	46.5	949	5 Q9Y0H4	Q9Y0H4 drosophila
25	40	46.5	2139	16 Q88YG6	Q88YG6 lactobacill
26	39	45.3	259	12 Q9Q8L5	Q9Q8L5 myxoma viru
27	39	45.3	263	17 Q97VB6	Q97VB6 sulfolobus
28	39	45.3	327	3 Q96VM0	Q96VM0 varrowia li
29	39	45.3	346	16 Q8ICM5	Q8ICM5 bacillus ce
30	39	45.3	369	5 Q93177	Q93177 caenorhabdi
31	39	45.3	430	16 Q8NRC7	Q8NRC7 corynebacte
32	39	45.3	439	16 Q926H4	Q926H4 rhizobium m
33	39	45.3	598	5 Q81PF9	Q81PF9 drosophila
34	39	45.3	604	5 Q8MSA8	Q8MSA8 drosophila
35	39	45.3	643	5 Q9VLP4	Q9VLP4 drosophila
36	39	45.3	735	2 Q24749	Q24749 acetobacter
37	39	45.3	766	10 Q8H6B0	Q8H6B0 zea mays (m
38	39	45.3	4368	5 Q61851	Q61851 caenorhabdi
39	38	44.2	235	5 Q23070	Q23070 caenorhabdi
40	38	44.2	251	13 Q3I9Q8	Q3I9Q8 brachydanio
41	38	44.2	252	16 Q87H76	Q87H76 vibrio para
42	38	44.2	276	4 Q8WV14	Q8WV14 homo sapien
43	38	44.2	285	16 Q8Z7N2	Q8Z7N2 salmonella
44	38	44.2	293	10 Q8VYU0	Q8VYU0 jatropha cu
45	38	44.2	293	10 Q8S452	Q8S452 jatropha cu

ALIGNMENTS

RESULT 1

Q8N683 PRELIMINARY; PRT; 209 AA.
AC Q8N683; 01-OCT-2002 (TREMREL. 22, Created)
DT 01-OCT-2002 (TREMREL. 22, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Fibroblast growth factor 21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC018404; AAH18404.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PD00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;

Query Match 100.0%; Score 86; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTAAH 16

DB 45 RQRYLYTDDAQQTAAH 60

RESULT 2

Q8V180 PRELIMINARY; PRT; 208 AA.
ID Q8V180

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AC Q8V180;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fibroblast growth factor 21.
GN FGF21.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB078901; BAB84299.1; -.
DR GO; GO:0008083; F: growth factor activity; IEA.
DR InterPro; IPR008996; Cytok IL1-like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD008831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 208 AA; 22857 MW; D232445902CDB8EA CRC64;

Query Match 87.2%; Score 75; DB 11; Length 208;
Best Local Similarity 87.5%; Pred. No. 3.1e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEAH 16
Db |||||:|||||
46 RQRYLYTDDQTEAH 61

RESULT 3
O64469 PRELIMINARY; PRT; 349 AA.
AC O64469;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Putative GDSL-motif lipase/hydrolase.
GN AT2G19060.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Mayhew L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrara A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RC Lin X.;
RL EMBL; AC002392; RAD12024.1; -.
DR FIR; T00526; T00526.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Hydrolase.

SQ SEQUENCE 349 AA; 38724 MW; 8836B8DF2AAE2AF7 CRC64;

Query Match 53.5%; Score 46; DB 10; Length 349;
Best Local Similarity 53.3%; Pred. No. 8.6;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEA 15
Db |||||:|||||
310 RERYVYWDNVHSTEA 324

RESULT 4
Q65610 PRELIMINARY; PRT; 233 AA.
AC Q65610;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE N protein.
OS Kairi virus.
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.
OC NCBI_TaxID=80939;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94172333; PubMed=8126455;
RA Dunn E., Pritlove D.C., Elliott R.M.;
RT "Evolutionary relationships of the Bunyavirus S genome segment.";
RL J. Gen. Virol. 75:597-608(1994).
DR EMBL; X73467; CAA51849.1; -.
DR GO; GO:0019013; C: viral nucleocapsid; IEA.
DR InterPro; IPR001784; Bunya_nucleocap.
DR Pfam; PF00952; Bunya_nucleocap; 1.
DR PRODOM; PD001909; Bunya_nucleocap; 1.
SQ SEQUENCE 233 AA; 26578 MW; 3D34022413505CF6 CRC64;

Query Match 50.0%; Score 43; DB 12; Length 233;
Best Local Similarity 50.0%; Pred. No. 19;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEAH 16
Db |||||:|||||
182 RQRYMNLDSQWTKH 197

RESULT 5
Q8IBCL PRELIMINARY; PRT; 1916 AA.
AC Q8IBCL;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein.
GN MAL8P1.1.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Seeger K., Murphy L., Harris D., Berriman M., Pain A., Hall N.,
RA Quail M., Barrell B.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL844507; CAD51085.1; -.
KW Hypothetical protein.
SQ SEQUENCE 1916 AA; 230013 MW; 68FF914B8A3519BD CRC64;

Query Match 50.0%; Score 43; DB 5; Length 1916;
Best Local Similarity 42.9%; Pred. No. 2.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTE 14
Db |||||:|||||
1299 KENYIIDGNETE 1312

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RESULT 6
O45881 ID O45881 PRELIMINARY; PRT; 2225 AA.
AC O45881
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE W01F3.3 protein.
GN W01F3.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]_TaxID=6239;
RN [1]_TaxID=6239;
RP SEQUENCE FROM N.A.
RA Cummings P.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z92815; CAB07294.1; -.
DR PIR; T26063; T26063.
DR HSP; P31713; LSHP.
DR WormPep; W01F3.3; CE16531.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR002223; Kunitz_BPTI.
DR InterPro; IPR000716; Thyrroglobulin_1.
DR InterPro; IPR006150; Worm repeat_1.
DR Pfam; PF00014; Kunitz_BPTI; 10.
DR Pfam; PF00086; thyroglobulin_1; 1.
DR PRINTS; PR00759; BASICPTASE.
DR ProDom; PD000222; Kunitz_BPTI; 10.
DR SMART; SM00131; KU; 10.
DR SMART; SM00211; TV; 1.
DR SMART; SM00289; WRI; 4.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 8.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 10.
DR PROSITE; PS00484; THYRGOLOBULIN_1; 1.
KW Protease inhibitor; Serine protease inhibitor.
SQ SEQUENCE 2225 AA; 242198 MW; A5DD8AE9D2A7B02A CRC64;

Query Match 50.0%; Score 43; DB 5; Length 2225;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
DB 477 QRYFYNDSQKE 489

RESULT 7
P71428 ID P71428 PRELIMINARY; PRT; 93 AA.
AC P71428;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Transposable element ISL1.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
[1]
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Group B; TRANSPOSON=ISL1;
RX MEDLINE=85295506; PubMed=2993817;
RA Shimizu-Kadota M., Kiwaki M., Hirokawa H., Tsuchida N.;
"ISL1: a new transposable element in Lactobacillus casei.";

RESULT 8
O7XAQ1 ID O7XAQ1 PRELIMINARY; PRT; 243 AA.
AC O7XAQ1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MADS-box transcription factor.
GN HCSBP1.
OS Houttuynia cordata (Chameleon plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Piperales; Saururaceae;
OC Houttuynia.
OX NCBI_TaxID=16752;
[1]
RN [1]
RP SEQUENCE FROM N.A.
RA Ito M., Imafuku M., Tanabe Y., Aoki S., Hasebe M.;
"MASS-box genes needed for determining petal identity express in
petal-like bracts of Houttuynia cordata (Saururaceae).";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB089157; BAC80253.1; -.
SQ SEQUENCE 243 AA; 27728 MW; 7B34DBEE4609DB88 CRC64;

Query Match 47.7%; Score 41; DB 10; Length 243;
Best Local Similarity 50.0%; Pred. No. 44;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
DB 168 RRLRLQLDDGSQTNP 183

RESULT 9
O64468 ID O64468 PRELIMINARY; PRT; 349 AA.
AC O64468;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative GDSL-motif lipase/hydrolase.
GN AT2G19050.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

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RL Mol. Gen. Genet. 200:193-198(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Group B; TRANSPOSON=ISL1;
RA Shimizu-Kadota M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02734; CAA26516.1; -.
DR PIR; S28726; S28726.
DR InterPro; IPR002514; Transposase_8.
DR Pfam; PF01527; Transposase_8; 1.
SQ SEQUENCE 93 AA; 10745 MW; 62584573F7F83DCE CRC64;

Query Match 47.7%; Score 41; DB 2; Length 93;
Best Local Similarity 61.5%; Pred. No. 15;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOT 13
DB 43 RWRKLYTEDGKQT 55

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RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Unayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eissen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002392; RAD12023.1; -.
DR FIR; T00525; T00525.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
KW Hydrolase.
SQ SEQUENCE 349 AA; 38577 MW; 05DAC363EA5F3D2A CRC64;

Query Match 47.7%; Score 41; DB 10; Length 349;
Best Local Similarity 46.7%; Pred. No. 67;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQOQTEA 15
Db 309 QRRYVWDNVHPTA 323

RESULT 10
Q9FSS1 PRELIMINARY; PRT; 355 AA.
AC Q9FSS1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative lipase/acylhydrolase.
GN H0212B02.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Zhou B., Feng Q., Huang Y.C., Chen Z.H., Li Y., Zhu J.J.,
RA Tang Y.S., Zhao Q., Liu Y.L., Mu J., Yu Z., Fan D.L., Chen L.,
RA Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X.,
RA Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.,
RA Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
RA "Oryza sativa indica (Guangluai4) genomic DNA, chromosome4, BAC
RT clone:H0212B02.9";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL442007; CAC03353.1; -.
DR Gramene; Q9FSS1; -.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR001087; Lipase_GDSL.
DR Pfam; PF00657; Lipase_GDSL; 1.
DR PROSITE; PS00038; HLH_1; 1.
KW Hydrolase.
SQ SEQUENCE 355 AA; 39580 MW; CFDEA2DDCCD52650 CRC64;

Query Match 47.7%; Score 41; DB 10; Length 355;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOQTEA 15
Db 322 EKYFYWDDVHPTA 335

RESULT 11
Q7XMQ2 PRELIMINARY; PRT; 355 AA.
AC Q7XMQ2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE OSUNB0059K02.9 protein.
GN OSUNB0059K02.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Liu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RA Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL606692; CAE04499.1; -.
DR EMBL; AL606692; CAE04499.1; -.
DR CFPDEBEADCCD52650 CRC64;
SQ SEQUENCE 355 AA; 39680 MW; CFPDEBEADCCD52650 CRC64;

Query Match 47.7%; Score 41; DB 10; Length 355;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOQTEA 15
Db 322 EKYFYWDDVHPTA 335

RESULT 12
Q48525 PRELIMINARY; PRT; 385 AA.
AC Q48525;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Transposase.
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Group B; TRANSPOSON-ISL1;
RX MEDLINE=85295506; PubMed=293817;
RA Shimizu-Kadota M., Kiwaki M., Hirokawa H., Tsuchida N.;
RT "ISL1: a new transposable element in Lactobacillus casei.";
RL Mol. Gen. Genet. 200:193-198(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Group B; TRANSPOSON-ISL1;
RA Shimizu-Kadota M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02734; CAA26518.1; -.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR002514; Transposase_8.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF01527; Transposase_8; 1.
DR Pfam; PF01527; Transposase_8; 1.
SQ SEQUENCE 385 AA; 44659 MW; D905D7AC279D8FF7 CRC64;

Query Match 47.7%; Score 41; DB 2; Length 385;
Best Local Similarity 61.5%; Pred. No. 75;

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RL J. Bacteriol. 0:0-0(2001):

RC STRAIN=VF5;
BY MEYTIME-99105555. PUBMED-9537320.

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.,
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus.";
 RL Nature 392:353-358(1998).
 DR EMBL; AF000717; AAC07076.1; -;
 DR FIC; C70385; C70385.
 DR InterPro; IPR005017; Toluene X.
 DR Pfam; PF03349; Toluene X; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 403 AA; 45861 MW; 04B04382A9F76D03 CRC64;

Query Match 46.5%; Score 40; DB 16; Length 403;
 Best Local Similarity 37.5%; Pred. No. 1.2e+02;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEAH 16
 :|||:|:|:
 Db 85 QKRYVYVDRSEDETH 100

RESULT 17

Q8L341 PRELIMINARY; PRT; 506 AA.
 AC Q8L341;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tnp protein.
 GN TNP.
 OS Vibrio cholerae 037.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=185332;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=1322-69;
 RX MEDLINE=21950561; PubMed=11953381;
 RA Li M., Shimada T., Morris J.G. Jr., Sulakvelidze A., Sozhamannan S.;
 RT "Evidence for the emergence of non-O1 and non-O139 Vibrio cholerae
 RT strains with pathogenic potential by exchange of O-antigen
 RT biosynthesis regions.";
 RL Infect. Immun. 70:2441-2453(2002).
 DR EMBL; AF390573; HAM22604.1; -;
 DR GO; GO:0003677; P:DNA binding; IEA.
 DR GO; GO:0006310; P:DNA recombination; IEA.
 DR InterPro; IPR007102; IS408_HTH.
 DR Pfam; PF00665; Irv; 1.
 SQ SEQUENCE 506 AA; 58610 MW; 06887234D0D27131 CRC64;

Query Match 46.5%; Score 40; DB 2; Length 506;
 Best Local Similarity 63.6%; Pred. No. 1.6e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQ 11
 :|||:|:|:
 Db 319 RQRYLYTETQ 329

RESULT 18

Q8TC08 PRELIMINARY; PRT; 518 AA.
 AC Q8TC08;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LD10565P (CG4244-PD).
 GN SU(DX) OR CG4244.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flesher C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin X.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J.J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissensbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RC SEQUENCE FROM N.A.
 RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J.Y., Beeson K.Y., Busan D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanavong S.,
 RA Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RC SEQUENCE FROM N.A.
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Brysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RP FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF069406; AAL39551.1; -;
 DR EMBL; AB003584; AAN10441.1; -;
 DR FlyBase; FBgn0003557; Su(dx).
 DR GO; GO:0007219; P:wing margin morphogenesis; IGI.
 DR GO; GO:0008587; P:wing vein morphogenesis; IGI.
 DR GO; GO:0008586; P:wing vein morphogenesis; IGI.
 DR InterPro; IPR000569; HECT domain.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR Pfam; PF00632; HECT; 1.
 DR Pfam; PF00397; WW; 2.
 DR SMART; SM00119; HECTC; 1.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS0237; HECT; 1.
 DR PROSITE; PS01159; WW DOMAIN 1; 2.
 DR PROSITE; PS0020; WW DOMAIN 2; 2.
 SQ SEQUENCE 518 AA; 61579 MW; 394240B85695856D CRC64;

Query Match 46.5%; Score 40; DB 5; Length 518;
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQTEA 15
 DB 19 QRYLYSQQQOQPTA 32

RESULT 19
 Q9F237
 ID Q9F237 PRELIMINARY; PRT; 529 AA.
 AC Q9F237;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Oligo-1,6-glucosidase.
 OS *Bacillus flavocaldarius*.
 OC Bacteria, Firmicutes; Bacilliales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=69408;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=KP1228;
 RC MEDLINE=98357218; PubMed=9692189;
 RX Kashiwabara S., Matsuki Y., Kishimoto T., Suzuki Y.;
 RA "Clustered proline residues around the active-site cleft in
 RT the most stable oligo-1,6-glucosidase of *Bacillus flavocaldarius*
 RT KP1228.";
 RL Biosci. Biotechnol. Biochem. 62:1093-1102 (1998).
 RL EMBL; AB003697; BAB18518.1; -;
 DR PIR; JE0181; JE0181.
 DR HSP; P21332; IUOK.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006589; Alp amyl cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 529 AA; 61470 MW; AB69611D41148B5 CRC64;

Query Match 46.5%; Score 40; DB 2; Length 529;

Best Local Similarity 43.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 QY 1 RORYLYTDDAQTEAH 16
 DB 227 RHEHLYTEQDPETAY 242
 RESULT 20
 Q9RA62
 ID Q9RA62 PRELIMINARY; PRT; 529 AA.
 AC Q9RA62;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Alpha-glucosidase.
 OS *Thermus caldophilus*.
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OX NCBI_TaxID=272;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=GK24; Lee S.Y., Lee D.S.;
 RA "Thermotable alpha-glucosidase gene from *Thermus aquaticus*
 RT caldophilus GK24.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF06282; RAD50603.1; -;
 DR HSP; P21332; IUOK.
 DR GO; GO:0004556; F:alpha-amylase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006047; Alpha amyl cat.
 DR InterPro; IPR006589; Alp amyl cat_sub.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 SQ SEQUENCE 529 AA; 61383 MW; 9C036E1C1F5118AA CRC64;

Query Match 46.5%; Score 40; DB 2; Length 529;
 Best Local Similarity 43.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQTEAH 16
 DB 227 RHEHLYTEQDPETAY 242

RESULT 21
 Q06696
 ID Q06696 PRELIMINARY; PRT; 566 AA.
 AC Q06696;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Chromosome XII COSMID 9931.
 GN VPS36 OR L9931.3 OR YLR417W.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=S288C;
 RC MEDLINE=97313267; PubMed=9169871;
 RX Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,
 RA Benes V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
 RA Entian K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
 RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,
 RA Louis E.J., Messenguy F., Mewes H.W., Miesga T., Mostl D.,
 RA Muller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
 RA Portetelle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
 RA Scharte M., Scherens B., Scholler P., Schwager C., Schwarz S.,
 RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
 RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,

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RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Favello A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Waterston R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U20162; AAB67493.1; -.
DR PIR; S59382; S59382.
DR SGD; S0004409; VPS36.
DR GO; GO:0005768; C:endosome; IDA.
DR GO; GO:0016299; P:regulator of G-protein signaling activity; IMP.
DR GO; GO:0045014; P:negative regulation of transcription by glu. .; IMP.
DR GO; GO:0045053; P:protein-Golgi retention; IMP.
DR GO; GO:0006623; P:protein-vacuolar targeting; IMP.
DR InterPro; IPR007261; Vps36.
DR Pfam; PF04132; Vps36; 1.
DR SMART; SM00547; Znf_RBZ; 2.
SQ SEQUENCE 566 AA; 64017 MW; 60DDDAEA3A620409 CRC64;

Query Match 46.5%; Score 40; DB 3; Length 566;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
Db ||| ||| :| :|
52 QRIIYIDDAKPTQ 64

RESULT 22
P89057 PRELIMINARY; PRT; 775 AA.
ID P89057
AC P89057;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VP4.
OS Rotavirus sp.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10970;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YR-1;
RA Ushijima H., Morikawa S., Mukoyama A., Nishio O.;
RT "Characterization of VP4 and VP7 of a murine rotavirus (YR-1) isolated in Japan.";
RL Jpn. J. Med. Sci. Biol. 48:237-247(1996).
DR EMBL; DA5215; BAA08147.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
SQ SEQUENCE 775 AA; 86306 MW; 4B4B90E49FCDC97 CRC64;

Query Match 46.5%; Score 40; DB 12; Length 775;
Best Local Similarity 42.9%; Pred. No. 2.5e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOTEAH 16
Db :||| ||| :| :|
301 QVYTRDGEVTAH 314

RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Favello A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Waterston R.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Cherry J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U20162; AAB67493.1; -.
DR PIR; S59382; S59382.
DR SGD; S0004409; VPS36.
DR GO; GO:0005768; C:endosome; IDA.
DR GO; GO:0016299; P:regulator of G-protein signaling activity; IMP.
DR GO; GO:0045014; P:negative regulation of transcription by glu. .; IMP.
DR GO; GO:0045053; P:protein-Golgi retention; IMP.
DR GO; GO:0006623; P:protein-vacuolar targeting; IMP.
DR InterPro; IPR007261; Vps36.
DR Pfam; PF04132; Vps36; 1.
DR SMART; SM00547; Znf_RBZ; 2.
SQ SEQUENCE 566 AA; 64017 MW; 60DDDAEA3A620409 CRC64;

Query Match 46.5%; Score 40; DB 3; Length 566;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
Db ||| ||| :| :|
52 QRIIYIDDAKPTQ 64

RESULT 23
Q8CED4 PRELIMINARY; PRT; 819 AA.
ID Q8CED4
AC Q8CED4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Zinc finger protein 27.
GN ZFP27.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK028500; BAC25981.1; -.
DR MGD; MGI:99174; Zfp27.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001909; KRAB.
DR Pfam; PF01352; KRAB; 1.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 21.
DR PROSITE; PS0805; KRAB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 21.
DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 22.
SQ SEQUENCE 819 AA; 92920 MW; C6782ECC0C379C4B CRC64;

Query Match 46.5%; Score 40; DB 11; Length 819;
Best Local Similarity 53.3%; Pred. No. 2.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTEAH 16
Db ||| ||| :| :|
19 QRSLYRDVVQETYSH 33

RESULT 24
Q9Y0H4 PRELIMINARY; PRT; 949 AA.
ID Q9Y0H4
AC Q9Y0H4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Su(dx) protein.
GN SU(DX) OR CG4244.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Bouck J., Bottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
 RA de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasner K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milehina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*."
 RT Science 287:2185-2195(2000).
 RL [2]
 RN
 RP SEQUENCE FROM N.A.
 RA Cornell M., Evans D.A.P., Mann R., Fostier M., Flaszka M.,
 RA Monthatong M., Artavanis-Tsakonas S., Baron M.,
 RT "The *Drosophila melanogaster* Suppressor of *deltex* gene, a regulator of
 RT the Notch receptor signalling pathway, is an E3 class ubiquitin
 RT ligase."
 RL Genetics 152:0-0(1999).
 CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 DR EMBL: AE003584; AAF51312.1; -;
 DR EMBL: AF152865; AAD38975.1; -;
 DR HSP; Q13526; IPIN.
 DR FlyBase: FBgn0003557; Su(dx).
 DR GO: GO:007219; P: N signaling pathway; IGI.
 DR GO: GO:0008587; P: wing margin morphogenesis; IGI.
 DR GO: GO:0008586; P: wing vein morphogenesis; IGI.
 DR InterPro: IPR000008; C2.
 DR InterPro: IPR008973; C2_CalB.
 DR InterPro: IPR000569; HECT domain.
 DR InterPro: IPR001202; WW_Rsp5_WWP.
 DR Pfam: PF00168; C2; 1.
 DR Pfam: PF00632; HECT; 1.
 DR Pfam: PF00397; WW; 4.
 DR SMART: SM00239; C2; 1.
 DR SMART: SM00119; HECT; 1.
 DR SMART: SM00456; WW; 3.
 DR PROSITE: PS50004; C2_DOMAIN_2; 1.
 DR PROSITE: PS50237; HECT; 1.
 DR PROSITE: PS01159; WW_DOMAIN_1; 3.
 DR PROSITE: PS50020; WW_DOMAIN_2; 2.
 DR SEQUENCE 949 AA; 107966 MW; 74B17A8B05AC6E6B CRC64;

Query Match 46.5%; Score 40; DB 5; Length 949;
 Best Local Similarity 57.1%; Pred. No. 3.2e+02;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQQTEA 15
 |||||: |||||
 Db 450 QRYLYSQQQQPTA 463

RESULT 25
 Q88YGG PRELIMINARY; PRT; 2139 AA.
 ID Q88YGG6;
 AC Q88YGG6;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cell surface protein precursor.
 DE LP_0800.
 OS Lactobacillus plantarum.
 OS Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OC NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCF51;
 RX MEDLINE=22480296; PubMed=12566566;
 RA Kleerebezem M., Boekhorst J., van Kraenenburg R., Molenaar D.,
 RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Sierzen R.J.;
 RT "Complete genome sequence of *Lactobacillus plantarum* WCF51."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
 DR EMBL: AL935254; CAD63387.1; -;
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR Pfam: PF00746; Gram_pos_anchor; 1.
 DR PROSITE: PS50847; GRAM_POS_ANCHORING; 1.
 KW Complete proteome.
 SQ SEQUENCE 2139 AA; 226353 MW; 71C8B7CDB8EC5838 CRC64;
 Query Match 46.5%; Score 40; DB 16; Length 2139;
 Best Local Similarity 77.8%; Pred. No. 8.1e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 5 LYTDDAQQT 13
 :|||||
 Db 1496 MYTDDLQQT 1504
 RESULT 26
 Q808L5 PRELIMINARY; PRT; 259 AA.
 ID Q808L5;
 AC Q808L5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE M085R.
 GN M085R.
 OS Myxoma virus (strain Lausanne).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Leporipoxvirus.
 OC NCBI_TaxID=31530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lausanne;
 RX MEDLINE=20032073; PubMed=10562494;
 RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
 RA Macaulay C., Willer D., Evans D., McFadden G.;
 RT "The complete DNA sequence of myxoma virus."
 RL Virology 264:298-318(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Lausanne;
 RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.-X.,
 RA Macaulay C., Willer D., Evans D., McFadden G.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF170726; AAF14973.1; -;
 DR InterPro: IPR000086; NUDIX_hydrolase.
 DR InterPro: IPR003301; Viral_VD10.
 DR Pfam: PF00293; NUDIX; 1.
 DR PRINTS: PR01364; VD10PROTEIN.
 DR PROSITE: PS00893; NUDIX; 1.

SQ SEQUENCE 259 AA; 30411 MW; 2ELC254DC626848D CRC64;
 Query Match 45.3%; Score 39; DB 12; Length 259;
 Best Local Similarity 58.3%; Pred. No. 1.1e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 QLYTDDAQOQTEA 15
 Db 25 YTWTTDDAQVSA 36
 | : ||||| : |
 | : ||||| : |

RESULT 27
 Q97YE6 PRELIMINARY; PRT; 263 AA.
 ID Q97YE6
 AC Q97YE6
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein SSO1380.
 GN SSO1380.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OC NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;
 RA MEDLINE=2132296; PubMed=11427726;
 RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
 RA Aways M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
 RA De Moors A., Etraou G., Fletcher C., Gordon P.M.K.,
 RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
 RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
 RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
 RA Garrett R.A., Ragan M.A., Senses C.W., Van der Oost J.;
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
 DR EMBL; AE06752; AAK41614.1; -.
 DR FIR; G90294; G90294.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 263 AA; 31204 MW; CEB2E3919CEB7F7 CRC64;
 Query Match 45.3%; Score 39; DB 17; Length 263;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQOQTEA 15
 Db 217 ERFLYLDNHDQIKA 230
 | : ||||| : |
 | : ||||| : |

RESULT 28
 Q96VMO PRELIMINARY; PRT; 327 AA.
 ID Q96VMO
 AC Q96VMO
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Putative dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
 GN TGD1.
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OC NCBI_TaxID=4952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SMS397A;
 RA Cheon S.A., Song Y., Kim J.Y.;
 RT "Molecular cloning of the YITGD1 gene in Yarrowia lipolytica.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY040633; AAK77226.1; -.
 DR GO; GO:0008460; F:dTDP-glucose 4,6-dehydratase activity; IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.

DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
 DR InterPro; IPR001509; Epimerase_Dh.
 DR Pfam; PF01370; Epimerase; 1.
 KW Lyase.
 SQ SEQUENCE 327 AA; 37099 MW; DC4F253E0B1ABD76 CRC64;
 Query Match 45.3%; Score 39; DB 3; Length 327;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RQRYLYTDD 9
 Db 220 RRRVYADD 228
 | : ||||| : |
 | : ||||| : |

RESULT 29
 Q81CWS PRELIMINARY; PRT; 346 AA.
 ID Q81CWS
 AC Q81CWS
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Penicillin-binding protein.
 GN BC2729.
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=226900;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=22608415; PubMed=12721630;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
 RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
 RA Grechkin Y., Pusch G., Haselkorn R., Foust M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis.";
 EL Nature 423:87-91(2003).
 DR EMBL; AE017006; AAP09683.1; -.
 DR InterPro; IPR001466; Beta_lactamase.
 DR Pfam; PF00144; beta-lactamase; 1.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
 KW Complete proteome.
 SQ SEQUENCE 346 AA; 38538 MW; 53189F477337A312 CRC64;
 Query Match 45.3%; Score 39; DB 16; Length 346;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQOQ 13
 Db 219 QTYVYKSDAQAT 230
 | : ||||| : |
 | : ||||| : |

RESULT 30
 Q93177 PRELIMINARY; PRT; 369 AA.
 ID Q93177
 AC Q93177
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DR C02C6.3 protein.
 GN C02C6.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swinburne J.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z79596; CAB01858.3; -.
 DR PIR; T18857; T18857.
 DR PIR; T18859; T18859.
 DR WormPep; C02C6.3; CE29169.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR Pfam; PF00560; LRR; 4.
 DR Pfam; PF01463; LRRCT; 1.
 DR SMART; SM00082; LRRCT; 1.
 SQ SEQUENCE 369 AA; 42639 MW; CFB127DC68B96D3A CRC64;

Query Match 45.3%; Score 39; DB 5; Length 369;
 Best Local Similarity 70.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDA 10
 ||| ||| |||
 DB 39 RQRYLYTDDA 48

RESULT 31
 Q8NRC7 PRELIMINARY; PRT; 430 AA.
 AC Q8NRC7;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mg/Co/Ni transporter MgtE (contains CBS domain).
 GN CGL1125.
 OS Corynebacterium glutamicum (Brevibacterium flavum).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
 OX NCBI_TaxID=1718;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
 RA Nakagawa S.;
 RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP005277; BAB98518.1; -.
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000644; CBS domain.
 DR InterPro; IPR006668; MgtE intracl.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF03448; MgtE N; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 1.
 KW Complete proteome.
 SQ SEQUENCE 430 AA; 47316 MW; 447DC6CE103D34B9 CRC64;

Query Match 45.3%; Score 39; DB 16; Length 430;
 Best Local Similarity 63.6%; Pred. No. 1.9e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 LYTTDDAQQTEA 15
 ||| ||| |||
 DB 368 LYADDSDQETAA 378

RESULT 32
 Q926H4 PRELIMINARY; PRT; 439 AA.
 ID Q926H4
 AC Q926H4;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative sugar uptake ABC transporter periplasmic solute-binding
 DE protein.
 GN RB0682 OR SBE21103. (Sinorhizobium meliloti).
 OS Rhizobium meliloti (megaplasmid 2).
 OG Plasmid psymb (megaplasmid 2).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396508; PubMed=11481431;
 RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorhoefer F.J., Hernandez-Lucas I., Becker A., Gouzy J.,
 RA Golding B., Puehler A.;
 RA "The complete sequence of the 1,683-kb psymb megaplasmid from the N2-
 RT fixing endosymbiont Sinorhizobium meliloti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 DR EMBL; AL603644; CAC49082.1; -.
 DR PIR; B95927; B95927.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR InterPro; IPR006059; SBP_bac_1.
 DR Pfam; PF01547; SBP_bac_1;
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Plasmid; Hypothetical protein; Complete proteome.
 SQ SEQUENCE 439 AA; 47505 MW; 274E8BDC80BF57D6 CRC64;

Query Match 45.3%; Score 39; DB 16; Length 439;
 Best Local Similarity 53.8%; Pred. No. 2e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQQTE 14
 ||| ||| ||| |||
 DB 152 QKSLYQDEAKTTE 164

RESULT 33
 Q8IPF9 PRELIMINARY; PRT; 598 AA.
 AC Q8IPF9;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CG7795-PB.
 GN CG7795.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabriella A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.D.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Sampson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banton J., Beeson K.Y., Buesam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.J., Bergman C., Bernert D., Frise E., de Grey A., Harris N.,
 RA Klomp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003620; AAN1163.1;
 DR FlyBase; FBgn0032019; CG7795.
 SQ SEQUENCE 598 AA; 67370 MW; 2B9CA0BE22421CC9 CRC64;

Query Match 45.3%; Score 39; DB 5; Length 598;
 Best Local Similarity 46.7%; Pred. No. 2.8e+02;
 Matches 7; Conservative 5; Mismatches 1; Indels 2; Gaps 1;
 OY 4 YLYT--DDAQOQTEAH 16
 DB 428 YLYTMEDESEETQRH 442

RESULT 34
 QMSA8
 ID QMSA8 PRELIMINARY; PRT; 604 AA.
 AC QMSA8;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE LD44821p.
 GN CG7795.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celnik S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY118966; AAMS0826.1; --
 DR FlyBase; FBgn0032019; CG7795.
 SQ SEQUENCE 604 AA; 68182 MW; D8B168E7BFBA07FF CRC64;

Query Match 45.3%; Score 39; DB 5; Length 604;
 Best Local Similarity 46.7%; Pred. No. 2.9e+02;
 Matches 7; Conservative 5; Mismatches 1; Indels 2; Gaps 1;
 OY 4 YLYT--DDAQOQTEAH 16
 DB 428 YLYTMEDESEETQRH 442

RESULT 35
 QSVLP4
 ID QSVLP4 PRELIMINARY; PRT; 643 AA.
 AC QSVLP4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE CG7795 protein.
 GN CG7795.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 RA Burris K.C., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foster C., Gabriella A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mozhrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003620; AAF52640.1; -;
 DR FlyBase; FBgn0032019; CG7795.
 SQ SEQUENCE 643 AA; 72867 MW; 94FFB937EB9CBB12 CRC64;

Query Match 45.3%; Score 39; DB 5; Length 643;
 Best Local Similarity 46.7%; Pred. No. 3.1e+02;
 Matches 7; Conservative 5; Mismatches 1; Indels 2; Gaps 1;

QY 4 YLYT--DQAQQTAAH 16
 |||||:|:|:|:|:
 Db 428 YLYTMEDESEETQRH 442

RESULT 36
 024749 PRELIMINARY; PRT; 735 AA.
 AC 024749;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Beta-glucosidase.
 GN BETA-GUJ
 OS Acetobacter xylinus.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Acetobacteraceae; Gluconacetobacter.
 OX NCBI_TaxID=28448;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BPR2001;
 RX MEDLINE=98028223; PubMed=9362130;
 RA Tonouchi N., Tahara N., Kojima Y., Nakai T., Sakai F., Hayashi T.,
 RA Tsuchida T., Yoshinaga F.;
 RT "A beta-glucosidase gene downstream of the cellulose synthase operon
 in cellulose-producing *Acetobacter*.";
 RL Biosci. Biotechnol. Biochem. 61:1789-1790(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BPR2001;
 RX Uneyama T., Tonouchi N.;
 RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BPR2001;
 RX MEDLINE=98296257; PubMed=9630539;
 RA Nakai T., Moriya A., Tonouchi N., Tsuchida T., Yoshinaga F.,
 RA Horinouchi S., Sone Y., Mori H., Sakai F., Hayashi T.;
 RT "Control of expression by the cellulose synthase (bcsA) promoter
 region from *Acetobacter xylinum* BPR 2001.";
 RL Gene 213:93-100(1998).
 DR EMBL; AB003689; BAA23595.1; -;
 DR EMBL; AB010645; BAA31467.1; -;
 DR PIR; JC5869; JC5869.
 GO; GO:0004553; F:Hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR002772; Glyco_hydro_3C.
 DR InterPro; IPR001764; Glyco_hydro_3N.
 DR Pfam; PF00933; Glyco_hydro_3; 1.
 DR Pfam; PF01915; Glyco_hydro_3_C; 1.
 DR PRINTS; PR00133; GLYHDLASE3.
 SQ SEQUENCE 735 AA; 78223 MW; 463DB8116F1C55E1 CRC64;

Query Match 45.3%; Score 39; DB 2; Length 735;
 Best Local Similarity 70.0%; Pred. No. 3.6e+02;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TDDAQQTAAH 16
 |||||:|:|:|:|:
 Db 718 TDDSQQTAAH 727

RESULT 37
 08H6B0 PRELIMINARY; PRT; 766 AA.
 AC 08H6B0;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE SET domain protein 113.
 GN SDG113.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. B73;
 RA Chandler V.L., Kaeppler S.M., Cone K.C.;
 RT "Sequences from the Plant Chromatin Consortium.";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. B73;
 RA Bergstrom D., Springer N.M., Schmitt L.T., Guthrie E., Sidorenko L.,
 RA Kaeppler S.M., Cone K.C.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF545813; AAN41253.1; -;
 DR InterPro; IPR003105; G9a.
 DR InterPro; IPR003616; PostSET.
 DR InterPro; IPR007728; Pre-SET.
 DR InterPro; IPR001214; SET.
 DR InterPro; IPR003606; Zn2-binding.
 DR Pfam; PF05033; Pre-SET; 1.
 DR Pfam; PF00856; SET; 1.
 DR Pfam; PF02182; YDC_SRA; 1.
 DR SMART; SM00468; PreSET; 1.
 DR SMART; SM00317; SET; 1.
 DR SMART; SM00466; SRA; 1.
 DR PROSITE; PS00868; POST SET; 1.
 DR PROSITE; PS00867; PRE SET; 1.
 DR PROSITE; PS0280; SET; 1.
 SQ SEQUENCE 766 AA; 83842 MW; D2778799EF9E9E4B8 CRC64;

Query Match 45.3%; Score 39; DB 10; Length 766;
 Best Local Similarity 53.8%; Pred. No. 3.8e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQQT 13
 |||||:|:|:|:|:
 Db 269 RRRHLQLDEAQT 281

RESULT 38
 061851 PRELIMINARY; PRT; 4368 AA.
 ID 061851
 AC 061851;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN F55F10.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Pauley A., Gattling S., Scheet P.;
 RT "The sequence of C. elegans cosmid F55F10.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL EMBL; AF067621; AAC17540.2; -.
 DR PIR; T33163; T33163.
 DR WormPep; F55F10.1; CE30377.
 DR GO; GO:0005524; E:ATP binding; IEA.
 DR GO; GO:0003677; E:DNA binding; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR002078; Sig54 interact.
 DR InterPro; IPR002035; VWFA_A.
 DR Pfam; PF00092; vwa; 1.
 DR SMART; SM00382; AAA; 6.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00675; SIGMA54_INTERACT_1; 1.
 DR PROSITE; PS0234; VWFA; 1.
 KW Hypothetical protein; ATP-binding.
 SQ SEQUENCE 4368 AA; 492651 MW; 6CE6A78E56A57969 CRC64;

 Query Match 45.3%; Score 39; DB 5; Length 4368;
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

 QY 1 RQRYLYTDDAQOQTEA 15
 DB 3953 RKRELATDDAPMEEA 3967

 RESULT 39
 Q23070 PRELIMINARY; PRT; 235 AA.
 AC Q23070;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN W01A11.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;

RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Blanchard M., Bradshaw H.;
 RT "The sequence of C. elegans cosmid W01A11.";
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64852; AAB04972.1; -.
 DR PIR; T33962; T33962.
 DR WormPep; W01A11.7; CE14402.
 KW Hypothetical protein.
 SQ SEQUENCE 235 AA; 26776 MW; C087F352ED5F9874 CRC64;

 Query Match 44.2%; Score 38; DB 5; Length 235;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

 QY 1 RQRYLYTDDAQOQTEAH 16
 DB 106 RQRYLSEGDIVVSAH 121

 RESULT 40
 Q91908 PRELIMINARY; PRT; 251 AA.
 AC Q91908;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mannose binding-like lectin precursor.
 GN MBL.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20456722; PubMed=11003389;
 RA Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;
 RT "The homologue of mannose-binding lectin in the carp family Cyprinidae
 RT is expressed at high level in spleen, and the deduced primary
 RT structure predicts affinity for galactose.";
 RL Immunogenetics 51:955-964(2000).
 DR EMBL; AF227738; AAF63469.1; -.
 DR HSSP; P19999; IAFB.
 DR ZFIN; ZDB-GENE-000427-2; mbl.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:007157; P:heterophilic cell adhesion; IEA.
 DR InterPro; IPR008161; Clg helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF01391; Collagen; 2.
 DR Pfam; PF00059; Lectin_C; 1.
 DR ProDom; PD000007; Clg helix; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
 KW Collagen; Lectin; Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 251 MANNOSE BINDING-LIKE LECTIN.
 FT VARIANT 21 21 M -> L.
 FT VARIANT 204 204 K -> N.
 SQ SEQUENCE 251 AA; 26829 MW; 12D0ABD06B63B11 CRC64;

Query Match 44.2%; Score 38; DB 13; Length 251;
Best Local Similarity 50.0%; Pred.No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQQT 13
|:| ||| :|
Db 135 QRYVTDDVEET 146

Search completed: March 2, 2004, 16:07:19
Job time : 8.66667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:51:17 ; Search time 1.53333 Seconds
(without alignments)
543.341 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RQRYLYTDDAQQTAEH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	86	100.0	209	1 FGFL HUMAN	Q9naal homo sapien
2	75	87.2	210	1 FGFL MOUSE	O9jjn1 mus musculus
3	41	47.7	415	1 HEMI NEIGO	O9zhd6 neisseria g
4	41	47.7	1121	1 DPOI_ADEG1	O64751 avian adeno
5	40	46.5	543	1 ZN08 HUMAN	P17098 homo sapien
6	40	46.5	776	1 VP4_ROTPI	P25174 porcine rot
7	40	46.5	1587	1 SUR2 CABEL	Q10669 caenorhabdi
8	39	45.3	215	1 IF4E APLCA	O77210 aplysia cal
9	39	45.3	627	1 2AD2 SCHPO	P78759 schizosacch
10	38	44.2	457	1 CUSC_ECOLI	P26451 human rotav
11	38	44.2	460	1 CUSC_ECO57	P77211 escherichia
12	38	44.2	460	1 CUSC_ECOL6	Q8cwa4 escherichia
13	38	44.2	460	1 SYR_STAEP	Q8ctn9 staphylococ
14	38	44.2	553	1 VP4_NCDV	P17465 nebraska ca
15	38	44.2	775	1 VP4_ROTPI	P39034 feline rota
16	38	44.2	775	1 VP4_ROTPI	P39033 human rotav
17	38	44.2	775	1 VP4_ROTPI	P04508 simian 11 r
18	38	44.2	776	1 VP41_ROTPI	P12976 simian 11 r
19	38	44.2	776	1 VP42_ROTPI	P36305 bovine rota
20	38	44.2	776	1 VP4_ROTPI	P08713 bovine rota
21	38	44.2	776	1 VP4_ROTPI	P17463 simian 11 r
22	38	44.2	776	1 VP4_ROTPI	P17454 simian 11 r
23	38	44.2	776	1 VP4_ROTPI	Q9pf41 xylella fas
24	38	44.2	792	1 OSTA_XYLFA	Q87ai9 xylella fas
25	38	44.2	792	1 OSTA_XYLFT	P14381 xenopus lae
26	38	44.2	1308	1 YTX2_XENLA	Q04561 lelystad vi
27	38	44.2	3859	1 RPOA_LELV	P53515 escherichia
28	37	43.0	101	1 RFAA_ECOLI	P21049 vaccinia vi
29	37	43.0	273	1 VE08_VACCC	P23372 vaccinia vi
30	37	43.0	273	1 VE08_VACCV	P33820 variola vir
31	37	43.0	273	1 VE08_VARV	Q9spe5 arabidopsis
32	37	43.0	291	1 SNAG_ARATH	P73655 synchocyst
33	37	43.0	337	1 SYW_SYNY3	

RESULT 1
FGFL HUMAN STANDARD; PRT; 209 AA.
AC Q9NSX1:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21) (UNQ31115/PRO10196).
GN FGF21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
the liver.";
RL Biochim. Biophys. Acta 1492:203-206 (2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brueh J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Ratton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Marks M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.

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CC -----
CC EMBL: AB021975; BAA99415.1; -;
CC DR EMBL: AB021975; BAA99415.1; -;
CC DR EMBL: AB021975; BAA99415.1; -;
CC DR HSSP: P03968; 1BAR.
CC DR HSSP: P03968; 1BAR.
CC DR GO: GO:0005576; C:extracellular; TAS.
CC DR GO: GO:0005576; C:soluble fraction; TAS.
CC DR GO: GO:0007267; P:cell-cell signaling; TAS.
CC DR GO: GO:0007165; P:signal transduction; TAS.
CC DR InterPro: IPR008996; Cytok_1111_like.
CC

34 37 43.0 415 1 SIP2 YEAST P34164 saccharomyc
35 37 43.0 435 1 FIXC RHISN Q53208 rhizobium s
36 37 43.0 470 1 STE3 YEAST P06783 saccharomyc
37 37 43.0 553 1 SYR_STAAM Q932f6 staphylococ
38 37 43.0 553 1 SYR_STAAM Q99w05 staphylococ
39 37 43.0 553 1 SYR_STAAM Q8nxt8 staphylococ
40 37 43.0 593 1 DSBD VIBVU O8dcz0 vibrio vuln
41 37 43.0 605 1 UBP2 HUMAN O75504 homo sapien
42 37 43.0 616 1 MUTA_STRCM Q05064 streptomyce
43 37 43.0 746 1 PFEA_PSEAE Q05098 pseudomonas
44 37 43.0 775 1 VP4_ROTPI Q01541 human rotav
45 37 43.0 776 1 VP4_ROTPI Q08778 human rotav

ALIGNMENTS

```
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 209
FT CONFLICT 23 23
SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;

Query Match 100.0%; Score 86; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTEAH 16
Db 45 RQRYLYTDDAQQTEAH 60

RESULT 2
FGFL MOUSE
ID FGFL MOUSE STANDARD; PRT; 210 AA.
AC Q9JUN1
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21).
GN FGF21.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in
RT the liver.";
RL Biochim. Biophys. Acta 1492:203-206 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli K., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: Most abundantly expressed in the liver, also
CC expressed in the thymus at lower levels.
CC -1- SIMILARITY: Belongs to the heparin-binding growth factors family.
CC
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-----
DR EMBL; AB025718; BAA99416.1; -.
DR EMBL; AK007574; BAB25115.1; -.
DR HSSP; PO3968; 1BAR.
DR MGD; MGI:1861377; Fgf21.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28
FT CHAIN 29 210
FT CONFLICT 23 23
FT CONFLICT 23 23
SQ SEQUENCE 210 AA; 23237 MW; AE02AABA6477E6F0 CRC64;

Query Match 87.2%; Score 75; DB 1; Length 210;
Best Local Similarity 87.5%; Pred. No. 3.4e-06;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQTEAH 16
Db 46 RQRYLYTDDAQQTEAH 61

RESULT 3
HEMI NEIGO
ID HEMI NEIGO STANDARD; PRT; 415 AA.
AC Q9ZHD6;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutaryl-tRNA reductase (EC 1.2.1.-) (GLUTR).
GN HEMA.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 700825 / FA 1090;
RX MEDLINE=99030330; PubMed=9811666;
RA Lewis L.A., Sung M., Gipson M., Hartman K., Dyer D.W.;
RT "Transport of intact porphyrin by HmuAB, the hemoglobin-haptoglobin
RT utilization system of Neisseria meningitidis.";
RL J. Bacteriol. 180:6043-6047 (1998).
CC -1- CATALYTIC ACTIVITY: Glutamyl-tRNA (Glu) + NADPH = glutamate-1-
CC semialdehyde + NADP(+) + tRNA(Glu).
CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.
CC -1- SIMILARITY: Belongs to the glutaryl-tRNA reductase family.
CC
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-----
DR EMBL; AF067426; AAC79428.1; -.
DR HSSP; O42843; 1B29.
DR HAMAP; MF_00087; -.
DR InterPro; IPR000343; Glutr.
DR Pfam; PF00745; Glutr dimer; 1.
DR Pfam; PF05201; Glutr N; 1.
DR Pfam; PF05200; Glutr NAD bind; 1.
DR TIGRfams; TIGR01035; hema; 1.
DR PROSITE; PS00747; GLUTR; 1.
```

KW Porphyrin biosynthesis; Oxidoreductase; NADP.
 FT ACT_SITE 50 50 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 94 94 BASE (BY SIMILARITY).
 SQ SEQUENCE 415 AA; 45453 MW; 054D366586CBB32F CRC64;
 Query Match 47.7%; Score 41; DB 1; Length 415;
 Best Local Similarity 61.5%; Pred. No. 9.7;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YLYTDDAQTEAH 16
 |||||
 Db 82 YLYTLDQETVRH 94

RESULT 4
 ID DPOL ADEG1 STANDARD; PRT; 1121 AA.
 AC Q64751;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 GN POL.
 OS Avian adenovirus gall (strain Phelps) (Fowl adenovirus 1) (CELO).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
 OX NCBI_TaxID=10553;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=96186720; PubMed=8627769;
 RA Chocca S., Kurzbaue R., Schaffner G., Baker A., Mautner V.,
 RA Cotten M.;
 RT "The complete DNA sequence and genomic organization of the avian
 RT adenovirus CELO.";
 RL J. Virol. 70:2939-2949 (1996).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA}(N).
 CC -!- MISCELLANEOUS: This DNA polymerase requires a protein as a primer.
 CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
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 CC
 CC EMBL; U46933; AAC54904.1; -;
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR004968; DNA_pol_B_2.
 DR Pfam; PF03175; DNA_pol_B_2; 1.
 DR PRINTS; PR00106; DNAPOLB.
 DR SMART; SM00486; POLBG; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 DR Transferase; DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding.
 KW SEQUENCE 1121 AA; 129395 MW; A55B9B6A54D3BDE1 CRC64;
 SQ SEQUENCE 1121 AA; 129395 MW; A55B9B6A54D3BDE1 CRC64;
 Query Match 47.7%; Score 41; DB 1; Length 1121;
 Best Local Similarity 50.0%; Pred. No. 30;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTE 14
 ||::|||
 Db 731 RQFRYADDPQEE 744

RESULT 5
 ZN08_HUMAN STANDARD; PRT; 543 AA.
 ID ZN08_HUMAN
 AC P17098;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein 8 (Zinc finger protein HF.18) (Fragment).
 GN ZNF8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90169993; PubMed=2106481;
 RA Lania L., Donti E., Panucci A., Pascucci A., Pengue G.,
 RA Feliciello I., Ia Mantia G., Lanfrancone L., Felicci P.-G.;
 RT "cDNA isolation, expression analysis, and chromosomal localization of
 RT two human zinc finger genes.";
 RL Genomics 6:333-340 (1990).
 CC -!- FUNCTION: May function as a transcription factor.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- TISSUE SPECIFICITY: UBIQUITOUSLY PRESENT IN MANY HUMAN CELL LINES
 CC OF DIFFERENT EMBRYOLOGICAL DERIVATION.
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -!- SIMILARITY: Contains 1 KRAB domain.
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 CC
 CC EMBL; M29581; AAA61314.1; -;
 DR PIR; B34612; B34612.
 DR HSP; P08046; 1A1H.
 DR Genew; HGNC:13154; ZNF8.
 DR MIM; 194532; -;
 DR GO; GO:0005634; C:nucleus; NAS.
 DR GO; GO:0003677; F:DNA binding; NAS.
 DR GO; GO:0008270; F:zinc ion binding; NAS.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 DR InterPro; IPR001909; KRAB.
 DR InterPro; IPR007087; Znf_C2H2.
 DR InterPro; IPR007086; Znf_C2H2_sub.
 DR Pfam; PF01352; KRAB; 1.
 DR Pfam; PF00096; zf-C2H2; 7.
 DR PRINTS; PR00048; ZINCFINGER.
 DR SMART; SM00349; KRAB; 1.
 DR SMART; SM00355; Znf_C2H2; 7.
 DR PROSITE; PS50805; KRAB; 1.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 7.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 7.
 DR Transcription regulation; DNA-binding; zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.
 KW NON_TER 1 1
 FT DOMAIN <1 64 KRAB.
 FT ZN_FING 225 247 C2H2-TYPE.
 FT ZN_FING 253 275 C2H2-TYPE.
 FT ZN_FING 281 303 C2H2-TYPE.
 FT ZN_FING 309 331 C2H2-TYPE.
 FT ZN_FING 337 359 C2H2-TYPE.
 FT ZN_FING 365 387 C2H2-TYPE.
 FT ZN_FING 435 457 C2H2-TYPE.
 SQ SEQUENCE 543 AA; 61772 MW; ADD987504ECAC019 CRC64;

Query Match 46.5%; Score 40; DB 1; Length 543;
 Best Local Similarity 53.3%; Pred. No. 20;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTE 15
 |||||
 Db 164 RGEYLYTDSQITDS 178

```

DE Protein sur-2.
GN SUR-2 OR F39B2.4.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORM A).
RC STRAIN=Bristol N2;
RX MEDLINE=96018822; PubMed=7557379;
RA Singh N., Han M.;
RT "sur-2, a novel gene, functions late in the let-60 ras-mediated
RT signaling pathway during Caenorhabditis elegans vulval induction.";
RL Genes Dev. 9:2251-2265(1995).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Dobson R.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN REVISIONS, AND ALTERNATIVE SPLICING.
RA Durbin R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Functions in the let-60 ras signaling pathway; acts
CC downstream of let-60 during C.elegans vulval induction.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=a;
CC Name=b;
CC IsoId=Q10669-1; Sequence=Displayed;
CC IsoId=Q10669-2; Sequence=VSP_004435;
CC Note=No experimental confirmation available;
CC -!- DEVELOPMENTAL STAGE: Highest levels in embryos and larvae.
CC -----
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CC -----
EMBL; U33051; AAA45507.1; -
DR EMBL; Z92834; CAB07385.2; -
DR EMBL; Z92834; CAB07394.2; -
DR WormPep; F39B2.4a; CE28023.
DR WormPep; F39B2.4b; CE28024.
KW Alternative splicing.
FT DOMAIN 1387 1404 ACIDIC.
FT DOMAIN 1405 1587 GLN/HIS-RICH.
FT VARSPPLIC 505 505 Y -> FLD (in isoform b).
FT /FTID=VSP_004435.
SQ SEQUENCE 1587 AA; 183906 MW; A125FCA74922B11C CRC64;

Query Match 46.5%; Score 40; DB 1; Length 1587;
Best Local Similarity 43.8%; Pred. No. 68;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RQVLYTDDAQOTEAH 16
Db :|||:|
1553 QQQYLYMQQLQHQH 1568

RESULT 8
IF4E APLCA
ID IF4E APLCA STANDARD; PRT; 215 AA.
AC O7710;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Eukaryotic translation initiation factor 4E (eIF4E) (eIF-4E) (mRNA
DE cap-binding protein) (eIF-4F 25 kDa subunit).
OS Aplysia californica (California sea hare).

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DE VP4_ROTTPY
ID VP4_ROTTPY STANDARD; PRT; 776 AA.
AC P25174;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8].
GN S4.
OS Porcine rotavirus (strain YM).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10919;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=91251227; PubMed=1645789;
RA Lopez S., Lopez I.V., Romero P., Mendez E., Soberon X., Arias C.F.;
RT "Rotavirus YM gene 4: analysis of its deduced amino acid sequence and
RT prediction of the secondary structure of the VP4 protein.";
RL J. Virol. 65:3738-3745(1991).
CC -!- SUBCELLULAR LOCATION: Outer capsid.
CC -!- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
CC product is VP5.
CC -!- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; M63931; AAA47100.1; -
DR EMBL; A40342; VPXRYM.
DR InterPro; IPR000416; Cap_VP4.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 776
FT CHAIN 1 776 OUTER CAPSID PROTEIN VP4.
FT CHAIN 248 776 OUTER CAPSID PROTEIN VP8.
FT CHAIN 1 776 OUTER CAPSID PROTEIN VP5.
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 325 325 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 670 670 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 776 AA; 86772 MW; B6A6C9CF81541014 CRC64;

Query Match 46.5%; Score 40; DB 1; Length 776;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOTEAH 16
Db :|||:|
302 QVYTRDGEQITAH 315

RESULT 7
SUR2_CABEL
ID SUR2_CABEL STANDARD; PRT; 1587 AA.
AC Q10669; O45497; Q9U3G5;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

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DR EMBL; AB041232; BAB40598.1; -.
DR EMBL; Z98533; CAB11096.1; -.
DR EMBL; D89107; BAA13770.1; -.
DR GeneDB_Spombe; SPAC6F12.12; -.
DR GO; GO:0007049; P:cell cycle; ISS.
DR GO; GO:0016043; P:cell organization and biogenesis; ISS.
DR GO; GO:0016288; P:cytokinesis; ISS.
DR GO; GO:0007067; P:mitosis; ISS.
DR InterPro; IPR002554; B56.
DR Pfam; PF01603; B56; 1.
DR Nuclear protein.
KW SEQUENCE 627 AA; 72464 MW; 82AD6F5EA5097C3 CRC64;
SQ
Query Match 45.3%; Score 39; DB 1; Length 627;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YLYTDDAQOQTEAH 16
DB 37 YVETDVKRHTDTH 49

RESULT 10
VP4_ROT66 STANDARD; PRT; 776 AA.
AC P26451;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8].
GN S4.
OS Human rotavirus (serotype 1 / strain 69M).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OC NCBI_TaxID=10947;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91220682; PubMed=1850912;
RA Qian Y., Green K.Y.;
RT "Human rotavirus strain 69M has a unique VP4 as determined by amino acid sequence analysis.";
RL Virology 182:407-412(1991).
CC -! SUBCELLULAR LOCATION: Outer capsid.
CC -! PTM: VP8 is one of two trypsin cleavage products of VP4; the other product is VP5.
CC -! SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC
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CC
DR EMBL; M60600; AAA47336.1; -.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
DR Coat protein; Glycoprotein.
KW CHAIN 1 776
FT CHAIN 1 241 OUTER CAPSID PROTEIN VP4.
FT CHAIN 248 776 OUTER CAPSID PROTEIN VP5 (POTENTIAL).
FT CARBOHYD 32 32 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 776 AA; 86466 MW; 70C0E9A53FCE13C1 CRC64;
Query Match 45.3%; Score 39; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOQTEAH 16
DB 302 QYTYTRDGEVNAH 315

RESULT 11
CUSC_ECOLI STANDARD; PRT; 457 AA.
AC P77211; Q9LSY3; Q9X444;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cation efflux system protein cusc precursor.
DE CUSC OR IBBB OR B0572.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin D., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RC MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba T., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampaui G., Seki Y., Takami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horituchi I.;
RT "A 718-Kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K1 / RS218 / O18:K1:H7;
RC MEDLINE=9242786; PubMed=10225861;
RA Huang S.-H., Chen Y.-H., Fu Q., Stins M., Wang Y., Wess C., Kim K.S.;
RT "Identification and characterization of an Escherichia coli invasion gene locus, ibeB, required for penetration of brain microvascular endothelial cells.";
RT Infect. Immun. 67:2103-2109(1999).
RN [5]
RP SEQUENCE OF 1-340 FROM N.A.
RC STRAIN=K12 / DH5-alpha;
RC MEDLINE=20461235; PubMed=11004187;
RA Munson G.P., Lam D.L., Outten F.W., O'Halloran T.V.;
RT "Identification of a copper-responsive two-component system on the chromosome of Escherichia coli K-12.";
RL J. Bacteriol. 182:5864-5871(2000).
RN [6]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RC MEDLINE=99420866; PubMed=10493123;
RA Pountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography.";
RL Electrophoresis 20:2181-2195(1999).
RN [7]

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DR PIR; E85555; E85555.
DR InterPro; IPR003423; OEP.
DR Pfam; PF02321; OEP; 2.
DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
KW Outer membrane; Signal; Lipoprotein; Palmitate; Complete proteome.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 460 CATION EFFLUX SYSTEM PROTEIN CUSC.
FT LIPID 18 18 N-palmitoyl cysteine (Probable).
FT LIPID 18 18 S-diacylglycerol cysteine (Probable).
SQ SEQUENCE 460 AA; 50715 MW; FE79EDB715ABC922 CRC64;

Query Match 44.2%; Score 38; DB 1; Length 460;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQ 12
DB 148 RQNYLATEEAQR 159

RESULT 13

CUSC_ECOL6
ID CUSC_ECOL6 STANDARD; PRT; 460 AA.
AC Q8CWA4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cation efflux system protein cusc precursor.
GN CUSC OR C0658.

OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O6:H1 / CFT073 / ATCC 700928;

RX MEDLINE=22388234; PubMed=12471157;

RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

RA Mayhew G.F., Rose D.B., Zhou S., Schwartz D.C., Perna N.T.,

RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

RT "Extensive mosaic structure revealed by the complete genome sequence

of uropathogenic Escherichia coli."

RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

CC -!- FUNCTION: Part of a cation efflux system that mediates resistance
to copper and silver (By similarity).

CC -!- SUBUNIT: The cusc efflux system is composed of cusa, cusb, cusc and
cuscF (By similarity).

CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid

anchor (Potential).

CC -!- INDUCTION: Transcriptionally regulated by cusr in response to

copper and silver ions (Probable).

CC -!- SIMILARITY: Belongs to the fusA/nodT family.

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CC EMBL; AB016757; AAN79133.1; --

DR InterPro; IPR003423; OEP.

DR InterPro; IPR000437; Prok_lipoprot_S.

DR Pfam; PF02321; OEP; 2.

DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

KW Outer membrane; Signal; Lipoprotein; Palmitate; Complete proteome.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 460 CATION EFFLUX SYSTEM PROTEIN CUSC.

FT LIPID 18 18 N-palmitoyl cysteine (Probable).

FT LIPID 18 18 S-diacylglycerol cysteine (Probable).

SQ SEQUENCE 460 AA; 50709 MW; 4C1D618F06AD6B9 CRC64;
Query Match 44.2%; Score 38; DB 1; Length 460;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQQ 12
DB 148 RQNYLATEEAQR 159

RESULT 14

SYR_STAEP

ID SYR_STAEP STANDARD; PRT; 553 AA.

AC Q8CTN9;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS).

GN ARG5 OR SE0380.

OS Staphylococcus epidermidis.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1282;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 12228;

RX PubMed=12950922;

RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M., Chen Z.,

RT "Genome-based analysis of virulence genes in a non-biofilm-forming

Staphylococcus epidermidis strain (ATCC 12228)."

RL Mol. Microbiol. 49:1577-1593 (2003).

CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +

diphosphate + L-arginyl-tRNA(Arg).

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.

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CC EMBL; AB016745; AA003977.1; --

DR HAMAP; MF_00123; --; 1.

DR InterPro; IPR001278; Arg_tRNA-synt_1c.

DR InterPro; IPR005148; N.

DR InterPro; IPR008909; tRNA-synt_1d_C.

DR InterPro; IPR001412; tRNA-synt_1.

DR Pfam; PF03485; N-Arg; 1.

DR Pfam; PF00750; tRNA-synt_1d; 1.

DR Pfam; PF05746; tRNA-synt_1d_C; 1.

DR PRINTS; PR01038; TRNASYNTHARG.

DR TIGRFAMs; TIGR00456; argS; 1.

DR PROSITE; PS00178; AA tRNA_LIGASE I; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;

Complete proteome.

FT SITE 130 140 "HIGH" REGION.

SQ SEQUENCE 553 AA; 62535 MW; EB776F5242F36AB1 CRC64;

Query Match 44.2%; Score 38; DB 1; Length 553;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TDDAQQTQEAH 16

DB 518 TDDTEKTKAAH 527

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RESULT 15
VP4_NCDV
ID VP4_NCDV STANDARD; PRT; 775 AA.
AC P17465;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8].
GN S4.
OS Nebraska calf diarrhea virus (strain Lincoln) (NCDV).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OC NCBI_TaxID=10932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89012172; PubMed=2845121;
RA Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K.,
RA Kapikian A.Z., Chanock R.M., Gorziglia M.;
RT "Comparative analysis of the VP3 gene of divergent strains of the
RT rotaviruses simian Sali and bovine Nebraska calf diarrhea virus.";
RL J. Virol. 62:4022-4026(1988).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
CC product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC
DR PIR; C31159; VPXRT2.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 775
FT CHAIN 1 775
FT CHAIN 248 775
FT CARBOHYD 56 56
FT CARBOHYD 97 97
FT CARBOHYD 132 132
FT CARBOHYD 151 151
FT CARBOHYD 183 183
FT CARBOHYD 198 198
FT CARBOHYD 456 456
FT CARBOHYD 507 507
FT CARBOHYD 596 596
FT CARBOHYD 602 602
FT SEQUENCE 775 AA; 86549 MW; F5D28332747FD9AB CRC64;
Query Match 44.2%; Score 38; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTTDDAQOQTEAH 16
DB 302 QYTYTRDGEVTAH 315
RESULT 16
VP4_ROT1
ID VP4_ROT1 STANDARD; PRT; 775 AA.
AC P35034;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8].
GN S4.
OS Feline rotavirus (serotype G3 / strain FRV-1).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OC NCBI_TaxID=39009;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92356070; PubMed=1322955;
RA Isegawa Y., Nakagomi O., Nakagomi T., Ueda S.;
RT "A VP4 sequence highly conserved in human rotavirus strain AU-1 and
RT feline rotavirus strain FRV-1.";
RL J. Gen. Virol. 73:1939-1946(1992).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
CC product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC
DR PIR; JQ1639; JQ1639.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 775
FT CHAIN 248 775
FT CARBOHYD 56 56
FT CARBOHYD 97 97
FT CARBOHYD 132 132
FT CARBOHYD 151 151
FT CARBOHYD 183 183
FT CARBOHYD 198 198
FT CARBOHYD 456 456
FT CARBOHYD 507 507
FT CARBOHYD 596 596
FT CARBOHYD 602 602
FT SEQUENCE 775 AA; 87138 MW; 8C22E881D82F2823 CRC64;
Query Match 44.2%; Score 38; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTTDDAQOQTEAH 16
DB 302 QYTYTRDGEVTAH 315
RESULT 17
VP4_ROT3
ID VP4_ROT3 STANDARD; PRT; 775 AA.
AC P39033;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8].
GN S4.
OS Human rotavirus (serotype G3 / strain AU-1).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OC NCBI_TaxID=39013;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92356070; PubMed=1322955;
RA Isegawa Y., Nakagomi O., Nakagomi T., Ueda S.;
RT "A VP4 sequence highly conserved in human rotavirus strain AU-1 and
RT feline rotavirus strain FRV-1.";
RL J. Gen. Virol. 73:1939-1946(1992).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
CC product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC
DR PIR; JQ1639; JQ1639.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 775
FT CHAIN 248 775
FT CARBOHYD 56 56
FT CARBOHYD 97 97
FT CARBOHYD 132 132
FT CARBOHYD 151 151
FT CARBOHYD 183 183
FT CARBOHYD 198 198
FT CARBOHYD 456 456
FT CARBOHYD 507 507
FT CARBOHYD 596 596
FT CARBOHYD 602 602
FT SEQUENCE 775 AA; 87138 MW; 8C22E881D82F2823 CRC64;
Query Match 44.2%; Score 38; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTTDDAQOQTEAH 16
DB 302 QYTYTRDGEVTAH 315

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CC CC or send an email to license@isb-sib.ch).
CC CC -----
DR DR EMBL; D10970; BAA01747.1; -.
DR DR PIR; J01638; J01638.
DR DR InterPro; IPR000416; Cap VP4.
DR DR InterPro; IPR008985; ConA_like Lec_gl.
DR DR Pfam; PF00426; VP4; 1.
DR DR Coat protein; Glycoprotein.
DR DR CHAIN 1 775
DR DR CHAIN 1 241
DR DR CHAIN 248 775
DR DR CARBOHYD 17 17
DR DR CARBOHYD 32 32
DR DR CARBOHYD 97 97
DR DR CARBOHYD 132 132
DR DR CARBOHYD 183 183
DR DR CARBOHYD 198 198
DR DR CARBOHYD 237 237
DR DR CARBOHYD 567 567
DR DR CARBOHYD 613 613
DR DR SEQUENCE 775 AA; 87092 MW; 41480C91A89B18A CRC64;
SQ SEQUENCE 775 AA; 87092 MW; 41480C91A89B18A CRC64;

Query Match 44.2%; Score 38; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQTEAH 16
Db 302 QYTTDRGEEVTAH 315

RESULT 18
VP41 ROT1
ID VP41 ROT1 STANDARD; PRT; 776 AA.
AC P04508;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8] (Version 1).
GN S4.
OS Simian 11 rotavirus (strain Sall-Both).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=37137;
RN [1]
RP SEQUENCE OF 4-750 FROM N.A.
RX MEDLINE=86045932; PubMed=2998038;
RA Lopez S., Arias C.F., Bell J.R., Strauss J.H., Espejo R.T.;
RT "Primary structure of the cleavage site associated with trypsin
RT enhancement of rotavirus Sall infectivity.";
RL Virology 144:11-19 (1985).
RN [2]
RP SEQUENCE OF 1-3 AND 751-776 FROM N.A.
RX MEDLINE=87231047; PubMed=3035499;
RA Lopez S., Arias C.F.;
RT "The nucleotide sequence of the 5' and 3' ends of rotavirus Sall gene
RT 4.";
RL Nucleic Acids Res. 15:4691-4691 (1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (26 ANGSTROMS).
RX MEDLINE=94178243; PubMed=8131735;
RA Yeager M., Berriman J.A., Baker T.S., Bellamy A.R.;
RT "Three-dimensional structure of the rotavirus haemagglutinin VP4 by
RT cryo-electron microscopy and difference map analysis.";
RL EMBO J. 13:1011-1018 (1994).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
CC product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC -1- CAUTION: SEE ALSO VERSION 2 OF THIS PROTEIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR DR EMBL; X14204; CAA32420.1; -.
DR DR PIR; S03611; S03611.
DR DR InterPro; IPR000416; Cap VP4.
DR DR InterPro; IPR008985; ConA_like Lec_gl.
DR DR Pfam; PF00426; VP4; 1.

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CC -----
DR DR EMBL; Y00336; CAA68424.1; -.
DR DR PIR; A04129; VPR48.
DR DR InterPro; IPR000416; Cap VP4.
DR DR InterPro; IPR008985; ConA_like Lec_gl.
DR DR Pfam; PF00426; VP4; 1.
DR DR Coat protein; Glycoprotein.
DR DR CHAIN 1 776
DR DR CHAIN 1 241
DR DR CHAIN 248 776
DR DR CARBOHYD 32 32
DR DR CARBOHYD 56 56
DR DR CARBOHYD 97 97
DR DR CARBOHYD 132 132
DR DR CARBOHYD 151 151
DR DR CARBOHYD 198 198
DR DR CARBOHYD 456 456
DR DR CARBOHYD 507 507
DR DR CARBOHYD 602 602
DR DR SEQUENCE 776 AA; 86725 MW; FD63962AC6B85E52 CRC64;
SQ SEQUENCE 776 AA; 86725 MW; FD63962AC6B85E52 CRC64;

Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQTEAH 16
Db 302 QYTTDRGEEVTAH 315

RESULT 19
VP42 ROT1
ID VP42 ROT1 STANDARD; PRT; 776 AA.
AC P12976;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)
DE [Contains: Outer capsid proteins VP5 and VP8] (Version 2).
GN S4.
OS Simian 11 rotavirus (strain Sall-Both).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=37137;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89183617; PubMed=2538804;
RA Mitchell D.B., Both G.W.;
RT "Complete nucleotide sequence of the simian rotavirus Sall VP4 gene.";
RL Nucleic Acids Res. 17:2122-2122 (1989).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
CC product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC -1- CAUTION: SEE ALSO VERSION 1 OF THIS PROTEIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR DR EMBL; X14204; CAA32420.1; -.
DR DR PIR; S03611; S03611.
DR DR InterPro; IPR000416; Cap VP4.
DR DR InterPro; IPR008985; ConA_like Lec_gl.
DR DR Pfam; PF00426; VP4; 1.

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Coat protein; Glycoprotein.		OUTER CAPSID PROTEIN VP4.
KW	CHAIN 1 776	OUTER CAPSID PROTEIN VP8 (POTENTIAL).
FT	CHAIN 1 241	OUTER CAPSID PROTEIN VP5 (POTENTIAL).
FT	CHAIN 248 776	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 32 32	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 56 56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 97 97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 116 116	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 132 132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 149 149	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 198 198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 386 386	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 776 AA; 86774 MW; EA9B43CE96CC53CF CRC64;	
Query Match 44.2%; Score 38; DB 1; Length 776;		
Best Local Similarity 42.9%; Pred. No. 69;		
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;		
QY	3 RYLYTDDAQQTAEH 16	
DB	302 QYTYTRDGEVTAH 315	
RESULT 20		
VP4_ROTBS		
ID	VP4_ROTBS STANDARD; PRT; 776 AA.	
AC	P36305;	
DT	01-JUN-1994 (Rel. 29, Created)	
DT	01-JUN-1994 (Rel. 29, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)	
DE	[Contains: Outer capsid proteins VP5 and VP8].	
GN	S4.	
OS	Bovine rotavirus (serotype 8 / strain A5).	
OC	Viruses; dsRNA viruses; Reoviridae; Rotavirus.	
OX	NCBI_TaxID=36440;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=93286580; PubMed=839807;	
RA	Taniguchi K., Urasawa T., Urasawa S.;	
RT	"Independent segregation of the VP4 and the VP7 genes in bovine rotaviruses as confirmed by VP4 sequence analysis of G8 and G10	
RT	bovine rotavirus strains.";	
RL	J. Gen. Virol. 74:1215-1221(1993).	
CC	-1- SUBCELLULAR LOCATION: Outer capsid.	
CC	-1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other	
CC	product is VP5.	
CC	-1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.	
CC		
EMBL; Y00127; CAA68325.1; -		
DR	InterPro; IPR000416; Cap VP4.	
DR	InterPro; IPR008985; ConA_like lec_g1.	
DR	Pfam; PF00426; VP4; 1.	
KW	Coat protein; Glycoprotein.	
FT	CHAIN 1 776	OUTER CAPSID PROTEIN VP4.
FT	CHAIN 1 241	OUTER CAPSID PROTEIN VP8.
FT	CHAIN 248 776	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 32 32	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 56 56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 97 97	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 132 132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 151 151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 183 183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 198 198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 456 456	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 507 507	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 596 596	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 602 602	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 776 AA; 86768 MW; 69945BBA19CB5BBA CRC64;	
Query Match 44.2%; Score 38; DB 1; Length 776;		
Best Local Similarity 42.9%; Pred. No. 69;		
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;		
QY	3 RYLYTDDAQQTAEH 16	
DB	302 QYTYTRDGEVTAH 315	
RESULT 22		
VP4_ROTBS		
ID	VP4_ROTBS STANDARD; PRT; 776 AA.	
AC	P17463;	
DT	01-AUG-1990 (Rel. 15, Created)	
DT	01-AUG-1990 (Rel. 15, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4)	
DE	[Contains: Outer capsid proteins VP5 and VP8].	

GN S4.
OS Simian 11 rotavirus (strain SALL1-FEM).
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10925;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=69012172; PubMed=2845121;
RA Nishikawa K., Taniguchi K., Torres A., Hoshino Y., Green K.,
RA Kapikian A.Z., Chanock R.M., Gorziglia M.,
RT "Comparative analysis of the VP3 gene of divergent strains of the
rotavirus simian SALL1 and bovine Nebraska calf diarrhea virus.";
RL J. Virol. 62:4022-4026(1988).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
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or send an email to license@isb-sib.ch).
CC -----
EMBL; M23188; AAA47355.1; ALT_SEQ.
DR PIR; B31159; VPXRT1.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 776
FT CHAIN 1 241
FT CHAIN 248 776
FT CARBOHYD 32 32
FT CARBOHYD 56 56
FT CARBOHYD 97 97
FT CARBOHYD 132 132
FT CARBOHYD 151 151
FT CARBOHYD 198 198
FT CARBOHYD 456 456
FT CARBOHYD 507 507
FT CARBOHYD 596 596
FT CARBOHYD 602 602
FT CARBOHYD 776 AA; 86692 MW; 3F7DE298DB298FC7 CRC64;
SQ SEQUENCE 776 AA; 86692 MW; 3F7DE298DB298FC7 CRC64;
Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLYTDDAQOTEAH 16
DB 302 QYTYTRDGEVTAH 315
OSTA_XYLFA STANDARD; PRT; 776 AA.
RESULT 24
OSTA_XYLFA
ID OSTA_XYLFA STANDARD; PRT; 792 AA.
AC Q9P41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Organic solvent tolerance protein precursor.
GN IMP OR OSTA OR XF0837.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RT "Comparative analysis of the VP3 gene of divergent strains of the
rotaviruses simian SALL1 and bovine Nebraska calf diarrhea virus.";
RL J. Virol. 62:4022-4026(1988).
CC -1- SUBCELLULAR LOCATION: Outer capsid.
CC -1- PTM: VP8 is one of two trypsin cleavage products of VP4; the other
product is VP5.
CC -1- SIMILARITY: Belongs to the rotaviruses VP4 protein family.
CC PIR; A31159; VPXRS1.
DR InterPro; IPR000416; Cap VP4.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR Pfam; PF00426; VP4; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 776
FT CHAIN 248 776
FT CARBOHYD 32 32
FT CARBOHYD 56 56
FT CARBOHYD 97 97
FT CARBOHYD 116 116
FT CARBOHYD 132 132
FT CARBOHYD 149 149
FT CARBOHYD 198 198
FT CARBOHYD 386 386
FT CARBOHYD 776 AA; 86770 MW; 683BAAE24B329674 CRC64;
SQ SEQUENCE 776 AA; 86770 MW; 683BAAE24B329674 CRC64;
Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLYTDDAQOTEAH 16
DB 302 QYTYTRDGEVTAH 315
OSTA_XYLFA STANDARD; PRT; 792 AA.
RESULT 24
OSTA_XYLFA
ID OSTA_XYLFA STANDARD; PRT; 792 AA.
AC Q9P41;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Organic solvent tolerance protein precursor.
GN IMP OR OSTA OR XF0837.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,

RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovskij-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";
CC Nature 406:151-159 (2000).
CC
CC -!- FUNCTION: Determines N-hexane tolerance. Involved in outer
CC membrane permeability. Essential for envelope biogenesis. Could be
CC part of a targeting/usher system for outer membrane components (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -!- SIMILARITY: Belongs to the imp/osta family.
CC
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CC
CC EMBL; AE003923; AAP83647.1; -;
CC PIR; B82756; B82756.
CC HAMAP; MF 01411; -; 1.
CC InterPro; IPR007543; Osta_C.
CC Pfam; PF04453; Osta_C; 1.
CC Outer membrane; Signal; Complete proteome.
CC SIGNAL 1 22 POTENTIAL
CC CHAIN 23 792 ORGANIC SOLVENT TOLERANCE PROTEIN.
CC SEQUENCE 792 AA; 91001 MW; EB97FF8CFD35A422 CRC64;
CC
CC Query Match 44.2%; Score 38; DB 1; Length 792;
CC Best Local Similarity 61.5%; Pred. No. 70;
CC Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 3 RYLTYDDAQQTGA 15
CC ||||| |||||
CC 273 RYLTYDDGKWQTRA 285
CC
CC Db
CC
CC RESULT 25
CC OSTA_XYLFT STANDARD; PRT; 792 AA.
CC AC O87A19;
CC DT 10-OCT-2003 (Rel. 42, Created)
CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
CC DE Organic solvent tolerance protein precursor.
CC GN IMP OR OSTA OR PD1836.
CC OS *Xylella fastidiosa* (strain Temecula / ATCC 700964).
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
CC CC Xanthomonadaceae; *Xylella*.
CC ON NCBI_TaxID=183190;
CC RX [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=22421331; PubMed=12533478;
CC RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
CC RA Miyaki C.Y., Furlan L.R., Machado L.E.A., da Silva A.C.R., Moon D.H.,
CC RA Takita M.A., Lemos E.G.M., Lemos M.V.F., El-Dorri H., Tsai S.M.,
CC RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
CC RA Carter H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.O.,
CC RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.B.,
CC RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
CC RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
CC RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
CC RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassiaki F.T., Sena J.A.D.,
CC RA de Souza A.A., Truffi D., Teukumo F., Yanai G.M., Zaros L.G.,
CC RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
CC RA Kitajima J.P.;
CC RT "Comparative analyses of the complete genome sequences of Pierce's
CC RT disease and citrus variegated chlorosis strains of *Xylella*
CC RT *fastidiosa*.";
CC RT J. Bacteriol. 185:1018-1026 (2003).
CC RL

CC -!- FUNCTION: Determines N-hexane tolerance. Involved in outer
CC membrane permeability. Essential for envelope biogenesis. Could be
CC part of a targeting/usher system for outer membrane components (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -!- SIMILARITY: Belongs to the imp/osta family.
CC
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CC
CC EMBL; AE012560; AAO29668.1; -;
CC HAMAP; MF 01411; -; 1.
CC InterPro; IPR007543; Osta_C.
CC Pfam; PF04453; Osta_C; 1.
CC Outer membrane; Signal; Complete proteome.
CC SIGNAL 1 22 POTENTIAL
CC CHAIN 23 792 ORGANIC SOLVENT TOLERANCE PROTEIN.
CC SEQUENCE 792 AA; 90768 MW; 70637D6FA7B62DAD CRC64;
CC
CC Query Match 44.2%; Score 38; DB 1; Length 792;
CC Best Local Similarity 61.5%; Pred. No. 70;
CC Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 3 RYLTYDDAQQTGA 15
CC ||||| |||||
CC 273 RYLTYDDGKWQTRA 285
CC
CC Db
CC
CC RESULT 26
CC YTX2_XENLA STANDARD; PRT; 1308 AA.
CC AC P14381;
CC DT 01-JAN-1990 (Rel. 13, Created)
CC DT 01-JAN-1990 (Rel. 13, Last sequence update)
CC DT 01-APR-1990 (Rel. 14, Last annotation update)
CC DE Transposon TX1 hypothetical 149 kDa protein (ORF 2).
CC OS *Xenopus laevis* (African clawed frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
CC OC Xenopodinae; *Xenopus*.
CC ON NCBI_TaxID=8355;
CC RX [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=89384562; PubMed=2550791;
CC RA Garrett J.E., Knutson D.S., Carroll D.;
CC RT "Composite transposable elements in the *Xenopus laevis* genome.";
CC RL Mol. Cell. Biol. 9:3018-3027 (1989).
CC
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CC
CC EMBL; M26915; AAA49976.1; -;
CC PIR; B32494; B32494.
CC InterPro; IPR005135; Exo_endo_phos.
CC DR InterPro; IPR000477; RVTFse.
CC Pfam; PF03372; Exo_endo_phos; 1.
CC Pfam; PF00078; rvt; 1.
CC DR Hypothetical protein; Transposable element.
CC KW SEQUENCE 1308 AA; 149577 MW; C9A9C98CDC169C19 CRC64;
CC SQ
CC
CC Query Match 44.2%; Score 38; DB 1; Length 1308;
CC Best Local Similarity 63.6%; Pred. No. 1.2e+02;
CC Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy	2 QRYLYTDDAQ 12	InterPro; IPR007095; RNA_pol_DS_PS.
Db	878 QRYLYADPSPQ 888	InterPro; IPR007094; RNA_pol_PSVir.
		InterPro; IPR000606; Viral_helicase1.
		InterPro; IPR005159; WCCH.
		Pfam; PF05410; Peptidase_C31; 1.
		Pfam; PF05411; Peptidase_C32; 1.
		Pfam; PF05412; Peptidase_C33; 1.
		Pfam; PF05579; Peptidase_S32; 1.
		Pfam; PF01443; Viral_helicase1; 1.
		Pfam; PF03716; WCCH; 1.
		RNA-directed RNA polymerase; Transferase; Helicase; ATP-binding;
		Hydrolase; Serine protease; Zinc-finger.
		CHAIN 1 2396
		ORF1B.
		CYS-RICH.
		CYS-RICH.
		CYS-RICH.
		HELICASE.
		CYS-RICH.
		TRYPSIN-LIKE SERINE PROTEASE.
		CYS-RICH.
		POLYMERASE.
		CHARGE RELAY SYSTEM (BY SIMILARITY).
		CHARGE RELAY SYSTEM (BY SIMILARITY).
		CHARGE RELAY SYSTEM (BY SIMILARITY).
		ATP (BY SIMILARITY).
		BY SIMILARITY.
		T -> V (IN REF. 3).
		V -> I (IN REF. 3).
		CONFLICT 3744 3744
		SEQUENCE 3859 AA; 421758 MW; 8C5E945AC6895CEE CRC64;
		Query Match 44.2%; Score 38; DB 1; Length 3859;
		Best Local Similarity 54.5%; Pred. No. 4.3e+02;
		Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy	6 YTDDAQOTEAH 16	
Db	2278 YTDDSRYTQDH 2288	
		RESULT 28
		AFAP_AFCOLI STANDARD; PRT; 101 AA.
		AC P53515;
		DT 01-OCT-1996 (Rel. 34; Created)
		DT 01-NOV-1997 (Rel. 35; Last sequence update)
		DT 01-NOV-1997 (Rel. 35; Last annotation update)
		DE AFA-III adhesin operon regulatory protein.
		GN AFAA.
		OS Escherichia coli.
		OG Plasmid pIL1055.
		OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
		OC Enterobacteriaceae; Escherichia.
		OX NCBI_TaxID=562;
		[1]
		RP SEQUENCE FROM N.A.
		RC STRAIN=A30;
		RX MEDLINE=95095929; PubMed=8002584;
		RA Garcia M.-I., Labigne A., le Bouguenec C.L.;
		RT "Nucleotide sequence of the afimbrial-adhesin-encoding afa-3 gene
		cluster and its translocation via flanking IS1 insertion sequences.";
		RL J. Bacteriol. 176:7601-7613(1994).
		CC -1- FUNCTION: REGULATES THE TRANSCRIPTION OF GENES INVOLVED IN THE
		BIOSYNTHESIS OF AFIMBRIAL ADHESIN-III.
		CC -1- SIMILARITY: HIGH TO E.COLI DATA; SOME, TO E.COLI PAPB.
		CC -1- CAUTION: It is uncertain whether Met-1 or Met-17 is the initiator.
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Wed Mar 3 08:19:49 2004

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CC EMBL; X76688; CRA54113.1; -
DR EMBL; X76688; CRA54114.1; ALT_INIT.
DR PIR; D55545; D55545.
DR InterPro; IPR004356; Fim_regulat.
DR Pfam; PF03333; PapB; 1
DR PRINTS; PR01554; FIMREGULATRY.
DR Transcription regulation; Activator; Trans-acting factor; Plasmid.
KW SEQUENCE 101 AA; 11743 MW; F55914BC263BDD6B CRC64;
SQ

Query Match 43.0%; Score 37; DB 1; Length 101;
Best Local Similarity 58.3%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQVLYTDDAQ 12
DB 2 RRYLYLADTPQ 13

RESULT 29
VE08_VACCC STANDARD; PRT; 273 AA.
AC P21049;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein E8.
GN E8R.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OC NCBI_TaxID=10249;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91021027; PubMed=2219722;
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "The complete DNA sequence of vaccinia virus.";
RL Virology 179:247-266(1990).
[2]
RP COMPLETE GENOME.
RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA Paoletti E.;
RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL Virology 179:517-563(1990).
[3]
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CC -----
CC EMBL; M36339; AAB59828.1; -
DR InterPro; IPR005057; Pox_E8.
DR Pfam; PF03394; Pox_E8; 1
DR PIRSF; PIRSF015690; VAC_E8R; 1.
SQ SEQUENCE 273 AA; 31888 MW; 6C274DCEE6353629 CRC64;

Query Match 43.0%; Score 37; DB 1; Length 273;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYLYTDDAQ 11
DB 157 RYVYTDNAK 165

RESULT 31
VE08_VARV STANDARD; PRT; 273 AA.
AC P33820;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Protein E8.
GN E8R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OC NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=94151514; PubMed=8109158;
RA Shchelkunov S.N., Blinov V.M., Resenchuk S.M., Totmenin A.V.,
RA Sandakhchiev L.S.;
RT "Analysis of the nucleotide sequence of a 43 kbp segment of the
RT genome of variola virus India-1967 strain.";
RL Virus Res. 30:239-258(1993).
[2]
RP COMPLETE GENOME.
RP STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms.";
RL FEBS Lett. 319:80-83(1993).
[3]
RP SEQUENCE FROM N.A.
RP STRAIN=Bangladesh-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Massung R.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,

```

RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.,
RT "Potential virulence determinants in terminal regions of variola
RL smallpox virus genome";
RL Nature 366:748-751(1993).
CC -----
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CC -----
DR EMBL; X69198; AAA48990.1; -;
DR EMBL; L22579; AAA60797.1; -;
DR PIR; B36842; B36842.
DR PIR; T28487; T28487.
DR InterPro; IPR005057; Pox_E8.
DR Pfam; PF03394; Pox_E8; 1.
DR PIRSF; PIRSF015690; VAC_E8R; 1.
SQ SEQUENCE 273 AA; 31898 MW; 02859D3F756A53AE CRC64;
Query Match 43.0%; Score 37; DB 1; Length 273;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 RLYLTDAAQ 11
DB 157 RYVYDQNAK 165
|||||:
RESULT 32
ID SNAG ARATH STANDARD; PRT; 291 AA.
AC Q9SP55; Q9SUN8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Gamma-soluble NSF attachment protein (Gamma-SNAP) (N-ethylmaleimide-
DE sensitive factor attachment protein, gamma).
GN GSNAP OR A74G20410 OR F9F13.50.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
OX [1]_TaxID=3702;
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20193631; PubMed=10727946;
RA Weidenhaupt M., Bruckert F., Louwagie M., Garin J., Satre M.,
RA Pohl T., Duesterhoef A., Striekema W., Etian K.-D., Terryn N.,
RA Harris B., Ansgore W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Bontroy M., Bancroft I.,
RA Vos P., Honeisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Billham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenecker T., Bothe G., Rampersger U., Hilbert H., Braun M.,

RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moeljan P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Bernier S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysschaert C., Gielens J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Ouail M.A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartman B., Grandrath K., Dauner D., Herzl A.,
RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Glabaud G., Muendlein A., Felber R.,
RA Schnabi S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Furnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threiden J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Spieth J., Ryan E., Andrews S., Geisel C., Hillier L.W.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshua C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana";
RL Nature 402:769-777(1999).
RN SEQUENCE FROM N.A.
RP Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.A.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required for vesicular transport between the endoplasmic
CC reticulum and the Golgi apparatus. Binds to SNARE complex and then
CC recruits NSF to disassemble it (by similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic peripheral membrane protein (By
CC similarity).
CC -!- SIMILARITY: Belongs to the SNAP family.
CC -!- CAUTION: Ref.2 sequences differ from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
DR EMBL; AF177990; AAF01285.1; -;
DR EMBL; AL080253; CAB45807.1; ALT_SEQ.
DR EMBL; AL161553; CAB79041.1; ALT_SEQ.
DR EMBL; AY086673; CAB63730.1; -;
DR InterPro; IPR000744; NSF_attach.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF02071; NSF; 1.
KW Transport; Protein transport; Endoplasmic reticulum; Golgi stack;
KW Multigene family.
FT CONFLICT 45 46 NK -> KN (IN REF. 3).
FT CONFLICT 129 129 A -> S (IN REF. 3).
SQ SEQUENCE 291 AA; 32360 MW; 3EECE3B64D038BAD CRC64;
Query Match 43.0%; Score 37; DB 1; Length 291;
Best Local Similarity 63.6%; Pred. No. 34;

```
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YLYTDDAQTE 14
DB 200 YLYAHDLOQAE 210

RESULT 33
SYW_SYNY3
ID SYW_SYNY3 STANDARD; PRT; 337 AA.
AC P7355;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TPRS)
GN TRPS OR SLR1884.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimoda S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
RC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA(Trp).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC
CC EMBL; D50908; BAAL7700.1; ALT_INIT.
CC HSP; P00953; ID2R.
CC HAMAP; MF_00140; -, 1.
CC InterPro; IPR002305; tRNA-synt_1b.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002306; Trp tRNA-synt_1b.
CC Pfam; PF00579; tRNA-synt_1b; 1.
CC PRINTS; PR10139; TRNASYNTHTRP.
CC TIGRFAMs; TIGR00233; trps; 1.
CC PROSITE; PS00178; AA tRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 12 20 "HIGH" REGION
CC SITE 199 203 "KMSKS" REGION.
CC FT BINDING 202 202 ATP (BY SIMILARITY).
CC SEQUENCE 337 AA; 37763 MW; A780860A78D312D CRC64;

Query Match 43.0%; Score 37; DB 1; Length 337;
Best Local Similarity 46.7%; Pred. No. 40;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQTEAH 16
DB 232 QRGWFDDEPRPECH 246

RESULT 34
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```
SIP2_YEAST
ID SIP2_YEAST STANDARD; PRT; 415 AA.
AC P34164;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SIP2 protein (SPM2 protein).
GN SIP2 OR SPM2 OR YGL208W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX Drobot M.A., Janema D., Himmelfarb H.J., Friesen J.D.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=95112798; PubMed=7813428;
RA Yang X., Jiang R., Carlson M.;
RT "A family of proteins containing a conserved domain that mediates
RT interaction with the yeast SNF1 protein kinase complex."
RL EMBO J. 13:5878-5886(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97298309; PubMed=9153757;
RA Feuerhann M., Simeonava L., Souciet J.-L., Potier S.;
RT "Analysis of 21.7 kb DNA sequence from the left arm of chromosome VII
RT reveals 11 open reading frames: two correspond to new genes."
RL Yeast 13:475-477(1997).
RN [4]
RP SEQUENCE OF 1-283 FROM N.A.
RX STRAIN=S288C;
RX MEDLINE=96408772; PubMed=8813766;
RA Kail M., Juettner E., Vaux D.;
RT "Lambda clone B22 contains a 7676 bp genomic fragment of
RT Saccharomyces cerevisiae chromosome VII spanning the VAM7-SPM2
RT intergenic region and containing three novel transcribed open reading
RT frames."
RL Yeast 12:799-807(1996).
CC -!- FUNCTION: Not known; interacts with the SNF1 protein kinase.
CC Could be an adaptor that promote the activity of SNF1 towards
CC specific targets.
CC -!- PTM: Phosphorylated by SNF1 in vitro.
CC -!- SIMILARITY: Belongs to the 5'-AMP-activated protein kinase beta
CC subunit family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z14128; CAA78503.1; -.
CC EMBL; L31592; AAC37420.1; -.
CC EMBL; Z72730; CAA396922.1; -.
CC EMBL; U33754; AAC49497.1; -.
CC PIR; S51792; S51792.
CC Germonline; 141256; -.
CC SGD; S0003176; SIF2.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0004679; F:SNF1/AMP-activated protein kinase activity; IMP.
CC GO; GO:0007574; P:cell aging (sensu Saccharomycetes); IMP.
CC GO; GO:0030447; P:filamentous growth; IMP.
CC GO; GO:0008468; P:protein amino acid phosphorylation; IMP.
CC GO; GO:0007165; P:signal transduction; IMP.
CC InterPro; IPR006828; AMPKBI.
CC Pfam; PF04739; AMPKBI; 1.
CC Phosphorylation.
KW
```

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SQ SEQUENCE 415 AA; 46404 MW; CBB4FCE0070A563F CRC64;
Query Match 43.0%; Score 37; DB 1; Length 415;
Best Local Similarity 58.3%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQOT 13
Db 320 ERYYYTLDRQOS 331

RESULT 35
FIXC_RHISN STANDARD; PRT; 435 AA.
AC Q53208;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FixC protein.
DE FIXC OR Y4UP.
GN Rhizobium sp. (strain NGR234).
OG Plasmid sym pNGR234.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97305956; PubMed=9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RA "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96389014; PubMed=8796346;
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RA "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase': a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -!- FUNCTION: COULD BE REQUIRED FOR THE FORMATION OF A FUNCTIONAL
CC NITROGENASE FE PROTEIN. PROBABLY ACCEPTS ELECTRONS FROM FIXA/FIXB
CC AND REDUCES A QUINONE.
CC -!- COFACTOR: FAD (Potential).
CC -!- SIMILARITY: Belongs to the Etf-QO / fixC family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z68203; CAA92415.1; -
CC EMBL; AE000100; AAB91888.1; -
CC InterPro: IPR001327; FAD_pyr_redox.
CC PRINTS; PR00368; FADPNR.
CC Nitrogen fixation; Oxidoreductase; FAD; Flavoprotein; plasmid.
KW NP BIND 8 22 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 435 AA; 47536 MW; 5C4113C66F84BA61 CRC64;

Query Match 43.0%; Score 37; DB 1; Length 435;
Best Local Similarity 46.7%; Pred. No. 54;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QRYLYTDDAQOTEAH 16
Db 75 QRFWTTDTSHTGMH 89

RESULT 36
STE3_YEAST

```

```

ID STE3_YEAST STANDARD; PRT; 470 AA.
AC P06783;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pheromone A factor receptor.
DE STE3 OR YKL178C.
GN Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86149315; PubMed=3006051;
RA Hagen D.C., McCaffrey G., Sprague G.F. Jr.;
RA "Evidence the yeast STE3 gene encodes a receptor for the peptide
RT pheromone a factor: gene sequence and implications for the structure
RT of the presumed receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1418-1422(1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Nakayama N., Miyajima A., Arai K.;
RA "Nucleotide sequences of STE2 and STE3, cell type-specific sterile
RT genes from Saccharomyces cerevisiae.";
RL EMBO J. 4:2643-2648(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94205264; PubMed=8154185;
RA Wiemann S., Voss H., Schwager C., Rupp T., Stegemann J.,
RA Zimmermann J., Grothues D., Sensen C., Erfle H., Hewitt N.,
RA Banerji A., Ansoorge W.;
RA "Sequencing and analysis of 51.6 kilobases on the left arm of
RT chromosome XI from Saccharomyces cerevisiae reveals 23 open reading
RT frames including the PAS1 gene.";
RL Yeast 9:1343-1348(1993).
CC -!- FUNCTION: Receptor for the peptide pheromone a factor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor family 4.
CC
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CC
CC EMBL; M12239; AAA35113.1; -
CC EMBL; X03011; CAA26795.1; -
CC EMBL; X74151; CAA52261.1; -
CC EMBL; Z28177; CAA82019.1; -
CC PIR; B24670; B24670.
CC GeneOnline; 139933; -
CC SGD; S0001661; STE3.
CC GO; GO:0005887; C:Integral to plasma membrane; IDA.
CC GO; GO:0004933; F:mating-type a-factor pheromone receptor act. .; IMP.
CC GO; GO:000750; P:signal transduction during conjugation with. .; IMP.
CC InterPro: IPR001499; STE3_GPCR.
CC Pfam; PF02076; STE3_1.
CC PRINTS; PR00899; GPCRSTE3.
KW Transmembrane; G-protein coupled receptor; Pheromone response.
FT TRANSMEM 6 23 POTENTIAL.
FT TRANSMEM 30 53 POTENTIAL.
FT TRANSMEM 71 98 POTENTIAL.
FT TRANSMEM 117 134 POTENTIAL.
FT TRANSMEM 156 183 POTENTIAL.
FT TRANSMEM 206 228 POTENTIAL.
FT TRANSMEM 267 285 POTENTIAL.
FT DOMAIN 300 470 HYDROPHILIC.
SQ SEQUENCE 470 AA; 53708 MW; 5DBF611076B8CA91 CRC64;

Query Match 43.0%; Score 37; DB 1; Length 470;
Best Local Similarity 46.2%; Pred. No. 59;

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Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 YLYTDDAQTEAH 16
DB 226 YTFVQDLQVEGH 238

RESULT 37
SYR STAAW
ID - SYR STAAW STANDARD; PRT; 553 AA.
AC Q93766
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine-tRNA ligase) (ArgRS).
GN ARG5 OR SAV0607.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=213111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL: AP003359; BAB56769.1; -
CC HAMAP: MF_00123; -; 1.
CC InterPro: IPR001278; Arg_tRNA-synt_1c.
CC InterPro: IPR005148; N.
CC InterPro: IPR008909; tRNA-synt_1d_C.
CC Pfam: PF03485; N-Arg; 1.
CC PRINTS: PR01038; TRNASYNTHARG.
CC TIGRFAMs: TIGR00456; argS; 1.
CC PROSITE: PS00178; AA TRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 132 140 "HIGH" REGION.
CC SEQUENCE 553 AA; 62346 MW; 86F27FB94CDA9A9 CRC64;

Query Match 43.0%; Score 37; DB 1; Length 553;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TDDAQTEAH 16
DB 518 TDDIEKTKAH 527

RESULT 38
SYR STAAW
ID - SYR STAAW STANDARD; PRT; 553 AA.
AC Q93766
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine-tRNA ligase) (ArgRS).
GN ARG5 OR SAV0607.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=213111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC
CC -----
CC EMBL: AP003359; BAB56769.1; -
CC HAMAP: MF_00123; -; 1.
CC InterPro: IPR001278; Arg_tRNA-synt_1c.
CC InterPro: IPR005148; N.
CC InterPro: IPR008909; tRNA-synt_1d_C.
CC InterPro: IPR001412; tRNA-synt_1.
CC Pfam: PF03485; N-Arg; 1.
CC PRINTS: PR01038; TRNASYNTHARG.
CC TIGRFAMs: TIGR00456; argS; 1.
CC PROSITE: PS00178; AA TRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 132 140 "HIGH" REGION.
CC SEQUENCE 553 AA; 62346 MW; 86F27FB94CDA9A9 CRC64;

Query Match 43.0%; Score 37; DB 1; Length 553;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TDDAQTEAH 16
DB 518 TDDIEKTKAH 527

RESULT 39
SYR STAAW
ID - SYR STAAW STANDARD; PRT; 553 AA.
AC Q93766
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine-tRNA ligase) (ArgRS).
GN ARG5 OR SAV0607.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=213111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC
CC -----
CC EMBL: AP003359; BAB56769.1; -
CC HAMAP: MF_00123; -; 1.
CC InterPro: IPR001278; Arg_tRNA-synt_1c.
CC InterPro: IPR005148; N.
CC InterPro: IPR008909; tRNA-synt_1d_C.
CC InterPro: IPR001412; tRNA-synt_1.
CC Pfam: PF03485; N-Arg; 1.
CC PRINTS: PR01038; TRNASYNTHARG.
CC TIGRFAMs: TIGR00456; argS; 1.
CC PROSITE: PS00178; AA TRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 132 140 "HIGH" REGION.
CC SEQUENCE 553 AA; 62365 MW; 84FOAAA2212E30C CRC64;

Query Match 43.0%; Score 37; DB 1; Length 553;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TDDAQTEAH 16
DB 518 TDDIEKTKAH 527

RESULT 39
SYR STAAW
ID - SYR STAAW STANDARD; PRT; 553 AA.
AC Q93766
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine-tRNA ligase) (ArgRS).
GN ARG5 OR SAV0607.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=213111952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC
CC -----
CC EMBL: AP003359; BAB56769.1; -
CC HAMAP: MF_00123; -; 1.
CC InterPro: IPR001278; Arg_tRNA-synt_1c.
CC InterPro: IPR005148; N.
CC InterPro: IPR008909; tRNA-synt_1d_C.
CC InterPro: IPR001412; tRNA-synt_1.
CC Pfam: PF03485; N-Arg; 1.
CC PRINTS: PR01038; TRNASYNTHARG.
CC TIGRFAMs: TIGR00456; argS; 1.
CC PROSITE: PS00178; AA TRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 132 140 "HIGH" REGION.
CC SEQUENCE 553 AA; 62365 MW; 84FOAAA2212E30C CRC64;

Query Match 43.0%; Score 37; DB 1; Length 553;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 TDDAQTEAH 16
DB 518 TDDIEKTKAH 527

```

```

DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine-tRNA ligase) (ARGRS).
GN ARGS OR MW0571.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12043378;
RA Baba T., Takeuchi F., Kuroda M., Tuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359.1819-1827(2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC
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CC
CC -----
CC EMBL; AF004824; BAB94436.1; -.
CC HAMAP; MF 00123; -.
CC InterPro; IPR001278; Arg_tRNA-synt_1c.
CC InterPro; IPR005148; N.
CC InterPro; IPR008909; tRNA-synt_1d_C.
CC InterPro; IPR001412; tRNA-synt_1.
CC Pfam; PF03485; N-Arg; 1.
CC Pfam; PF00750; tRNA-synt_1d; 1.
CC Pfam; PF05746; tRNA-synt_1d_C; 1.
CC PRINTS; PR01039; TRNASYNTHARG.
CC TIGRfam; TIGR00456; argS; 1.
CC PROSITE; PS00178; AA tRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 132 140 "HIGH" REGION.
CC SEQUENCE 553 AA; 62381 MW; 9B10A85C212B30C CRC64;
Query Match 43.0%; Score 37; DB 1; Length 553;
Best Local Similarity 60.0%; Pred. No. 71;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 7 TDDAQCTEAAH 16
DB 518 TDDIEKTKAH 527
RESULT 40
DSBD VIBVU STANDARD; PRT; 593 AA.
AC QSDCZ0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thiol:disulfide interchange protein dsbD precursor (EC 1.8.1.8)
DE (Protein-disulfide reductase) (Disulfide reductase).
GN DSBD OR VVI1247.
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;

```

```

RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RT Submitted (DRC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Required to facilitate the formation of correct
CC disulfide bonds in some periplasmic proteins and for the assembly
CC of the periplasmic c-type cytochromes. Acts by transferring
CC electrons from cytoplasmic thioredoxin to the periplasm. This
CC reaction involves a cascade of disulfide bond formation and
CC reduction steps (By similarity).
CC -!- CATALYTIC ACTIVITY: Protein dithiol + NAD(P)+ = protein disulfide
CC + NAD(P)H.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -!- SIMILARITY: Belongs to the thioredoxin family. DsbD subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; AE016801; AA009703.1; -.
CC HAMAP; MF 00399; -.
CC InterPro; IPR003834; Cytochc_TM.
CC InterPro; IPR006662; ThioRed.
CC InterPro; IPR006663; Thioredox_dom2.
CC Pfam; PF02683; DsbD; 1.
CC Pfam; PF00085; thioRed; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Oxidoreductase; Redox-active center; Electron transport; NAD;
CC Transmembrane; Inner membrane; Cytochrome c-type biogenesis; Signal;
CC Complete proteome.
CC SIGNAL 1 21
CC CHAIN 22 593
CC TRANSMEM 193 215
CC TRANSMEM 235 257
CC TRANSMEM 269 291
CC TRANSMEM 318 340
CC TRANSMEM 347 369
CC TRANSMEM 384 401
CC TRANSMEM 408 425
CC TRANSMEM 440 462
CC DISULFID 130 136
CC DISULFID 207 328
CC DISULFID 508 511
CC SEQUENCE 593 AA; 64815 MW; A6B029712A5C9B73 CRC64;
Query Match 43.0%; Score 37; DB 1; Length 593;
Best Local Similarity 54.5%; Pred. No. 76;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 4 YLYTDDAQCTE 14
DB 460 YWFTDSSQQTQ 470
Search completed: March 2, 2004, 16:05:26
Job time : 3.53333 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 2, 2004, 16:00:38 ; Search time 2.26667 Seconds
(without alignments)
678.999 Million cell updates/sec

Title: US-10-060-765-7

Perfect score: 86

Sequence: 1 RORYLYTDDAQOQTEAH 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	46	53.5	349	2 T00526	probable GDSL-moti
2	43	50.0	2225	2 T26063	hypothetical prote
3	41	47.7	93	2 S28726	hypothetical prote
4	41	47.7	349	2 T00525	probable GDSL-moti
5	40	46.5	332	2 T25023	hypothetical prote
6	40	46.5	403	2 C70385	hypothetical prote
7	40	46.5	529	2 JE0181	oligo-1,6-glucosid
8	40	46.5	543	2 B34612	zinc finger protei
9	40	46.5	566	2 S59382	hypothetical prote
10	40	46.5	776	1 VPXRYM	outer layer protei
11	40	46.5	1661	2 T21986	hypothetical prote
12	40	46.5	1663	2 T21993	hypothetical prote
13	39	45.3	259	2 C36819	Cil protein - rabb
14	39	45.3	263	2 G90294	hypothetical prote
15	39	45.3	278	2 T18857	hypothetical prote
16	39	45.3	439	2 B95927	probable sugar upt
17	39	45.3	627	2 T11663	probable phosphor
18	39	45.3	735	2 JC5869	beta-glucosidase
19	38	44.2	235	2 T33962	hypothetical prote
20	38	44.2	285	2 A10633	probable membrane
21	38	44.2	344	2 T01629	probable GDSL-moti
22	38	44.2	457	2 B64790	yc1B protein - Esc
23	38	44.2	460	2 B90705	probable resistanc
24	38	44.2	460	2 B85555	probable resistanc
25	38	44.2	580	2 F81042	hemolysin activati
26	38	44.2	580	2 A81989	probable periplasm
27	38	44.2	747	1 VPX84S	outer layer protei
28	38	44.2	775	1 JQ1638	outer layer protei
29	38	44.2	775	1 JQ1639	outer layer protei

30	38	44.2	775	1 VPXRT2	outer layer protei
31	38	44.2	776	1 VPXRT3	outer layer protei
32	38	44.2	776	1 VPXRE3	outer layer protei
33	38	44.2	776	1 JQ2022	outer layer protei
34	38	44.2	776	1 VPXRS1	outer layer protei
35	38	44.2	776	2 S03611	outer layer protei
36	38	44.2	776	2 S24410	hypothetical outer
37	38	44.2	792	2 B82756	organic solvent to
38	38	44.2	1051	2 T48933	WD repeat domain p
39	38	44.2	1308	2 B32494	transposable eleme
40	38	44.2	1426	2 A39580	hypothetical prote
41	38	44.2	1619	2 T18499	hypothetical prote
42	38	44.2	1645	2 AG1897	two-component hybr
43	38	44.2	2396	2 B36861	orf la protein - L
44	37	43.0	101	2 D55545	afaa protein - Esc
45	37	43.0	145	2 AE3288	hypothetical prote

ALIGNMENTS

RESULT 1

T00526

Probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T20K24.7

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 02-Feb-2001

C:Accession: T00526; A84572

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,

submitted to the EMBL Data Library, July 1997

A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.

A:Reference number: Z14167

A:Accession: T00526

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-349 <ROU>

A:Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176708

A:Experimental source: cultivar Columbia

Rubin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Niernman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: A84572

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-349 <STO>

A:Cross-references: GB:AE002093; NID:g3176708; PIDN:AAI2024.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g19060; T20K24.7

A:Map position: 2

A:Introns: 81/1; 122/3; 197/3; 282/1

C:Superfamily: myrosinase-associated protein MyAP

Query Match 53.5%; Score 46; DB 2; Length 349;

Best Local Similarity 53.3%; Pred. No. 2.1;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RORYLYTDDAQOQTEA 15

Db 310 RERYVVDNVHSTEA 324

RESULT 2

T26063

hypothetical protein W01F3.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T26063

R:Cummings, P.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20145

A:Accession: T26063
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2225 <WIL>
A:Cross-references: EMBL:Z92815; PIDN:CAB07294.1; GSPDB:GN00023; CESP:W01F3.3
A:Experimental source: clone W01F3
C:Genetics:
A:Gene: CESP:W01F3.3
A:Map position: 5
A:Introns: 33/1; 56/1; 100/1; 142/3; 271/3; 451/1; 525/3; 774/1; 1093/1; 1178/1; 1221/1;
Query Match 50.0%; Score 43; DB 2; Length 2225;
Best Local Similarity 53.8%; Pred. No. 61;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 2 QRYLYTDDAQQT 14
DB 477 QRYFYEDSKCE 489
RESULT 3
S28726
hypothetical protein 1 (insertion sequence ISL1) - Lactobacillus casei
C:Species: Lactobacillus casei
C>Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 20-Jun-2000
C:Accession: S28726
R:Shimizu-Kadota, M.; Kiwaki, M.; Hirokawa, H.; Tsuchida, N.
Mol. Gen. Genet. 200, 193-198, 1985
A:Title: ISL1: a new transposable element in Lactobacillus casei.
A:Reference number: S28726; MUID:85295506; PMID:2993817
A:Accession: S28726
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-93 <SHI>
A:Cross-references: EMBL:X02734; NID:G1279518; PIDN:CAA26516.1; PID:G43974
A:Experimental source: insertion sequence ISL1; strain C239
C:Genetics:
A:Mobile element: insertion sequence ISL1
C:Superfamily: Shigella flexneri conserved hypothetical protein tnpJ
Query Match 47.7%; Score 41; DB 2; Length 93;
Best Local Similarity 61.5%; Pred. No. 3.7;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQT 13
DB 43 RWRKLYTDEGKQT 55
RESULT 4
T00525
Probable GDSL-motif lipase/hydrolase [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T20K24.6
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T00525; H84571
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, July 1997
A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
A:Reference number: Z14167
A:Accession: T00525
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-349 <ROU>
A:Cross-references: EMBL:AC002392; NID:G3176701; PID:G3176707
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84571

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <STO>
A:Cross-references: GB:AB002093; NID:G3176707; PIDN:AAD12023.1; GSPDB:GN00139
C:Genetics:
A:Gene: T20K24.6; At2g19050
A:Map position: 2
A:Introns: 82/1; 123/3; 198/3; 281/1
C:Superfamily: myrosinase-associated protein MyAP
Query Match 47.7%; Score 41; DB 2; Length 349;
Best Local Similarity 46.7%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQT 15
DB 309 QRYVYWDNVHTEA 323
RESULT 5
T25023
hypothetical protein T20B3.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25023
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19970
A:Accession: T25023
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-332 <WIL>
A:Cross-references: EMBL:Z81593; PIDN:CAB04743.1; GSPDB:GN00023; CESP:T20B3.5
A:Experimental source: clone T20B3
C:Genetics:
A:Gene: CESP:T20B3.5
A:Map position: 5
A:Introns: 110/1; 246/3
C:Superfamily: Caenorhabditis hypothetical protein C49G7.2
Query Match 46.5%; Score 40; DB 2; Length 332;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 RQRYLYTDDAQQT 16
DB 8 RTDYHTADFOOTVILH 23
RESULT 6
C70385
hypothetical protein aq_985 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: C70385
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O. Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70385
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-403 <AQF>
A:Cross-references: GB:AE000717; NID:G2983492; PIDN:AAC07076.1; PID:G2983498; GB:AE0006
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_985
Query Match 46.5%; Score 40; DB 2; Length 403;
Best Local Similarity 37.5%; Pred. No. 30;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```

QY 1 RQRYLYTDDAQOTEAH 16
Db 85 QKRYVYVDRSEDETH 100

RESULT 7
JE0181
oligo-1,6-glucosidase (EC 3.2.1.10) - Bacillus flavocaldarius KP1228
C:Species: Bacillus flavocaldarius KP1228
C>Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 20-Sep-1999
C:Accession: JE0181
R:Kashiwabara, S.; Matsuki, Y.; Kishimoto, T.; Suzuki, Y.
Biosci. Biotechnol. Biochem. 62, 1093-1102, 1998
A:Title: Clustered proline residues around the active-site cleft in thermostable oligo-1
A:Reference number: JE0181; MUID:98357218; PMID:9692189
A:Accession: JE0181
A:Molecule type: DNA
A:Residues: 1-529 <KAS>
A:Cross-references: DDBJ:AB003697
C:Superfamily: alpha-glucosidase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase

Query Match 46.5%; Score 40; DB 2; Length 529;
Best Local Similarity 43.8%; Pred. No. 41;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 16
Db 227 RHEHLYTDEQPEYAY 242

RESULT 8
B34612
zinc finger protein ZNF8 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jun-1990 #sequence_revision 09-Oct-1992 #text_change 01-Dec-2000
C:Accession: B34612
R:Lanka, L.; Dotti, E.; Pannuti, A.; Pascucci, A.; Pengue, G.; Feliciello, I.; La Mantia
Genomics 6, 333-340, 1990
A:Title: cDNA isolation, expression analysis, and chromosomal localization of two human
A:Reference number: A34612; MUID:90169993; PMID:2106481
A:Accession: B34612
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-543 <LAN>
A:Cross-references: GB:M29581; NID:G340447; PIDN:AAA61314.1; PID:G340448; GB:J04751
C:Genetics:
A:Gene: GDB:ZNF8
A:Cross-references: GDB:120510; OMIM:194532
A:Map position: 20q13-20q13
C:Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C:Keywords: DNA binding; zinc finger

Query Match 46.5%; Score 40; DB 2; Length 543;
Best Local Similarity 53.3%; Pred. No. 42;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTEAH 15
Db 164 RGEYLYTDSQITDS 178

RESULT 9
S59382
hypothetical protein YLR417w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L9931.3
C:Species: Saccharomyces cerevisiae
C>Date: 30-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 29-Oct-1999
C:Accession: S59382
R:Favella, A.
submitted to the EMBL Data Library, January 1995
A:Description: The sequence of S. cerevisiae cosmid 9931.
A:Reference number: S59376

A:Accession: S59382
A:Molecule type: DNA
A:Residues: 1-566 <FAV>
A:Cross-references: EMBL:U20162; NID:G632669; PIDN:AAB67493.1; PID:G632672; MIPS:YLR417w
A:Experimental source: strain S288C (AB972)
C:Genetics:
A:Gene: SGD:VPS36
A:Cross-references: SGD:S0004409; MIPS:YLR417w
A:Map position: 12R

Query Match 46.5%; Score 40; DB 2; Length 566;
Best Local Similarity 53.8%; Pred. No. 44;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
Db 52 QRIVYDDAKPTQ 64

RESULT 10
VPRYM
outer layer protein VP3 - porcine rotavirus C (strain YM)
N:Alternate names: hemagglutinin; VP4 protein
N:Contains: outer layer protein VP5; outer layer protein VP8
C:Species: porcine rotavirus C
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: A40342
R:Lopez, S.; Lopez, I.; Romero, P.; Mendez, E.; Soberon, X.; Arias, C.F.
J. Virol. 65, 3738-3745, 1991
A:Title: Rotavirus YM gene 4: analysis of its deduced amino acid sequence and prediction
A:Reference number: A40342; MUID:91251227; PMID:1645789
A:Accession: A40342
A:Molecule type: genomic RNA
A:Residues: 1-776 <LOP>
A:Cross-references: GB:M63231; NID:G333323; PIDN:AAA47100.1; PID:G333324
C:Superfamily: rotavirus outer layer protein VP3
C:Keywords: capsid protein, coat protein; glycoprotein; hemagglutinin
F:1-241/Product: outer layer protein VP8 #status predicted <VP8>
F:242-247/Region: cleavage processing #status predicted
F:248-776/Product: outer layer protein VP5 #status predicted <VP5>
F:17,32,56,97,116,132,151,178,183,198,325,670/Binding site: carbohydrate (Asn) (covalent

Query Match 46.5%; Score 40; DB 1; Length 776;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLYTDDAQOTEAH 16
Db 302 QYTYTDEGEITAH 315

RESULT 11
T21986
hypothetical protein F39B2.4a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21986
R:Dobson, R.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19498
A:Accession: T21986
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1661 <WIL>
A:Cross-references: EMBL:Z92834; PIDN:CAB07385.1; GSPDB:GN000019; CESP:F39B2.4a
A:Experimental source: clone F39B2
C:Genetics:
A:Gene: CESP:F39B2.4a
A:Map position: 1
A:Introns: 37/3; 102/2; 229/3; 317/3; 375/2; 505/3; 546/1; 668/3; 833/1; 904/2; 941/3; 9

Query Match 46.5%; Score 40; DB 2; Length 1661;
Best Local Similarity 43.8%; Pred. No. 1.5e+02;

```


A:Contents: annotation
 C:Genetics:
 A:Gene: SWB21103
 A:Genome: plasmid

Query Match 45.3%; Score 39; DB 2; Length 439;
 Best Local Similarity 53.8%; Pred. No. 50;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQOTE 14
 | : | | : | : |
 Db 152 QKSLYQDEAKTTE 164

RESULT 17

T11663
 Probable phosphoprotein phosphatase (EC 3.1.3.16) regulatory chain - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
 C:Accession: T11663; T42084

R:Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1997

A:Reference number: Z17305
 A:Accession: T11663

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-627 <BAR>
 A:Cross-references: EMBL:Z98533; NID:e1071719; PID:e334113

R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
 DNA Res. 4, 363-369, 1997

A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
 A:Reference number: Z17323; MUID:98162722; PMID:9501991

A:Accession: T42084
 A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 215-627 <YOS>

A:Cross-references: EMBL:D89107; NID:gl749421; PIDN:BAAL3770.1; PID:gl749422
 A:Note: SPAC6F12.12

C:Genetics:
 A:Map position: 1L

A:Introns: 131/3; 213/1; 278/3; 410/2
 A:Note: SPAC6F12.12

C:Keywords: phosphoric monoester hydrolase

Query Match 45.3%; Score 39; DB 2; Length 627;
 Best Local Similarity 46.2%; Pred. No. 75;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YLYTDDAQOTE 16
 | : | | : | : |
 Db 37 YVETDDVKEHTDTH 49

RESULT 18

JC5869
 beta-glucosidase (EC 3.2.1.21) precursor - Acetobacter xylinus subsp. sucrofermentans

C:Species: Acetobacter xylinus subsp. sucrofermentans
 C>Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000

C:Accession: JC5869; PC4505
 R:Tonouchi, N.; Tahara, N.; Kojima, Y.; Nakai, T.; Sakai, F.; Hayaashi, T.; Tauchida, T.;

Bioc. Biotechnol. Biochem. 61, 1789-1790, 1997
 A:Title: A beta-glucosidase gene downstream of the cellulose synthase operon in cellulose

A:Reference number: JC5869; MUID:98028223; PMID:9362130
 A:Accession: JC5869

A:Molecule type: DNA
 A:Residues: 1-735 <TON>

A:Cross-references: DDBJ:AB003689; NID:g2641692; PIDN:BAR23595.1; PID:g2641693
 A:Experimental source: strain BPR2001

A:Accession: PC4505
 A:Molecule type: protein

A:Residues: 27-55 <TO2>
 A:Experimental source: strain BPR2001

A:Note: the residues and 714 and 715 are interchanged in the authors' translation

C:Comment: This enzyme is involved in cellulose synthesis and its degradation.
 C:Superfamily: beta-glucosidase
 C:Keywords: glycosidase; hydrolase
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-735/Product: beta-glucosidase #status predicted <MAT>

Query Match 45.3%; Score 39; DB 2; Length 735;
 Best Local Similarity 70.0%; Pred. No. 90;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 TDDAQOTEAH 16
 | : | | : | : |
 Db 718 TDDSQQTMMH 727

RESULT 19

T33962

hypothetical protein F46E10.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Nov-1999

C:Accession: T33962; T29650
 R:Johnson, D.; Bradshaw, H.

submitted to the EMBL Data Library, February 1999
 A:Description: The sequence of C. elegans cosmid F46E10.

A:Reference number: Z21446
 A:Accession: T33962

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-235 <JOH>
 A:Cross-references: EMBL:AF125955; PIDN:AAD14716.1; GSPDB:GN00023; CESP:F46E10.6

A:Experimental source: strain Bristol N2; clone F46E10
 R:Blanchard, M.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996
 A:Description: The sequence of C. elegans cosmid W01A11.

A:Reference number: Z20658
 A:Accession: T29650

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA

A:Residues: 1-235 <BLA>
 A:Cross-references: EMBL:U64852; PIDN:AAB04972.1; GSPDB:GN00023; CESP:W01A11.7

A:Experimental source: strain Bristol N2; clone W01A11
 C:Genetics:

A:Gene: CESP:F46E10.6; CESP:W01A11.7
 A:Map position: 5

A:Introns: 93/3; 140/3; 185/3

Query Match 44.2%; Score 38; DB 2; Length 235;
 Best Local Similarity 50.0%; Pred. No. 37;
 Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQOTE 16
 | : | | : | : |
 Db 106 RQRYLSEGDIVVSAH 121

RESULT 20

AI0633

probable membrane transporter STY1164 [imported] - Salmonella enterica subsp. enterica s
 C:Species: Salmonella enterica subsp. enterica serovar typhi

A:Note: this species has also been called Salmonella typhi
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AI0633
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerston, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AI0633
 A>Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-285 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08252.1; PID:gl6502299; GSPDB:GN00176
 C:Genetics:
 A:Gene: STV1164

Query Match 44.2%; Score 38; DB 2; Length 285;
 Best Local Similarity 46.2%; Pred. No. 46;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQTE 14
 |||: ||| :||:
 Db 46 QRYIVTDSIEETK 58

RESULT 21

T01629
 Probable GDSL-motif lipase/hydrolase At2g19010 [imported] - Arabidopsis thaliana
 N:Alternate names: APG protein homolog F19F24.21; hypothetical protein T20K24.2
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 19-Feb-1999 #sequence revision 19-Feb-1999 #text_change 16-Feb-2001
 C:Accession: T01629; T00521; D84571
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, April 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence.
 A:Reference number: Z14153
 A:Accession: T01629

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-344 <ROW>
 A:Cross-references: EMBL:AC003673; NID:g3004543; PID:g3004563
 A:Experimental source: cultivar Columbia
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
 submitted to the EMBL Data Library, July 1997
 A:Description: Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence.
 A:Reference number: Z14167
 A:Accession: T00521

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-344 <ROW>
 A:Cross-references: EMBL:AC002392; NID:g3176701; PID:g3176703
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: D84571
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-344 <STO>
 A:Cross-references: GB:AE002093; NID:g3176703; PIDN:AAD12019.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g19010; F19F24.21; T20K24.2

A:Map position: 2

A:Introns: 77/1; 118/3; 193/3; 276/1

C:Superfamily: myrosinase-associated protein MyAP

Query Match 44.2%; Score 38; DB 2; Length 344;
 Best Local Similarity 46.7%; Pred. No. 57;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQTEA 15
 |||: ||| :||:
 Db 304 RTEYVFWDLLHSTEA 318

RESULT 22

B64790
 YlcB protein - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence revision 17-Sep-1997 #text_change 01-Mar-2002
 C:Accession: B64790
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cd

A.: Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: B64790
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-457 <BLAT>
 A:Cross-references: GB:AE000162; GB:U00096; NID:gl786782; PIDN:AAC73673.1; PID:gl786785
 A:Experimental source: strain K-12, substrain MGL655
 C:Genetics:

A:Gene: ylcB

C:Superfamily: modulation protein modT

C:Keywords: transmembrane protein

F:6-22/Domain: transmembrane #status predicted <TMM>

Query Match 44.2%; Score 38; DB 2; Length 457;
 Best Local Similarity 58.3%; Pred. No. 79;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQO 12
 |||: ||| :||:
 Db 148 RQNYLATEEAQR 159

RESULT 23

B90705
 Probable resistance protein [imported] - Escherichia coli (strain O157:H7, substrain RI
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: B90705
 R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
 sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: B90705

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-460 <HAV>

A:Cross-references: GB:BA000007; PIDN:BA034033.1; PID:gl3360068; GSPDB:GN00154

A:Experimental source: strain O157:H7, substrain RMD 050952

C:Genetics:

A:Gene: ECS0610

C:Superfamily: modulation protein modT

Query Match 44.2%; Score 38; DB 2; Length 460;
 Best Local Similarity 58.3%; Pred. No. 79;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RQRYLYTDDAQO 12
 |||: ||| :||:
 Db 148 RQNYLATEEAQR 159

RESULT 24

B85555
 Probable resistance protein ylcB [imported] - Escherichia coli (strain O157:H7, substra
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: B85555

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoukis, K.; Apodaca

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: B85555

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-460 <STO>

A:Cross-references: GB:AE005174; NID:gl2513457; PIDN:AAG54905.1; GSPDB:GN00145; UWGP:Z0

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

VPX84S		outer layer protein VP3 - simian rotavirus SA11 (fragment)				
A;Gene: ylcB		C;Species: simian rotavirus SA11				
C;Superfamily: modulation protein nodT		A;Note: host (monkey)				
Query Match		44.2%; Score 38; DB 2; Length 460;				
Best Local Similarity		58.3%; Pred. No. 79;				
Matches	7; Conservative	3; Mismatches	0; Gaps			
2; Indels						
QY	1 RQRYLYTDDAQ 12	: :				
Db		148 RQNYLATEAQR 159		: :		
RESULT 25				F81042		
hemolysin activation protein HecB, probable NMB1780 [imported] - Neisseria meningitidis				C;Species: Neisseria meningitidis		
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001				C;Accession: F81042		
R;Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.				Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;		
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.				Science 287, 1809-1815, 2000		
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve				A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.		
A;Reference number: AB1000; MUID:20175755; PMID:10710307				A;Accession: F81042		
A;Status: preliminary				A;Molecule type: DNA		
A;Residues: 1-580 <TET>				A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42120.1; PID:g722703		
A;Experimental source: serogroup B, strain MCS8				C;Genetics:		
A;Gene: NMB1780		Query Match				
Best Local Similarity	7; Conservative	44.2%; Score 38; DB 2; Length 580;				
Matches		63.6%; Pred. No. 1e+02;				
1; Mismatches	3; Indels	0; Gaps	0;			
QY		1 RQRYLYTDDAQ 11				
Db	361 RQYKYIDDAE 371	: :				
RESULT 26		A81989				
probable periplasmic protein NMA0687 [imported] - Neisseria meningitidis (strain Z2491)		C;Species: Neisseria meningitidis				
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001		C;Accession: A81989				
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel		; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,				
Nature 404, 502-506, 2000		A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.				
A;Reference number: A81775; MUID:20222556; PMID:10761919		A;Accession: A81989				
A;Status: preliminary		A;Molecule type: DNA				
A;Residues: 1-580 <PAR>		A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83973.1; PID:g737941				
A;Experimental source: serogroup A, strain Z2491		C;Genetics:				
A;Gene: NMA0686; NMA0687		Query Match				
Best Local Similarity	7; Conservative	44.2%; Score 38; DB 2; Length 580;				
Matches		63.6%; Pred. No. 1e+02;				
1; Mismatches	3; Indels	0; Gaps	0;			
QY		1 RQRYLYTDDAQ 11				
Db	361 RQYKYIDDAE 371	: :				
RESULT 27		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.		J. Gen. Virol. 73, 1939-1946, 1992				
A;Title: A VP4 sequence highly conserved in human rotavirus strain AU-1 and feline rotav		Query Match				
Best Local Similarity	6; Conservative	44.2%; Score 38; DB 1; Length 775;				
Matches		42.9%; Pred. No. 1.4e+02;				
3; Mismatches	5; Indels	0; Gaps	0;			
QY		3 RYLYTDDAQQTAAH 16				
Db	302 QYTYTRDGEVTAH 315	: :				
RESULT 29		JQ1639				
outer layer protein VP4 - feline rotavirus A (serotype G3, strain FRV-1)		N;Alternate names: hemagglutinin; outer capsid protein VP4				
N;Contains: outer layer protein VP5; outer layer protein VP8		C;Species: feline rotavirus A				
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jun-2000		C;Accession: JQ1639				
R;Isegawa, Y.; Nakagomi, O.; Nakagomi, T.; Ueda, S.</						

A;Reference number: JQ1638; MUID:92356070; PMID:1322955
A;Accession: JQ1639
A;Molecule type: genomic RNA
A;Residues: 1-775 <ISE>
A;Cross-references: DDBJ:D10971; NID:g222536; PIDN:BA01748.1; PID:g222537
C;Genetics:
A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;242-247/Region: cleavage processing #status predicted
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;17,32,97,132,183,198,567,613/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 44.2%; Score 38; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTYDDAQOQTEAH 16
:|||||:|:
Db 302 QYTYRDEEVTAAH 315

RESULT 30
VPXRT2
outer layer protein VP3 - Nebraska calf diarrhea virus (strain NCDV-Lincoln)
N;Alternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: Nebraska calf diarrhea virus
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 12-Apr-1996
C;Accession: C31159
J;Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan
J. Virol. 62, 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si
A;Reference number: A94694; MUID:89012172; PMID:2845121
A;Accession: C31159
A;Molecule type: genomic RNA
A;Residues: 1-775 <NIS>
C;Genetics:
A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;248-775/Product: outer layer protein VP5 #status predicted <VP5>
F;56,97,132,151,183,198,456,507,596,602/Binding site: carbohydrate (Asn) (covalent) #sta
Query Match 44.2%; Score 38; DB 1; Length 775;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTYDDAQOQTEAH 16
:|||||:|:
Db 302 QYTYRDEEVTAAH 315

RESULT 31
VPXRT1
outer layer protein VP3 - simian rotavirus Sall1 (strain Sall1-FEM)
N;Alternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: simian rotavirus Sall1
A;Note: host (monkey)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 12-Apr-1996
C;Accession: B31159
J;Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan
J. Virol. 62, 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si
A;Reference number: A94694; MUID:89012172; PMID:2845121
A;Accession: B31159
A;Molecule type: genomic RNA
A;Residues: 1-775 <NIS>
C;Genetics:
A;Map position: segment 4

C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
F;32,56,97,132,151,198,456,507,602/Binding site: carbohydrate (Asn) (covalent) #status
Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTYDDAQOQTEAH 16
:|||||:|:
Db 302 QYTYRDEEVTAAH 315

RESULT 32
VPXRB3
outer layer protein VP3 - bovine rotavirus A (strain C486)
N;Alternate names: hemagglutinin
C;Species: bovine rotavirus A
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A29529
R;Potter, A.A.; Cox, G.; Parker, M.; Babiuk, L.A.
Nucleic Acids Res. 15, 4361, 1987
A;Title: The complete nucleotide sequence of bovine rotavirus C486 gene 4 cDNA.
A;Reference number: A29529; MUID:87231020; PMID:3035492
A;Accession: A29529
A;Molecule type: genomic RNA
A;Residues: 1-776 <POT>
A;Cross-references: GB:Y00127; NID:g61854; PIDN:CAA68325.1; PID:g61855
C;Genetics:
A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin
F;32,56,97,132,151,183,198,456,507,596,602/Binding site: carbohydrate (Asn) (covalent)
Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 3 RYLTYDDAQOQTEAH 16
:|||||:|:
Db 302 QYTYRDEEVTAAH 315

RESULT 33
JQ2022
outer layer protein VP4 - bovine rotavirus A (serotype 5)
N;Alternate names: hemagglutinin; outer capsid protein VP4
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: bovine rotavirus A
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 02-Jun-2000
C;Accession: JQ2022
R;Taniguchi, K.; Urasawa, T.; Urasawa, S.
J. Gen. Virol. 74, 1215-1221, 1993
A;Title: Independent segregation of the VP4 and the VP7 genes in bovine rotaviruses as
A;Reference number: JQ2022; MUID:93286580; PMID:8389807
A;Accession: JQ2022
A;Molecule type: genomic RNA
A;Residues: 1-776 <TAN>
A;Cross-references: GB:D13395; NID:g393327
A;Note: this translation is not annotated in GenBank entry ROBA5VP4, release 113.0
C;Genetics:
A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;242-247/Region: cleavage processing #status predicted
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
F;56,97,132,151,198,456,507,670/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;

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us-10-060-765-7.rpr

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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-Feb-1999
C;Accession: S24410
C;Mation, N.M.; Estes, M.K.
Arch. Virol. 120, 109-113, 1991
A;Title: Sequence of a rotavirus gene 4 associated with unique biologic properties.
A;Reference number: S24410; MUID:92028406; PMID:1656916
A;Accession: S24410
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-776 <MAT>
A;Cross-references: EMBL:X57319
C;Superfamily: rotavirus outer layer protein VP3

Query Match 44.2%; Score 38; DB 2; Length 776;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQQTAAH 16
:|||||:
DB 302 QYTYTRDGEVTAH 315

RESULT 37
B82756
organic solvent tolerance precursor XF0837 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B82756
R;Anonymous; B82756
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82756
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-792 <SIM>
A;Cross-references: GB:AE003323; GB:AE003849; NID:99105736; PIDN:AAF83647.1; GSPDB:GN001
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.B.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0837

Query Match 44.2%; Score 38; DB 2; Length 792;
Best Local Similarity 61.5%; Pred. No. 1.5e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQQTAAH 15
:|||||:
DB 273 RYLTYDDGKQWTRA 285

RESULT 38
T48933
WD repeat domain protein - Arabidopsis thaliana
N;Alternate names: protein F1412.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T48933
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;

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Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQQTAAH 16
:|||||:
DB 302 QYTYTRDGEVTAH 315

RESULT 34
VPXR51
outer layer protein VP3 - simian rotavirus SA11 (strain SA11-SEM)
N;Alternate names: glycoprotein VP3; hemagglutinin; outer capsid protein VP3
N;Contains: outer layer protein VP5; outer layer protein VP8
C;Species: simian rotavirus SA11
A;Note: host (monkey)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 16-Jul-1999
C;Accession: A31159
R;Nishikawa, K.; Taniguchi, K.; Torres, A.; Hoshino, Y.; Green, K.; Kapikian, A.Z.; Chan
J. Virol. 62, 4022-4026, 1988
A;Title: Comparative analysis of the VP3 gene of divergent strains of the rotaviruses si
A;Reference number: A94694; MUID:89012172; PMID:2845121
A;Accession: A31159
A;Molecule type: genomic RNA
A;Residues: 1-776 <NIS>
A;Cross-references: GB:M23188; NID:9515742; PIDN:AAA47355.1; PID:9515743
C;Genetics:
A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3
C;Keywords: glycoprotein; hemagglutinin; outer capsid protein
F;1-241/Product: outer layer protein VP8 #status predicted <VP8>
F;248-776/Product: outer layer protein VP5 #status predicted <VP5>
F;32,56,97,116,132,149,198,386/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 44.2%; Score 38; DB 1; Length 776;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQQTAAH 16
:|||||:
DB 302 QYTYTRDGEVTAH 315

RESULT 35
S03611
outer layer protein VP3 - simian rotavirus SA11
C;Species: simian rotavirus SA11
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Sep-1999
C;Accession: S03611
R;Mitchell, D.B.; Both, G.W.
Nucleic Acids Res. 17, 2122, 1989
A;Title: Complete nucleotide sequence of the simian rotavirus SA11 VP4 gene.
A;Reference number: S03611; MUID:89183617; PMID:2538804
A;Accession: S03611
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-776 <MIT>
A;Cross-references: EMBL:X14204; NID:961891; PIDN:CAA32420.1; PID:961892
C;Genetics:
A;Map position: segment 4
C;Superfamily: rotavirus outer layer protein VP3

Query Match 44.2%; Score 38; DB 2; Length 776;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RYLTTDDAQQTAAH 16
:|||||:
DB 302 QYTYTRDGEVTAH 315

RESULT 36
S24410
hypothetical outer capsid protein - simian rotavirus SA11
C;Species: simian rotavirus SA11

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submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25008
A:Accession: T48933
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1051 <JUR>
A:Cross-references: EMBL:AL353818; GSPDB:GN00061; ATSP:F14L2.80
A:Experimental source: cultivar Columbia; BAC clone F14L2
C:Genetics:
A:Gene: ATSP:F14L2.80
A:Map position: 3
A:Introns: 36/3; 121/3; 205/3; 336/2; 668/3; 739/1; 773/1; 853/2; 894/2; 932/3

Query Match 44.2%; Score 38; DB 2; Length 1051;
Best Local Similarity 70.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 TDDAQTEAH 16
||| |||
Db 855 TDDGTQTRAH 864

RESULT 39

B32494
transposable element Txlc protein 2 - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 21-Jul-2000
C:Accession: B32494
R:Garrett, J.E.; Knutson, D.S.; Carroll, D.
Mol. Cell. Biol. 9, 3018-3027, 1989
A:Title: Composite transposable elements in the Xenopus laevis genome.
A:Reference number: A32494; MUID:89384562; PMID:2550791
A:Accession: B32494
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1308 <GAR>
A:Cross-references: GB:M26915; NID:G214844; PIDN:AAA49976.1; PID:G214846
C:Superfamily: pol polyprotein

Query Match 44.2%; Score 38; DB 2; Length 1308;
Best Local Similarity 63.6%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QRYLYTDDAQQ 12
||| |||
Db 878 QRYLYADPSFQ 888

RESULT 40

A99580
hypothetical protein MYPU 5450 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: A99580
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: A99580
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1426 <KUR>
A:Cross-references: GB:AL445566; PID:g14089960; PIDN:CAC13718.1; GSPDB:GN00153
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 5450
A:Genetic code: SGC3
C:Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain

Query Match 44.2%; Score 38; DB 2; Length 1426;
Best Local Similarity 72.7%; Pred. No. 2.9e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLYTDDAQOTE 14
||| |||
Db 1192 YLDQDDASQTE 1202

Search completed: March 2, 2004, 16:08:06
Job time : 4.26667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 16:07:28 ; Search time 5.0625 Seconds
(without alignments)
625.639 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	89	100.0	68	9 US-09-801-968-36	Sequence 36, Appl
3	89	100.0	68	10 US-09-802-154-36	Sequence 36, Appl
4	89	100.0	136	9 US-09-901-938-33	Sequence 33, Appl
5	89	100.0	136	14 US-10-379-334-33	Sequence 33, Appl
6	89	100.0	208	9 US-09-755-695-2	Sequence 2, Appl
7	89	100.0	208	14 US-10-227-884-78	Sequence 78, Appl
8	89	100.0	208	14 US-10-230-163-78	Sequence 78, Appl
9	89	100.0	208	14 US-10-230-338-78	Sequence 78, Appl
10	89	100.0	208	14 US-10-218-631-78	Sequence 78, Appl
11	89	100.0	208	14 US-10-230-414-78	Sequence 78, Appl
12	89	100.0	208	14 US-10-216-159A-78	Sequence 78, Appl
13	89	100.0	208	14 US-10-218-849-78	Sequence 78, Appl
14	89	100.0	208	14 US-10-227-873-78	Sequence 78, Appl
15	89	100.0	208	14 US-10-227-883-78	Sequence 78, Appl

16	89	100.0	208	14	US-10-219-076-78	Sequence 78, Appl
17	89	100.0	208	14	US-10-230-434-78	Sequence 78, Appl
18	89	100.0	208	14	US-10-219-003-78	Sequence 78, Appl
19	89	100.0	208	14	US-10-219-075-78	Sequence 78, Appl
20	89	100.0	208	14	US-10-219-484-78	Sequence 78, Appl
21	89	100.0	208	14	US-10-219-466-78	Sequence 78, Appl
22	89	100.0	208	14	US-10-219-479-78	Sequence 78, Appl
23	89	100.0	208	14	US-10-219-481-78	Sequence 78, Appl
24	89	100.0	208	14	US-10-230-260-78	Sequence 78, Appl
25	89	100.0	208	14	US-10-232-231-78	Sequence 78, Appl
26	89	100.0	208	14	US-10-232-233-78	Sequence 78, Appl
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28	89	100.0	208	14	US-10-218-956-78	Sequence 78, Appl
29	89	100.0	208	14	US-10-219-468-78	Sequence 78, Appl
30	89	100.0	208	14	US-10-219-478-78	Sequence 78, Appl
31	89	100.0	208	14	US-10-219-536-78	Sequence 78, Appl
32	89	100.0	208	14	US-10-233-205-78	Sequence 78, Appl
33	89	100.0	208	14	US-10-219-072-78	Sequence 78, Appl
34	89	100.0	208	14	US-10-219-479-78	Sequence 78, Appl
35	89	100.0	208	14	US-10-219-524-78	Sequence 78, Appl
36	89	100.0	208	14	US-10-219-528-78	Sequence 78, Appl
37	89	100.0	208	14	US-10-227-880-78	Sequence 78, Appl
38	89	100.0	208	14	US-10-227-881-78	Sequence 78, Appl
39	89	100.0	208	14	US-10-230-436-78	Sequence 78, Appl
40	89	100.0	208	14	US-10-232-223-78	Sequence 78, Appl
41	89	100.0	208	14	US-10-232-225-78	Sequence 78, Appl
42	89	100.0	208	14	US-10-232-227-78	Sequence 78, Appl
43	89	100.0	208	14	US-10-232-227-78	Sequence 78, Appl
44	89	100.0	208	14	US-10-232-227-78	Sequence 78, Appl
45	89	100.0	208	14	US-10-232-229-78	Sequence 78, Appl

ALIGNMENTS

RESULT 1

US-10-060-765-8
; Sequence 8, Application US/10060765
; Publication No. US20020164713A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020164713A1uyuki
; APPLICANT: Kavanaugh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-21 GENE AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-16758.001/201130.408
; CURRENT APPLICATION NUMBER: US/10/060,765
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/715,805
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-765-8

Query Match 100.0%; Score 89; DB 13; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.4e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

OY 1 HLPGNKSPHRDPAPR 15

DB 1 HLPGNKSPHRDPAPR 15

RESULT 2

US-09-801-968-36
; Sequence 36, Application US/09801968
; Patent No. US20020082205A1
; GENERAL INFORMATION:
; APPLICANT: Itoh, No. US20020082205A1uyuki
; APPLICANT: Kavanaugh, W. Michael

; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-17150.001/201130.40901
; CURRENT APPLICATION NUMBER: US/09/801,968
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-968-36

Query Match 100.0%; Score 89; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 4 HLPGNKSPHRDPAPR 18

RESULT 3
US-09-802-154-36
; Sequence 36, Application US/09802154
; Publication No. US20030105302A1
; GENERAL INFORMATION:
; APPLICANT: Kavanagh, W. Michael
; TITLE OF INVENTION: HUMAN FGF-23 GENE AND GENE EXPRESSION
; FILE OF INVENTION: PRODUCTS
; FILE REFERENCE: PP-17149.001/201130.409
; CURRENT APPLICATION NUMBER: US/09/802,154
; CURRENT FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-154-36

Query Match 100.0%; Score 89; DB 10; Length 68;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 4 HLPGNKSPHRDPAPR 18

RESULT 4
US-09-901-938-33
; Sequence 33, Application US/09901938
; Patent No. US20020156001A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/09/901,938
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-938-33

Query Match 100.0%; Score 89; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 107 HLPGNKSPHRDPAPR 121

RESULT 5
US-10-379-334-33
; Sequence 33, Application US/10379334
; Publication No. US20030181379A1
; GENERAL INFORMATION:
; APPLICANT: ECONS, Michael
; APPLICANT: WHITE, Kenneth
; APPLICANT: STROM, Tim
; APPLICANT: MEITINGER, Thomas
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR USE
; FILE REFERENCE: 053884-5001
; CURRENT APPLICATION NUMBER: US/10/379,334
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US/09/901,938
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/219,137
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 34
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US-10-379-334-33

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Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 HLPGNKSPHRDPAPR 121

RESULT 6
US-09-755-695-2
; Sequence 2, Application US/09755695
; Patent No. US20020081663A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Chen, Zhi
; TITLE OF INVENTION: NOVEL FGF HOMOLOG ZFGF11
; FILE REFERENCE: 00-03
; CURRENT APPLICATION NUMBER: US/09/755,695
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/174,526
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-695-2

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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

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US-10-227-884-78
; Sequence 78, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
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; PRIOR FILING DATE: 1999-01-12

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; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
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; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match          100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 8
US-10-230-163-78
; Sequence 78, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
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; PRIOR FILING DATE: 1998-08-11
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; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
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; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
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; PRIOR FILING DATE: 1998-11-17
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618

; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
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; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
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; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
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; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158

RESULT 9
US-10-230-338-78
; Sequence 78, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
```

Wed Mar 3 08:19:50 2004

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; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred.No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 11
US-10-230-414-78
; Sequence 78, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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Wed Mar 3 08:19:50 2004

us-10-060-765-8.rapb

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; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 12
US-10-216-159A-78
; Sequence 78, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; Prior Application removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 13
US-10-218-849-78
; Sequence 78, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 14
US-10-227-873-78
; Sequence 78, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; Prior Application removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-227-873-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158
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1	PRIOR APPLICATION NUMBER: 60/079294
2	PRIOR FILING DATE: 1998-03-25
3	PRIOR APPLICATION NUMBER: 60/079656
4	PRIOR FILING DATE: 1998-03-26
5	PRIOR APPLICATION NUMBER: 60/079728
6	PRIOR FILING DATE: 1998-03-27
7	PRIOR APPLICATION NUMBER: 60/081819
8	PRIOR FILING DATE: 1998-04-15
9	PRIOR APPLICATION NUMBER: 60/081955
10	PRIOR FILING DATE: 1998-04-15
11	PRIOR APPLICATION NUMBER: 60/082804
12	PRIOR FILING DATE: 1998-04-22
13	PRIOR APPLICATION NUMBER: 60/084441
14	PRIOR FILING DATE: 1998-05-06
15	PRIOR APPLICATION NUMBER: 60/085323
16	PRIOR FILING DATE: 1998-05-13
17	PRIOR APPLICATION NUMBER: 60/085579
18	PRIOR FILING DATE: 1998-05-15
19	PRIOR APPLICATION NUMBER: 60/086399
20	PRIOR FILING DATE: 1998-05-22
21	PRIOR APPLICATION NUMBER: 60/089532
22	PRIOR FILING DATE: 1998-06-17
23	PRIOR APPLICATION NUMBER: 60/089538
24	PRIOR FILING DATE: 1998-06-17
25	PRIOR APPLICATION NUMBER: 60/089905
26	PRIOR FILING DATE: 1998-06-18
27	PRIOR APPLICATION NUMBER: 60/090472
28	PRIOR FILING DATE: 1998-06-24
29	PRIOR APPLICATION NUMBER: 60/090557
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31	PRIOR APPLICATION NUMBER: 60/090691
32	PRIOR FILING DATE: 1998-06-25
33	PRIOR APPLICATION NUMBER: 60/090695
34	PRIOR FILING DATE: 1998-06-25
35	PRIOR APPLICATION NUMBER: 60/091982
36	PRIOR FILING DATE: 1998-07-07
37	PRIOR APPLICATION NUMBER: 60/095302
38	PRIOR FILING DATE: 1998-08-04
39	PRIOR APPLICATION NUMBER: 60/095318
40	PRIOR FILING DATE: 1998-08-04
41	PRIOR APPLICATION NUMBER: 60/095916
42	PRIOR FILING DATE: 1998-08-10
43	PRIOR APPLICATION NUMBER: 60/096146
44	PRIOR FILING DATE: 1998-08-11
45	PRIOR APPLICATION NUMBER: 60/096791
46	PRIOR FILING DATE: 1998-08-17
47	PRIOR APPLICATION NUMBER: 60/097986
48	PRIOR FILING DATE: 1998-08-26
49	PRIOR APPLICATION NUMBER: 60/098544
50	PRIOR FILING DATE: 1998-08-31
51	PRIOR APPLICATION NUMBER: 60/099596
52	PRIOR FILING DATE: 1998-09-09
53	PRIOR APPLICATION NUMBER: 60/099598
54	PRIOR FILING DATE: 1998-09-09
55	PRIOR APPLICATION NUMBER: 60/099803
56	PRIOR FILING DATE: 1998-09-10
57	PRIOR APPLICATION NUMBER: 60/099811
58	PRIOR FILING DATE: 1998-09-10
59	PRIOR APPLICATION NUMBER: 60/099812
60	PRIOR FILING DATE: 1998-09-10
61	PRIOR APPLICATION NUMBER: 60/099816
62	PRIOR FILING DATE: 1998-09-10
63	PRIOR APPLICATION NUMBER: 60/100338
64	PRIOR FILING DATE: 1998-09-11
65	PRIOR APPLICATION NUMBER: 60/100385
66	PRIOR FILING DATE: 1998-09-15
67	PRIOR APPLICATION NUMBER: 60/100390
68	PRIOR FILING DATE: 1998-09-15
69	PRIOR APPLICATION NUMBER: 60/100622
70	PRIOR FILING DATE: 1998-09-16
71	PRIOR APPLICATION NUMBER: 60/100848
72	PRIOR FILING DATE: 1998-09-18
73	PRIOR APPLICATION NUMBER: 60/100915

; PRIOR APPLICATION NUMBER: 60/145698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: 60/146222
 ; PRIOR FILING DATE: 1999-07-28
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 ; PRIOR APPLICATION NUMBER: 60/149320
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 ; PRIOR APPLICATION NUMBER: 60/164418
 ; PRIOR FILING DATE: 1999-11-09
 ; PRIOR APPLICATION NUMBER: 60/166361
 ; PRIOR FILING DATE: 1999-11-16
 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.00012;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15

Db 144 HLPGNKSPHRDPAPR 158

RESULT 15

US-10-227-883-78

; Sequence 78, Application US/10227883

; Publication No. US20030073817A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530PIC78

; CURRENT APPLICATION NUMBER: US/10/227,883

; CURRENT FILING DATE: 2002-08-26

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/081819

; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/081955
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082804
 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/084441
 ; PRIOR FILING DATE: 1998-05-06
 ; PRIOR APPLICATION NUMBER: 60/085323
 ; PRIOR FILING DATE: 1998-05-13
 ; PRIOR APPLICATION NUMBER: 60/085579
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/086392
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/089532
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089905
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090472
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090691
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 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/095302
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 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/097986
 ; PRIOR FILING DATE: 1998-08-26
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 ; PRIOR APPLICATION NUMBER: 60/101741
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; PRIOR APPLICATION NUMBER: 60/101786
 ; PRIOR FILING DATE: 1998-09-25
 ; PRIOR APPLICATION NUMBER: 60/101916
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 ; PRIOR APPLICATION NUMBER: 60/106178
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 ; PRIOR APPLICATION NUMBER: 60/106464
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 60/106905
 ; PRIOR FILING DATE: 1998-11-03
 ; PRIOR APPLICATION NUMBER: 60/108787
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 ; PRIOR APPLICATION NUMBER: 60/113296
 ; PRIOR FILING DATE: 1998-12-22
 ; PRIOR APPLICATION NUMBER: 60/113605
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: 60/113621
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 ; PRIOR APPLICATION NUMBER: 60/115558
 ; PRIOR FILING DATE: 1999-01-12
 ; PRIOR APPLICATION NUMBER: 60/115565
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 ; PRIOR APPLICATION NUMBER: 60/119549
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 ; PRIOR APPLICATION NUMBER: 60/123618
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 ; PRIOR FILING DATE: 1999-03-23
 ; PRIOR APPLICATION NUMBER: 60/126773
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 ; PRIOR FILING DATE: 1999-04-05
 ; PRIOR APPLICATION NUMBER: 60/130232
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 ; PRIOR APPLICATION NUMBER: 60/131022
 ; PRIOR FILING DATE: 1999-04-26
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 ; PRIOR APPLICATION NUMBER: 60/131291
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 ; PRIOR APPLICATION NUMBER: 60/140723
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 ; PRIOR APPLICATION NUMBER: 60/145698
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: 60/146222
 ; PRIOR FILING DATE: 1999-07-28
 ; PRIOR APPLICATION NUMBER: 60/146963
 ; PRIOR FILING DATE: 1999-08-03
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; PRIOR FILING DATE: 1999-08-17
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 ; PRIOR APPLICATION NUMBER: 60/151733
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 ; PRIOR APPLICATION NUMBER: 60/169445
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169495
 ; PRIOR FILING DATE: 1999-12-07
 ; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 DB 144 HLPGNKSPHRDPAPR 158

RESULT 16

US-10-219-076-78
 ; Sequence 78, Application US/10219076
 ; Publication No. US20030078379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC62
 ; CURRENT APPLICATION NUMBER: US/10/219,076
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 10/119,480
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/062287
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063549
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/069873
 ; PRIOR FILING DATE: 1997-12-17
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079294
 ; PRIOR FILING DATE: 1998-03-25
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 ; PRIOR FILING DATE: 1998-03-26
 ; PRIOR APPLICATION NUMBER: 60/079728
 ; PRIOR FILING DATE: 1998-03-27
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 246
 ; SEQ ID NO 78
 ; LENGTH: 208
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-219-076-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HLPGNKSPHRDPAPR 15
| | | | | | | | | | | | | | | | | |
DB 144 HLPGNKSPHRDPAPR 158

RESULT 17

US-10-230-434-78
; Sequence 78, Application US/10230434
; Publication No. US20030078380A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P530P1C82
; CURRENT APPLICATION NUMBER: US/10/230,434
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
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; PRIOR FILING DATE: 1998-04-15
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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-11-18
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; PRIOR FILING DATE: 1998-12-15

, PRIOR APPLICATION NUMBER: 60/113296
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 , PRIOR FILING DATE: 1998-12-23
 , PRIOR APPLICATION NUMBER: 60/113621
 , PRIOR FILING DATE: 1998-12-23
 , PRIOR APPLICATION NUMBER: 60/115558
 , PRIOR FILING DATE: 1999-01-12
 , PRIOR APPLICATION NUMBER: 60/115565
 , PRIOR FILING DATE: 1999-01-12
 , PRIOR APPLICATION NUMBER: 60/115733
 , PRIOR FILING DATE: 1999-01-12
 , PRIOR APPLICATION NUMBER: 60/119549
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 , PRIOR FILING DATE: 1999-12-07
 , PRIOR APPLICATION NUMBER: 60/169495
 , PRIOR FILING DATE: 1999-12-07
 , PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 DB 144 HLPGNKSPHRDPAPR 158

RESULT 18
 US-10-219-003-78
 ; Sequence 78, Application US/10219003
 ; Publication No. US2003008063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Philippe F.
 ; APPLICANT: Watanabe, Colin L.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3530PIC12
 ; CURRENT APPLICATION NUMBER: US/10/219,003
 ; PRIOR APPLICATION NUMBER: 2002-08-12
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: 60/059113
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 ; PRIOR FILING DATE: 1997-10-31
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 ; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/100848
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; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
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; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
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; PRIOR FILING DATE: 1998-11-17
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; PRIOR APPLICATION NUMBER: 60/108849
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
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; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 19
US-10-219-075-78
; Sequence 78, Application US/10219075
; Publication No. US2003008064A1
; GENERAL INFORMATION:

us-10-060-765-8.rapb

Wed Mar 3 08:19:50 2004

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC61
; CURRENT APPLICATION NUMBER: US/10/219,075
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-464-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 20
US-10-219-464-78
; Sequence 78, Application US/10219464
; Publication No. US2003008066A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC47
; CURRENT APPLICATION NUMBER: US/10/219,466
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-075-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 20
US-10-219-464-78
; Sequence 78, Application US/10219464
; Publication No. US2003008066A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC57
; CURRENT APPLICATION NUMBER: US/10/219,464
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; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-466-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 22
US-10-219-479-78
; Sequence 78, Application US/10219479
; Publication No. US2003008067A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C33
; CURRENT APPLICATION NUMBER: US/10/219,479
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-479-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 23
US-10-219-481-78
; Sequence 78, Application US/10219481
; Publication No. US2003008068A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C28
; CURRENT APPLICATION NUMBER: US/10/219,481
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-481-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
Db      144 HLPGNKSPHRDPAPR 158

RESULT 24
US-10-230-260-78
; Sequence 78, Application US/10230260
; Publication No. US2003008070A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C83
; CURRENT APPLICATION NUMBER: US/10/230,260
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-260-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 25
US-10-232-231-78
; Sequence 78, Application US/10232231
; Publication No. US2003008071A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C108
; CURRENT APPLICATION NUMBER: US/10/232,233
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 10/119,480

```

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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-231-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 26
US-10-232-233-78
; Sequence 78, Application US/10232233
; Publication No. US2003008072A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C108
; CURRENT APPLICATION NUMBER: US/10/232,233
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 10/119,480

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;; PRIOR APPLICATION NUMBER: 60/090695
;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/095302
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095318
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: 60/095916
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/096146
;; PRIOR FILING DATE: 1998-08-11
;; PRIOR APPLICATION NUMBER: 60/096791
;; PRIOR FILING DATE: 1998-08-17
;; PRIOR APPLICATION NUMBER: 60/097986
;; PRIOR FILING DATE: 1998-08-26
;; PRIOR APPLICATION NUMBER: 60/098544
;; PRIOR FILING DATE: 1998-08-31
;; PRIOR APPLICATION NUMBER: 60/099596
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099598
;; PRIOR FILING DATE: 1998-09-09
;; PRIOR APPLICATION NUMBER: 60/099803
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099811
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099812
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/099816
;; PRIOR FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: 60/100038
;; PRIOR FILING DATE: 1998-09-11
;; PRIOR APPLICATION NUMBER: 60/100385
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100390
;; PRIOR FILING DATE: 1998-09-15
;; PRIOR APPLICATION NUMBER: 60/100627
;; PRIOR FILING DATE: 1998-09-16
;; PRIOR APPLICATION NUMBER: 60/100848
;; PRIOR FILING DATE: 1998-09-18
;; PRIOR APPLICATION NUMBER: 60/100919
;; PRIOR FILING DATE: 1998-09-17
;; PRIOR APPLICATION NUMBER: 60/101477
;; PRIOR FILING DATE: 1998-09-23
;; PRIOR APPLICATION NUMBER: 60/101738
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101786
;; PRIOR FILING DATE: 1998-09-25
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101922
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/106178
;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/106248
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 60/106464
;; PRIOR FILING DATE: 1998-10-30
;; PRIOR APPLICATION NUMBER: 60/106905
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/108787
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108801
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113605

;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115733
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131445
;; PRIOR FILING DATE: 1999-04-28
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149638
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 29

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US-10-219-468-78
; Sequence 78, Application US/10219468
; Publication No. US20030092889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C34
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-468-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 30
US-10-219-468-78
; Sequence 78, Application US/10219478
; Publication No. US20030092889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C34
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-468-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 30
US-10-219-478-78
; Sequence 78, Application US/10219478
; Publication No. US20030092889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C67
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C30
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-478-78

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158

RESULT 31
US-10-219-536-78
; Sequence 78, Application US/10219536
; Publication No. US20030092890A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C67
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
```

```
; ORGANISM: Homo Sapien
US-10-233-205-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
      |||
Db      144 HLPGNKSPHRDPAPR 158
      |||

RESULT 33
US-10-219-072-78
; Sequence 78, Application US/10219072
; Publication No. US20030096959A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC45
; CURRENT APPLICATION NUMBER: US/10/219,072
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-072-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
      |||
Db      144 HLPGNKSPHRDPAPR 158
      |||

RESULT 34
US-10-219-470-78
; Sequence 78, Application US/10219470
```

```
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-536-78

Query Match      100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
      |||
Db      144 HLPGNKSPHRDPAPR 158
      |||

RESULT 32
US-10-233-205-78
; Sequence 78, Application US/10233205
; Publication No. US20030096362A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC15
; CURRENT APPLICATION NUMBER: US/10/233,205
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
```

```
; Publication No. US20030096960A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC59
; CURRENT APPLICATION NUMBER: US/10/219,470
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-470-78
```

```
Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158
```

```
RESULT 35
US-10-219-474-78
; Sequence 78, Application US/10219474
; Publication No. US20030096961A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
```

```
; FILE REFERENCE: P3530PIC36
; CURRENT APPLICATION NUMBER: US/10/219,474
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-474-78
```

```
Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 144 HLPGNKSPHRDPAPR 158
```

```
RESULT 36
US-10-219-524-78
; Sequence 78, Application US/10219524
; Publication No. US20030096962A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC37
; CURRENT APPLICATION NUMBER: US/10/219,524
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
```

```

; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 78
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-524-78

Query Match          100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLPGNKSPHRDPAPR 15
      |||||
Db      144 HLPGNKSPHRDPAPR 158

RESULT 37
US-10-219-528-78
; Sequence 78, Application US/10219528
; Publication No. US20030096963A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C68
; CURRENT APPLICATION NUMBER: US/10/219,528
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
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, PRIOR FILING DATE: 1999-11-09
, PRIOR APPLICATION NUMBER: 60/166361
, PRIOR FILING DATE: 1999-11-16
, PRIOR APPLICATION NUMBER: 60/169445
, PRIOR FILING DATE: 1999-12-07
, PRIOR APPLICATION NUMBER: 60/169495
, PRIOR FILING DATE: 1999-12-07
, PRIOR APPLICATION NUMBER: 60/169835
, PRIOR FILING DATE: 1999-11-09
, PRIOR APPLICATION NUMBER: 60/166361
, PRIOR FILING DATE: 1999-11-16
, PRIOR APPLICATION NUMBER: 60/169445
, PRIOR FILING DATE: 1999-12-07
, PRIOR APPLICATION NUMBER: 60/169495
, PRIOR FILING DATE: 1999-12-07
, PRIOR APPLICATION NUMBER: 60/169835
Query Match      100.0%; Scored
Best Local Similarity 100.0%; Pre-Matched
Matches 15; Conservative 0; Mismatches 0
QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158
RESULT 38
US-10-227-880-78
, Sequence 78, Application US/10227880
, Publication No. US20030096964A1
, GENERAL INFORMATION:
, APPLICANT: Baker, Kevin P.
, APPLICANT: Desnoyers, Luc
, APPLICANT: Gerritsen, Mary
, APPLICANT: Godward, Audrey
, APPLICANT: Goddard, Paul J.
, APPLICANT: Godowski, Paul J.
, APPLICANT: Grimaldi, J. Christophe
, APPLICANT: Gurney, Austin L.
, APPLICANT: Smith, Victoria
, APPLICANT: Stephan, Jean-Philippe
, APPLICANT: Watanabe, Colin L.
, APPLICANT: Wood, William I.
, TITLE OF INVENTION: SECRETED AND TRIMMED
, TITLE OF INVENTION: ACIDS ENCODINGS
, FILE REFERENCE: P530P1C74
, CURRENT APPLICATION NUMBER: US/10/227880
, CURRENT FILING DATE: 2002-08-26
, PRIOR APPLICATION NUMBER: 10/119,481
, PRIOR FILING DATE: 2002-04-09
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, PRIOR FILING DATE: 1998-05-15
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92 PRIOR FILING DATE: 1999-01-12
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94 PRIOR FILING DATE: 1999-01-12
95 PRIOR APPLICATION NUMBER: 60/119549
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Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HLPKNSPHRDPA 15
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Db      144 HLPKNSPHRDPA 158

RESULT 39
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; Sequence 78, Application US/10227881
; Publication No. US20030096965A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C80
; CURRENT APPLICATION NUMBER: US/10/227,881
; CURRENT FILING DATE: 2002-08-26
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Query Match 100.08; Score 89; DB 14; Length 208;

Best Local Similarity 100.08; Pred. No. 0.00012; Mismatches 0; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 144 HLPGNKSPHRDPAPR 158

RESULT 40

US-10-227-882-78
; Sequence 78, Application US/10227882
; Publication No. US20030096966A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C81
; CURRENT APPLICATION NUMBER: US/10/227,882
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
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;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131445
;; PRIOR FILING DATE: 1999-04-28
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149638
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 89; DB 14; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPCKNSPHRDPA 15
Dd 144 HLPCKNSPHRDPA 158

Search completed: March 2, 2004, 16:19:58
Job time : 5.0625 secs

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
| | | | | | | | | | | | | | |
Db 1 HLPGNKSPHRDPAPR 15

RESULT 2
ABB81312
ID ABB81312 standard; protein; 124 AA.
XX
AC ABB81312;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human FGF21 core structure amino acid sequence.

XX Fibroblast growth factor 9; FGF-9; cytostatic; vulnary; osteopathic;
KW antiarthritic; vasculogenesis; angiogenesis; FGFR; skeletal disorder;
KW fibroblast growth factor receptor; cancer; bone fracture healing;
KW bone growth; wound healing; achondroplasia; hypochondroplasia;
KW osteoporosis; cartilage defect; multiple myeloma.

XX Homo sapiens.

OS

XX WO200236732-A2.

PN

XX 10-MAY-2002.

PD

XX 18-OCT-2001; 2001WO-IL000962.

PF

XX 31-OCT-2000; 2000IL-00139380.

PR

XX (PROC-) PROCHON BIOTECH LTD.

PA

XX Bogin O, Adar R, Yayon A;

PI

XX WPI; 2002-479754/51.

DR

XX New variants of fibroblast growth factor, useful for treating skeletal

PT disorders including osteoporosis, malignancies and to enhance wound and

PT fracture healing.

PT

XX Disclosure; Fig 1; 74pp; English.

PS

XX The present invention describes an active variant (I) of a fibroblast

CC growth factor (FGF) having at least one mutation in the beta-8-beta-9

CC loop, having enhanced specificity for one receptor subtype compared to

CC the corresponding wild type FGF, by decreasing the biological activity

CC mediated by at least one receptor subtype while retaining the activity

CC mediated through another receptor subtype. (I) has cytostatic, vulnary,

CC osteopathic and antiarthritic activities. (I) can be used as a regulator

CC of vasculogenesis or angiogenesis. (I) is useful for preparing a

CC medicament and for treating a disease or disorder related to normal or

CC abnormal FGF receptors (FGFRs), especially skeletal disorders, cancer, to

CC enhance bone fracture healing or bone growth processes and wound healing

CC processes. (I) is useful in detection and treatment of various FGFR

CC related disorders including skeletal disorders e.g. achondroplasia,

CC hypochondroplasia, and osteoporosis, and cartilage defects, multiple

CC myeloma, epithelial cancers such as transitional cell carcinoma of the

CC bladder and cervical carcinoma. The novel mutants are useful in high

CC expression systems suitable for pharmaceutical production, targeting of

CC drugs or other agents to tissues and cells having specific FGFR subtypes,

CC and serve as template for the formation of improved agonists and

CC antagonists of FGFRs in various disorders such as skeletal disorders and

CC cancer. The present sequence represents a FGF core structure amino acid

CC sequence which is given in the exemplification of the present invention

XX

SQ Sequence 124 AA;

Query Match 100.0%; Score 89; DB 5; Length 124;

Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
| | | | | | | | | | | | | | |
Db 101 HLPGNKSPHRDPAPR 115

RESULT 3
AAU00965
ID AAU00965 standard; protein; 181 AA.
XX
AC AAU00965;

XX

DT 24-MAY-2001 (first entry)

XX

DE Human Fibroblast Growth Factor-like (FGF-like) polypeptide fragment.

XX

XX Fibroblast Growth Factor; FGF; treatment; cirrhosis; mucositis; diabetes;

KW inflammatory bowel disease; Crohn's disease; obesity; tubular necrosis;

KW renal tubule damage; gastrointestinal abnormality; wasting syndrome;

KW neurodegenerative disease; haematopoietic cell reconstruction; cachexia;

KW chemotherapy; corneal epithelium damage; retinal tissue damage; myopathy;

KW multiple sclerosis; short stature; delayed maturation; excessive growth;

KW acromegaly; premature maturation; alopecia; bronchopulmonary dysplasia;

KW androgen target organ abnormality; respiratory distress syndrome; stroke;

KW cancer; atherosclerosis; hypercholesterolemia; osteoporosis; baldness;

KW osteoarthritis; muscle atrophy; sarcopenia; wrinkles; increased fatigue;

KW decreased stamina; decreased cardiac function; immune system dysfunction;

KW Parkinson's disease; Alzheimer's disease; decreased cognitive function;

KW senile dementia; human.

XX

OS Homo sapiens.

XX

PN WO200118172-A2.

XX

PD 15-MAR-2001.

XX

PF 05-SEP-2000; 2000WO-US024373.

XX

PR 07-SEP-1999; 98US-00391861.

XX

PR 23-AUG-2000; 2000US-00644052.

XX

PA (AMGE-) AMGEN INC.

XX

PI Thomson AR, Liu B;

XX

DR WPI; 2001-226743/23.

XX

PT Novel isolated fibroblast growth factor-like polypeptide useful for

PT treating, preventing or ameliorating cirrhosis, inflammatory bowel

PT disease, mucositis, Crohn's disease, diabetes, obesity, stroke and

PT osteoporosis.

XX

PS Claim 14; Page 116-117; 138pp; English.

XX

CC The sequence represents a fragment of a fibroblast growth factor-like

CC (FGF-like) polypeptide. FGF-like protein and its associated nucleic acid

CC play a role in modulating body growth, maturation or life-span. They are

CC also useful for treating, preventing or ameliorating disorders such as

CC cirrhosis, inflammatory bowel disease, mucositis, Crohn's disease,

CC diabetes, obesity, gastrointestinal abnormalities, neurodegenerative

CC diseases, damage to renal tubules as a result of acute tubular necrosis,

CC haematopoietic cell reconstitution following chemotherapy, wasting

CC syndromes (e.g., cancer associated cachexia), damage to the corneal

CC epithelium, lens or retinal tissue, multiple sclerosis, myopathies, short

CC stature, delayed maturation, excessive growth (e.g. acromegaly),

CC premature maturation, alopecia, abnormalities of androgen target organs,

CC bronchopulmonary dysplasia, acute respiratory distress syndrome, tumours

CC of the eye or other tissues, atherosclerosis, hypercholesterolemia,

CC stroke, osteoporosis, osteoarthritis, muscle atrophy, sarcopenia,

CC baldness, wrinkles, increased fatigue, decreased stamina, decreased

CC cardiac function, immune system dysfunction, cancer, Parkinson's disease,

CC senile dementia, Alzheimer's disease, and decreased cognitive function
XX
SQ Sequence 181 AA;
Query Match 100.0%; Score 89; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 8e-05; 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDPAPR 15
|||
Db 117 HLPGNKSPHRDPAPR 131
|||
RESULT 4
AAE05078
ID AAE05078 standard; protein; 208 AA.
XX
AC AAE05078;
XX
XX 18-SEP-2001 (first entry)
XX Human fibroblast growth factor (FGF) homologue, zFGF11 protein.
XX
KW Human; fibroblast growth factor; FGF; zFGF11; chromosome 19; restenosis;
KW proliferation; mesenchymal cell; osteoblastic lineage cell; osteoporosis;
KW chromosomal disorder; chondrosarcoma; atherosclerosis; obesity; fracture;
KW bone formation; diabetes mellitus; neural cell development; angiogenesis;
KW amyotrophic lateral sclerosis; cerebrovascular stroke; neuropathy; ulcer;
KW congenital disorder; wound healing; cardiac function; glomerulonephritis;
KW surfactant production; anorectic; ischaemia; neogenesis; hyperplasia;
KW hypertension; cytosstatic; vasotropic; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= signal_peptide
FT Protein 28..208
FT /label= Human_mature_zFGF11_protein
FT Binding-site 44..46
FT /note= "Heparin binding domain"
XX
XX WO200149849-A1.
XX
XX 12-JUL-2001.
XX
XX 05-JAN-2001; 2001WO-US000324.
XX
XX 05-JAN-2000; 2000US-00477886.
XX (ZYMO) ZYMOGENETICS INC.
XX
XX Conklin DC, Chen Z;
XX
XX WPI; 2001-441880/47.
XX N-PSDB; AAD09151.
XX
XX Novel zFGF11 polypeptide and polynucleotide, a member of fibroblast
PT growth factor family, for stimulating proliferation of mesenchymal,
PT osteoblastic lineage cells and treating diabetes, obesity, osteoporosis,
PT cancer.
XX
XX Claim 1; Page 63; 69pp; English.
XX
XX The present sequence is human fibroblast growth factor (FGF) homologue,
CC zFGF11 protein. zFGF11 gene is located on chromosome 19. zFGF11 is useful
CC for stimulating proliferation of mesenchymal cells, osteoblastic lineage
CC cells. zFGF11 is useful for identifying chromosomal disorders associated
CC with abnormal expression of zFGF11 protein. zFGF11 is also useful for
CC stimulation, inhibition or proliferation of myocytes, smooth muscle
CC cells, adipocytes, chondrocytes, neural tube-derived stem cells, neural
CC crest stem cells and neuronal progenitors, pancreatic cells, prostate-
CC derived cells and endothelial cells and inhibiting chondrosarcomas,

CC atherosclerosis, restenosis and obesity. Stimulation of osteoblasts
CC results in bone formation useful for treating bone defects, fractures,
CC osteoporosis and other deficiencies in bone structure and formation.
CC zFGF11 is useful for treating disorders associated with diabetes
CC mellitus, neural cell development or degeneration, amyotrophic lateral
CC sclerosis, cerebrovascular stroke, neuropathy associated with lack of
CC maintenance of neuronal differentiation and congenital disorders of the
CC nervous system or lack of neuronal development, promoting angiogenesis
CC and wound healing, for revascularisation in eye, complications related to
CC poor circulation such as diabetic food ulcers, improving cardiac
CC function, modulating surfactant production in the lung epithelium, to
CC reduce damage to the tissue caused by ischaemia or ischaemia-reperfusion
CC events, particularly in the heart or brain and for inducing skeletal
CC muscle neogenesis and/or hyperplasia, kidney regeneration and/or for
CC treating of systemic and pulmonary hypertension. Antagonists of zFGF11
CC are useful for inhibiting disorders associated with kidney epithelium
CC such as glomerulonephritis
XX
XX Sequence 208 AA;
SQ
Query Match 100.0%; Score 89; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05; 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDPAPR 15
|||
Db 144 HLPGNKSPHRDPAPR 158
|||
RESULT 5
AAU83630
ID AAU83630 standard; protein; 208 AA.
XX
AC AAU83630;
XX
XX 08-MAY-2002 (first entry)
XX Human PRO protein, Seq ID No 78.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US021066.
XX
XX 20-JUL-2000; 2000US-0219556P.
XX 25-JUL-2000; 2000US-0220585P.
XX 25-JUL-2000; 2000US-0220605P.
XX 25-JUL-2000; 2000US-0220607P.
XX 25-JUL-2000; 2000US-0220624P.
XX 25-JUL-2000; 2000US-0220638P.
XX 25-JUL-2000; 2000US-0220664P.
XX 25-JUL-2000; 2000US-0220666P.
XX 26-JUL-2000; 2000US-0220893P.
XX 28-JUL-2000; 2000WO-US020710.
XX 01-AUG-2000; 2000US-0222425P.
XX 22-AUG-2000; 2000US-0227133P.
XX 23-AUG-2000; 2000WO-US023522.
XX 24-AUG-2000; 2000WO-US023328.
XX 10-NOV-2000; 2000WO-US030873.
XX 28-NOV-2000; 2000US-0253646P.
XX 01-DEC-2000; 2000WO-US032678.
XX 20-DEC-2000; 2000US-00747259.
XX 20-DEC-2000; 2000WO-US034956.
XX 28-FEB-2001; 2001WO-US006520.
XX 01-MAR-2001; 2001WO-US006666.

PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001WO-US017032.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Deanovers L, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABK33574.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX Claim 11; Fig 78; 359pp; English.
 PS The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 6
 ABG32358
 ID ABG32358 standard; protein; 208 AA.
 XX
 AC ABG32358;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Human fibroblast growth factor (FGF) homologue, zFGF11.
 XX
 KW Human; fibroblast growth factor; FGF; zFGF11; mesenchymal cell; FGFR11c;
 KW osteoblastic lineage cell; diabetes mellitus; neuropathy;
 KW neural cell development; amyotrophic lateral sclerosis;
 KW cerebrovascular stroke; neuronal differentiation; congenital disorder;
 KW nervous system disorder; cardiac function; wound healing.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..27 /label= Signal_sequence
 FT Protein 28..208 /note= "Mature fibroblast growth factor homologue,
 FT zFGF11. This sequence is specifically claimed in claim 4"
 XX

PN US2002081663-A1.
 XX 27-JUN-2002.
 XX 05-JAN-2001; 2001US-00755695.
 XX 05-JAN-2000; 2000US-0174526P.
 XX (CONK/) CONKLIN D C.
 XX (CHEN/) CHEN Z.
 XX Conklin DC, Chen Z;
 XX WPI; 2002-628540/67.
 DR N-PSDB; ABK91310.
 XX Isolated polypeptide for zFGF11 (fibroblast growth factor) useful in
 PT treatment of disorders associated with diabetes mellitus, neural cell
 PT development or degeneration, amyotrophic lateral sclerosis,
 PT cerebrovascular stroke.
 XX Claim 4; Fig 1; 35pp; English.
 PS The invention relates to an isolated human polypeptide (I) for zFGF11 (a
 CC fibroblast growth factor), and the encoding polynucleotide (II). (I) and
 CC (II) are used in methods of the invention stimulating proliferation of
 CC mesenchymal cells, detecting the presence of zFGF11 in a biological
 CC sample, detecting the presence of FGFR11c in a biological sample and
 CC stimulating proliferation of osteoblastic lineage cells. The
 CC polypeptides, nucleic acid and/or antibodies of the invention may be used
 CC in treatment of disorders associated with diabetes mellitus, neural cell
 CC development or degeneration, amyotrophic lateral sclerosis,
 CC cerebrovascular stroke, neuropathy associated with lack of maintenance of
 CC neuronal differentiation, and congenital disorders of the nervous system
 CC or lack of neuronal development. Molecules of the invention may also be
 CC useful for improving cardiac function and for promoting wound healing of
 CC the epidermis. The present sequence represents the amino acid sequence of
 CC human zFGF11
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 5; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 7
 AAE17601
 ID AAE17601 standard; protein; 208 AA.
 XX
 AC AAE17601;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human extracellular messenger (XMES)-3 protein.
 XX
 KW Human; extracellular messenger; neurological disorder; epilepsy; XMES-3;
 KW Alzheimer's disease; autoimmune disorder; renal tubular acidosis; stroke;
 KW acquired immune deficiency syndrome; AIDS; Addison's disease; cytostatic;
 KW developmental disorder; anaemia; Cushing's syndrome; endocrine disorder;
 KW vascular malformation; cell proliferative disorder; gene therapy; cancer;
 KW neuroprotective; trauma; hypopituitarism; hypothyroidism; antihelminthic;
 KW hyperthyroidism; gonadal steroid hormone; pancreatic disorder; nootropic;
 KW diabetes mellitus; immunosuppressive; anti-inflammatory; antibacterial;
 KW antiviral; antifungal; parasitic; protozoal; allergy.
 XX
 OS Homo sapiens.
 XX
 XX WO200194587-A2.
 PN

XX 13-DEC-2001.
XX 06-JUN-2001; 2001WO-US018476.
XX 06-JUN-2000; 2000US-0210233P.
XX 23-JUN-2000; 2000US-0213465P.
XX 14-NOV-2000; 2000US-0249019P.
XX (INCY-) INCYTE GENOMICS INC.
XX Lal P, Yue H, He A, Nguyen DB, Walia N, Gandhi AP, Azimzai Y;
XX Bandman O, Tang YT, Lu Y, Baughn MR, Duggan BM, Lee S, Hafalia A;
XX Policky JL;
XX WPI; 2002-154573/20.
XX N-PSDB; AAD28493.
XX New extracellular messenger polypeptides and polynucleotides encoding
XX them, useful for diagnosing, treating or preventing e.g. neurological,
XX autoimmune, inflammatory, developmental and endocrine disorders.
XX Claim 1; Page 111; 123pp; English.
XX The present invention relates to new extracellular messenger polypeptides
XX and polynucleotides encoding them. XMES is useful in the diagnosis,
XX treatment and prevention of neurological disorders (e.g. epilepsy,
XX stroke, or Alzheimer's disease), autoimmune/inflammatory disorders (e.g.
XX acquired immune deficiency syndrome, AIDS, Addison's disease, or
XX allergies), developmental disorders (e.g. renal tubular acidosis, anaemia
XX or Cushing's syndrome), endocrine disorders (e.g. hypophysectomy,
XX aneurysm or vascular malformation), and cell proliferative disorders
XX (e.g. cancer), and in the assessment of the effects of exogenous
XX compounds on the expression of nucleic acid and amino acid sequences of
XX extracellular messengers. XMES may also be used in the treatment of
XX viral, bacterial, fungal, parasitic, protozoal and helminthic
XX infections, trauma, disorders associated with hypopituitarism,
XX hypothyroidism, hyperthyroidism or gonadal steroid hormones, and
XX pancreatic disorders such as type I or type II diabetes mellitus. The
XX XMES may be used for somatic or germline gene therapy. The present
XX sequence is human XMES-3 protein
XX SQ Sequence 208 AA;
Query Match 100.0%; Score 89; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158
RESULT 8
ABU80777
ID ABU80777 standard; protein; 208 AA.
XX AC ABU80777;
XX DT 23-JUN-2003 (first entry)
XX DE Human PRO polypeptide #39.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX OS Homo sapiens.
XX PN US2003036635-A1.
XX PD 20-FEB-2003.
XX PF 28-AUG-2002; 2002US-00230163.

XX 25-JUL-2000; 2000US-0220638P.
XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
XX N-PSDB; ACA66879.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for the manufacture of a medicament for diagnosing or treating
XX tumor.
XX Claim 11; Fig 78; 314pp; English.
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides and polynucleotides are useful for preparing a medicament
XX useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
XX useful in diagnostic assays for PRO, by detecting its expression in
XX specific cells, tissues or serum, and for affinity purification of PRO
XX from recombinant cell culture or natural sources. ABU80739-ABU80860
XX represent the human PRO polypeptides of the invention. Note: The sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/psipadIDEntry.html
XX SQ Sequence 208 AA;
Query Match 100.0%; Score 89; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158
RESULT 9
ABO33743
ID ABO33743 standard; protein; 208 AA.
XX AC ABO33743;
XX DT 17-SEP-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO10196.
XX KW Human; secreted and transmembrane protein; PRO; cytostatic;
XX antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; bone disorder; cartilage disorder; sports injury;
XX arthritis; wound.
XX OS Homo sapiens.
XX PN US2003045687-A1.
XX PD 06-MAR-2003.
XX PF 12-AUG-2002; 2002US-00218631.
XX PR 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.

PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX WPI; 2003-512315/48.
 DR N-PSDB; ACD68631.
 XX New genes, and its encoded secreted and transmembrane polypeptides,
 PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
 PT pericyte proliferation, especially for treating lung tumors, arthritis or
 PT wounds in a mammal.
 XX Claim 11; Fig 78; 314pp; English.
 PS The invention describes an isolated nucleic acid molecule comprising a
 XX sequence with at least 80% identity to: (a) a nucleotide encoding any of
 CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
 CC fully defined in the specification; or (b) any of 122 nucleotide
 CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
 CC specification; or the full length coding sequence of any these 122
 CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
 CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
 CC particularly useful for detecting tumours (e.g. lung tumour, colon
 CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
 CC in a mammal, for stimulating the release of TNP-alpha from human blood,
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells, for stimulating proliferation of pericyte cells, or for modulating
 CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
 CC polypeptide is also useful for treating tumours or various bone and/or
 CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
 CC PRO polypeptides are useful in drug screening, particularly as targets
 CC for therapeutic intervention in these diseases, and in the diagnostic
 CC determination of the presence of these diseases. The PRO polypeptides are
 CC also useful as molecular weight markers, or for chromosome
 CC identification. The PRO genes are useful as hybridisation probes, or for
 CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
 CC also be used in gene therapy, particularly for replacing a defective
 CC gene. This is the amino acid sequence of a novel human secreted and
 CC transmembrane PRO polypeptide
 XX Sequence 208 AA;
 SQ Query Match 100.0%; Score 89; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 DB |||||
 144 HLPGNKSPHRDPAPR 158
 RESULT 10
 ABU82086
 ID ABU82086 standard; protein; 208 AA.
 XX ABU82086;
 AC 25-JUN-2003 (first entry)
 DT Human human secreted and transmembrane protein PRO10196.
 XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
 XX Homo sapiens.
 OS

PN US2003088063-A1.
 XX 08-MAY-2003.
 XX 12-AUG-2002; 2002US-00219003.
 XX 25-JUL-2000; 2000US-0220664P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PU;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;
 XX WPI; 2003-393229/37.
 DR N-PSDB; ACA68535.
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX Claim 11; Fig 78; 314pp; English.
 CC The invention describes one hundred and eighty seven nucleic acids
 CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
 CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
 CC treating or diagnosing a cardiovascular, endothelial or angiogenic
 CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
 CC related macular degeneration, atherosclerosis, hypertension, arterial
 CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
 CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
 CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
 CC have applications in molecular biology, including use as hybridisation
 CC probes, and in chromosome and gene mapping. This is the amino acid
 CC sequence of a novel human secreted and transmembrane PRO polypeptide
 XX Sequence 208 AA;
 SQ Query Match 100.0%; Score 89; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 DB |||||
 144 HLPGNKSPHRDPAPR 158
 RESULT 11
 ABP96156
 ID ABP96156 standard; protein; 208 AA.
 XX ABP96156;
 AC 12-MAY-2003 (first entry)
 DT Human fibroblast growth factor 21 protein SEQ ID NO:2.
 XX Human; fibroblast growth factor 21; FGF-21; chromosome 19; 19q13.1-qter;
 KW diabetes; obesity; antidiabetic; anorectic; type 2 diabetes;
 KW type 1 diabetes.
 XX Homo sapiens.
 OS WO2003011213-A2.
 PN 13-FEB-2003.
 XX 22-JUL-2002; 2002WO-US021290.
 PF 30-JUL-2001; 2001US-0308702P.
 PR 10-JAN-2002; 2002US-0347991P.
 PR

XX PA (ELIL) LILLY & CO ELLI.
 XX PI Glasebrook AL, Hammond LJ, Kharitonov A, Shiyanova TL;
 XX PS N-PSDB; ABZ79797.
 DR WPI; 2003-248106/24.
 XX N-PSDB; ABZ79797.
 XX PT Treating a mammal exhibiting Type 2 diabetes or Type 1 diabetes or
 PT obesity, by administering composition comprising fibroblast growth factor
 PT -21.
 XX Claim 3; Fig 1; 32pp; English.
 XX The present sequence represents human fibroblast growth factor 21 (FGF-
 CC 21). FGF-21 is located to chromosome 19, more specifically to 19q13.1-
 CC qter. The present invention describes a method for treating a mammal
 CC exhibiting type 2 diabetes or type 1 diabetes, or treating a mammal for
 CC obesity which comprises administering to the mammal a composition
 CC comprising FGF-21 which has at least 95% amino acid sequence identity to
 CC the 208 amino acid sequence given in ABP96156. Also described: (1)
 CC inducing an increase in glucose uptake in adipocyte cells by
 CC administering FGF-21 to induce an increase in glucose uptake; and (2)
 CC manufacturing a medicament for treating type 1 diabetes, type 2 diabetes
 CC or obesity in a mammal using FGF-21 having 95% amino acid sequence
 CC identity to ABP96156. FGF-21 has antidiabetic and anorectic activities.
 CC The method is useful for treating a mammal exhibiting type 2 or 1
 CC diabetes or for treating a mammal for obesity. The method is preferably
 CC useful for treating humans exhibiting type 1 or type 2 diabetes, and for
 CC treating domestic animals for obesity
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 DB 144 HLPGNKSPHRDPAPR 158
 RESULT 12
 ABU72266
 ID ABU72266 standard; protein; 208 AA.
 XX AC ABJ72266;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human PRO10196 protein.
 XX PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
 KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
 XX Homo sapiens.
 XX US2003050448-A1.
 XX 13-MAR-2003.
 XX 28-AUG-2002; 2002US-00230414.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-521818/49.

DR N-PSDB; ABT44264.
 XX New nucleic acid encoding for a PRO protein, useful for the manufacture
 PT of a medicament for diagnosing or treating tumors or for measuring or
 PT detecting expression of an associated gene.
 XX Claim 11; Fig 78; 315pp; English.
 XX The invention relates to a novel isolated nucleic acid encoding a fully
 CC defined PRO polypeptide. The molecules of the invention may be useful for
 CC stimulating proliferation or gene expression in pericyte cells or the
 CC release of TNF-alpha from human blood. Other possible uses include the
 CC stimulation or inhibition of chondrocyte proliferation or
 CC differentiation, the stimulation of human dermal fibroblast cell
 CC proliferation and the detection of the presence of a tumour within a
 CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
 CC of a medicament for diagnosing or treating a tumour within a mammal or
 CC for measuring or detecting the expression of an associated gene, as well
 CC as during gene therapy. The current sequence is that of the human PRO
 CC protein of the invention
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 6; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 DB 144 HLPGNKSPHRDPAPR 158
 RESULT 13
 ABU72394
 ID ABU72394 standard; protein; 208 AA.
 XX AC ABJ72394;
 XX DT 06-NOV-2003 (first entry)
 XX DE Human PRO10196 protein.
 XX PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
 KW tumour necrosis factor; proliferation; differentiation; gene therapy;
 KW dermal fibroblast.
 XX Homo sapiens.
 XX US2003027988-A1.
 XX 06-FEB-2003.
 XX 26-AUG-2002; 2002US-0027884.
 XX 01-JUN-2001; 2001WO-US017800.
 XX 29-JUN-2001; 2001WO-US021066.
 XX 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-503301/47.
 DR N-PSDB; ABT44547.
 XX New PRO protein encoding nucleic acid, useful for preparing PRO
 PT polypeptides and anti-PRO antibodies for detecting the presence of a
 PT tumor in a mammal.
 XX Claim 11; Fig 78; 324pp; English.
 XX The invention relates to a novel isolated PRO protein encoding nucleic

CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC tumour in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention

XX SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
|||||
Db 144 HLPGNKSPHRDPAPR 158

RESULT 14

ABO34289
ID ABO34289 standard; protein; 208 AA.

XX AC ABO34289;

XX DT 19-SEP-2003 (first entry)

XX DE Human secreted/transmembrane polypeptide PRO 10196.

KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.

XX OS Homo sapiens.

XX FN US200304934-A1.

XX PD 06-MAR-2003.

XX PF 28-AUG-2002; 2002US-00230338.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Deanoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX DR WPI; 2003-492274/46.

XX DR N-PSDB; ACD82214.

XX PT New transmembrane polypeptides and nucleic acids encoding the
XX PT polypeptides, useful in gene therapy, in chromosome identification, as
XX PT chromosome markers, or in generating probes.

XX PS Claim 19; Fig 78; 315pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
XX polypeptide. Nucleic acids that encode PRO can be used to generate either
XX transgenic animals or knock-out animals useful in developing and
XX screening of therapeutically useful reagents. The nucleic acids may also
XX be used in gene therapy for replacing defective gene, in chromosome
XX identification, as chromosome markers, or in generating probes to isolate
XX full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
XX stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
XX and for detecting the presence of tumour in a mammal. The PRO
XX polypeptides are useful as molecular markers for protein electrophoresis
XX and the isolated nucleic acids may be used for recombinantly expressing
XX those markers. The PRO polypeptides and nucleic acids may also be used in

CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The present sequence represents the amino acid sequence
CC of a human secreted/transmembrane PRO polypeptide

XX SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
|||||
Db 144 HLPGNKSPHRDPAPR 158

RESULT 15

ADA37038
ID ADA37038 standard; protein; 208 AA.

XX AC ADA37038;

XX DT 20-NOV-2003 (first entry)

XX DE Human fibroblast growth factor 21 SEQ ID NO:1.

XX KW mortality; morbidity; fibroblast growth factor 21; FGF-21;
XX KW antiinflammatory; respiratory; antibacterial; immunosuppressive;
XX KW vasotropic; haemostatic; nephrotropic; glucose level regulator;
XX KW glucose uptake stimulator; insulin sensitivity enhancer;
XX KW systemic inflammatory response syndrome; respiratory distress;
XX KW acute lung injury; acute respiratory distress syndrome;
XX KW multiple organ dysfunction syndrome; sepsis;
XX KW chronic obstructive pulmonary disease; emphysema; chronic bronchitis;
XX KW pancreatitis; ischaemia; multiple trauma; tissue injury; shock; renal failure.
XX KW haemorrhagic shock; immune-mediated organ injury; shock; renal failure.

XX OS Homo sapiens.

XX FN WO2003059270-A2.

XX PD 24-JUL-2003.

XX PF 08-JAN-2003; 2003WO-US000010.

XX PR 15-JAN-2002; 2002US-0348890P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Heuer JG, Kharitonov A;

XX DR WPI; 2003-618118/58.

XX PT Use of fibroblast growth factor 21 for reduction of mortality and
XX PT morbidity in patients suffering from e.g. systemic inflammatory response
XX PT syndrome and acute respiratory distress syndrome.

XX PS Disclosure; Page 15-16; 22pp; English.

XX The present invention describes a method for the reduction of mortality
XX and morbidity in critically ill patients, which involves the
XX administration of fibroblast growth factor 21 (FGF-21) (I). (I) has
XX antiinflammatory, respiratory, antibacterial, immunosuppressive,
XX vasotropic, haemostatic and nephrotropic activities, and can be used as a
XX glucose level regulator, a glucose uptake stimulator, and an insulin
XX sensitivity enhancer. (I) can be used in the manufacture of a medicament
XX for the reduction of morbidity and mortality in critically ill patients
XX suffering from systemic inflammatory response syndrome (SIRS),
XX respiratory distress, acute lung injury, acute respiratory distress
XX syndrome, multiple organ dysfunction syndrome, sepsis and chronic
XX obstructive pulmonary disease (e.g. emphysema, and chronic bronchitis).
XX The SIRS includes pancreatitis, ischaemia, multiple trauma and tissue
XX injury, haemorrhagic shock, immune-mediated organ injury, shock and renal

CC failure. FGF-12 regulates glucose levels in response to nutrient
CC digestion; affects the overall metabolic state and counter-acts negative
CC side effects that occur during the body's stress response to sepsis;
CC reduces morbidity and mortality that occurs in critically ill patients;
CC and stimulates glucose uptake and enhances insulin sensitivity. The
CC present sequence represents the human FGF-21 amino acid sequence, which
CC is given in the exemplification of the present invention.
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158
|||||
RESULT 16
ID ABJ72096 standard; protein; 208 AA.
XX
AC ABJ72096;
XX
DT 16-OCT-2003 (first entry)
XX
DE Human membrane bound receptor/protein PRO10196 amino acid sequence.
XX
KW Human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN US2003065147-A1.
XX
PD 03-APR-2003.
XX
PF 29-AUG-2002; 2002US-00232224.
XX
PR 28-JUL-1999; 99US-0146222P.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-522018/49.
DR N-PSDB; ABT43920.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX Claim 11; Fig 78; 315pp; English.
XX
CC This invention relates to one hundred and twenty two novel nucleic acids
CC encoding human PRO membrane bound proteins or receptors. Extracellular
CC proteins play important roles in the formation, differentiation and
CC maintenance of multicellular organisms. The fate of many individual cells
CC (for example proliferation, migration or differentiation) is typically
CC governed by information received from other cells and the immediate
CC environment. The information is often transmitted by secreted
CC polypeptides (for example mitogenic factors, survival factors, cytotoxic
CC factors, differentiation factors, neurotrophic and hormones) which are

CC received and interpreted by diverse cell receptors or membrane bound
CC proteins. These membrane bound proteins and receptors may be of use as
CC pharmaceutical and diagnostic agents, such as in the blocking of receptor
CC -ligand interactions. The current invention provides the amino acid
CC sequences of novel human membrane bound receptors and proteins, along
CC with the cDNA sequences encoding them. The novel proteins of the
CC invention may have cytostatic activities through the stimulation of
CC chondrocytes. The nucleic acids of the invention may be useful for the
CC manufacture of a medicament for diagnosing or treating a tumour in a
CC mammal. In addition, they may be useful for measuring or detecting the
CC expression of a tumour associated gene. The present sequence is the amino
CC acid sequence of a human PRO protein of the invention
XX
SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 144 HLPGNKSPHRDPAPR 158
|||||
RESULT 17
ID ADB83568 standard; protein; 208 AA.
XX
AC ADB83568;
XX
DT 04-DEC-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10196.
XX
KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
KW antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN US2003073814-A1.
XX
PD 17-APR-2003.
XX
PF 12-AUG-2002; 2002US-00218849.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX WPI; 2003-644806/61.
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-644806/61.
DR N-PSDB; ADB83567.
XX
PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
PT in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.
XX
PS Claim 11; Fig 78; 315pp; English.
XX
CC The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in

pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1192, PRO1244, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1279, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567, PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322, PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15

Db 144 HLPGNKSPHRDPAPR 158

RESULT 18
ADB80674

ID ADB80674 standard; protein; 208 AA.

AC ADB80674;

DT 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

Human; secreted and transmembrane protein; PRO; cytostatic; vulnary; antiarthritic; pericyte cell proliferation;
KW pericyte cell differentiation; chondrocyte cell proliferation;
KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
KW (TNF)-alpha release; dermal fibroblast cell proliferation;
KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; tissue typing; chromosome mapping; gene mapping;
gene therapy.

XX Homo sapiens.

XX US2003088068-A1.

XX 08-MAY-2003.

XX 13-AUG-2002; 2002US-00219481.

XX 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
DR N-PSDB; ADB80673.

XX WPI; 2003-657982/62.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or as
PT hybridization probes in chromosome and gene mapping.

PS Claim 11; Fig 78; 305pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
CC useful for stimulating the proliferation of or gene expression in
CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
CC are useful for stimulating the release of tumour necrosis factor (TNF)-
CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
CC PRO1025, PRO1181, PRO1126, PRO1192, PRO1244, PRO1274, PRO1412,
CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1279, PRO1340, PRO1338,
CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
CC stimulating the proliferation of normal human dermal fibroblasts cells.
CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
CC are useful for detecting the presence of tumour in a mammal which
CC involves comparing the level of expression of the above PRO polypeptides
CC in a test sample of cells taken from the mammal, and a control sample of
CC normal cells of the same cell type, where a higher level of expression of
CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
Best Local Similarity 100.0%; Pred. No. 9.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15

Db 144 HLPGNKSPHRDPAPR 158

RESULT 19
ADB73215

ID ADB73215 standard; protein; 208 AA.

XX ADB73215;

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003096968-A1.
 XX
 XX 22-MAY-2003.
 XX
 XX 29-AUG-2002; 2002US-00232223.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-765525/72.
 DR N-PSDB; ADB73214.
 XX
 XX New isolated PRO polypeptides useful as molecular weight markers in
 PT protein electrophoresis, useful for tissue typing, and for treating
 PT arthritis and tumors.
 XX
 XX Claim 11; Fig 78; 308pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO363, PRO531, PRO1083, PRO840, PRO214,
 CC PRO247, PRO337, PRO526, PRO357, PRO725, PRO1306, PRO1419, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9840, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

SQ Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 - Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 20
 ADB78297
 ID ADB78297 standard; protein; 208 AA.
 XX
 XX ADB78297;
 AC
 XX 04-DEC-2003 (first entry)
 DT
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 PN US2003092889-A1.
 XX
 XX 15-MAY-2003.
 XX
 XX 13-AUG-2002; 2002US-00219478.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2003-765495/72.
 DR N-PSDB; ADB78296.
 XX
 XX New isolated PRO polypeptide useful for tissue typing, gene therapy, as
 PT molecular weight markers in protein electrophoresis, and for treating
 PT arthritis and tumors.
 XX
 XX Claim 11; Fig 78; 308pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO363, PRO531, PRO1083, PRO840, PRO214,
 CC PRO247, PRO337, PRO526, PRO357, PRO725, PRO1306, PRO1419, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9840, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.

CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (III) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158

RESULT 21
 ADB84945
 ID ADB84945 standard; protein; 208 AA.

AC ADB84945;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.

XX Homo sapiens.

XX US2003073817-A1.

XX PD 17-APR-2003.

XX PF 26-AUG-2002; 2002US-00227883.

XX PR 01-AUG-2000; 2000US-0222425P.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;

XX DR WPI; 2003-730024/69.

XX DR N-PSDB; ADB84944.

XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 FT e.g. in gene therapy, disease diagnosis, chromosome identification and
 PT tissue typing.

XX Claim 11; Fig 78; 314pp; English.

XX The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.

XX SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158

RESULT 22
 ADB78051

ID ADB78051 standard; protein; 208 AA.

AC ADB78051;

XX
 DT 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.

XX US2003092886-A1.

XX PD 15-MAY-2003.

XX PF 09-AUG-2002; 2002US-00216165.

XX PR 25-JUL-2000; 2000US-0220607P.

XX PR 01-JUN-2001; 2001WO-US017800.

XX PR 29-JUN-2001; 2001WO-US021066.

XX PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-765494/72.
 DR N-PSDB; ADB78050.
 XX
 PT Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as
 PT molecular weight markers in protein electrophoresis, for treating
 PT arthritis, tumor.
 XX
 PS Claim 11; Fig 78; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1328, PRO1341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 CC Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 23
 ADB87117
 ID ADB87117 standard; protein; 208 AA.
 XX
 AC ADB87117;
 DT 04-DEC-2003 (first entry)
 XX
 DE Human PRO polypeptide #39.
 XX
 KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.

XX Homo sapiens.
 OS US2003088067-A1.
 XX
 PN 08-MAY-2003.
 XX
 PD 13-AUG-2002; 2002US-00219479.
 PF
 XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-657981/52.
 DR N-PSDB; ADB87116.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX
 PS Claim 11; Fig 78; 314pp; English.
 XX
 CC The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.
 XX
 CC Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 24
 ADB84699
 ID ADB84699 standard; protein; 208 AA.
 XX
 AC ADB84699;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human PRO polypeptide #39.
 XX

KW Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 XX US2003092890-A1.
 XX
 XX 15-MAY-2003.
 XX
 XX 14-AUG-2002; 2002US-00219536.
 XX
 XX 28-JUL-1999; 99US-0146222P.
 XX
 XX 24-FEB-2000; 2000WO-US005004.
 XX
 XX 02-MAR-2000; 2000WO-US005841.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 XX
 XX 29-JUN-2001; 2001WO-US021086.
 XX
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-777259/73.
 XX
 XX N-PSDB; ADB84698.
 XX
 XX New isolated PRO polypeptides, useful for tissue typing, gene therapy, as
 XX molecular weight markers in protein electrophoresis, and for treating
 XX arthritis and tumors.
 XX
 XX Claim 11; Fig 78; 308pp; English.
 XX
 XX The invention relates to human PRO polypeptides (secreted and
 XX transmembrane polypeptides) and the PRO polynucleotides encoding them.
 XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 XX diagnostics, biosensors or bioreactors. They are particularly useful for
 XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 XX prostate tumour, rectal tumour or liver tumour) in a mammal, for
 XX stimulating the release of tumour necrosis factor (TNF)-alpha from human
 XX blood, for stimulating the proliferation or differentiation of
 XX chondrocyte cells, for stimulating the proliferation of or gene
 XX expression in pericyte cells or for stimulating the proliferation of
 XX normal human dermal fibroblasts. The PRO nucleic acids are useful as
 XX hybridisation probes, in chromosome and gene mapping, in generating
 XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 XX technology, in generating transgenic animals or knock-out animals which
 XX may be used in the development and screening of therapeutically useful
 XX reagents, in gene therapy, in chromosome identification, as chromosome
 XX markers and in generating probes. The PRO polypeptides, or anti-PRO
 XX antibodies, are useful for preparing a medicament for treating a
 XX condition which is responsive to the PRO polypeptides or anti-PRO
 XX antibodies, such as pericyte-associated tumours and bone and/or cartilage
 XX disorders (e.g. arthritis, sports injuries), involving inducing the re-
 XX differentiation of chondrocytes. The PRO polypeptides are useful as
 XX molecular markers for protein electrophoresis, and in tissue typing. This
 XX sequence represents a human PRO polypeptide of the invention.
 XX
 XX Sequence 208 AA;
 XX
 XX Query Match 100.0%; Score 89; DB 7; Length 208;
 XX Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 HLPGNKSPHRDPAPR 15
 XX |||||
 XX DB 144 HLPGNKSPHRDPAPR 158
 XX
 XX RESULT 25
 XX ADB83814

ID ADB83814 standard; protein; 208 AA.
 XX
 XX ADB83814;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10196.
 XX
 XX human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US2003069397-A1.
 XX
 XX 10-APR-2003.
 XX
 XX 09-AUG-2002; 2002US-00216159.
 XX
 XX 25-JUL-2000; 2000US-0220607P.
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 XX
 XX 29-JUN-2001; 2001WO-US021066.
 XX
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 XX WPI; 2003-657584/62.
 XX
 XX N-PSDB; ADB83813.
 XX
 XX New isolated polypeptides designated PRO polypeptides including
 XX polypeptides useful for stimulating the proliferation or differentiation
 XX of specific cell types, and for diagnosing cancer.
 XX
 XX Claim 11; Fig 78; 314pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 XX useful for stimulating the proliferation of or gene expression in
 XX pericyte cells. PRO357, PRO1272 or PRO4405 polypeptide are useful
 XX for stimulating the proliferation or differentiation of chondrocyte
 XX cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 XX are useful for stimulating the release of tumour necrosis factor (TNF)-
 XX alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 XX PRO247, PRO337, PRO526, PRO531, PRO1083, PRO840, PRO1080,
 XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 XX PRO1025, PRO1181, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 XX PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1338,
 XX PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1317, PRO1760, PRO1567,
 XX PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4344, PRO4322,
 XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 XX stimulating the proliferation of normal human dermal fibroblasts cells.
 XX PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 XX PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 XX polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 XX are useful for detecting the presence of tumour in a mammal which
 XX involves comparing the level of expression of the above PRO polypeptides
 XX in a test sample of cells taken from the mammal, and a control sample of
 XX normal cells of the same cell type, where a higher level of expression of
 XX the PRO polypeptides in the test sample as compared to the control sample
 XX is indicative of the presence of tumour in the mammal. The tumour is lung
 XX tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 XX liver tumour. (I) is useful as molecular weight markers, for tissue

CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

SQ Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158

RESULT 26

ADB72969
 ID ADB72969 standard; protein; 208 AA.

XX ADB72969;

XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 XX antiarthritic; pericyte cell proliferation;
 XX pericyte cell differentiation; chondrocyte cell proliferation;
 XX (TNF)-alpha release; dermal fibroblast cell proliferation;
 XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 XX colon tumour; breast tumour; prostate tumour; rectal tumour;
 XX liver tumour; tissue typing; chromosome mapping; gene mapping;
 XX gene therapy.

XX Homo sapiens.

XX US2003092887-A1.

XX 15-MAY-2003.

XX 12-AUG-2002; 2002US-00218956.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-777258/73.

XX N-PSDB; ADB72969.

XX Novel isolated PRO polypeptide useful for tissue typing, gene therapy, as
 XX molecular weight markers, for treating arthritis, tumor.

XX Claim 11; Fig 78; 308pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,

CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7114, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158

RESULT 27

ADC36807

ID ADC36807 standard; protein; 208 AA.

XX ADC36807;

XX 18-DEC-2003 (first entry)

XX Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 XX cancer; lung; colon; breast; prostate; rectum; liver;
 XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 XX arthritis; sports injury; cytostatic; antiarthritic.

XX Homo sapiens.

XX US2003088065-A1.

XX 08-MAY-2003.

XX 14-AUG-2002; 2002US-00219464.

XX 01-JUN-2001; 2001WO-US017800.

XX 29-JUN-2001; 2001WO-US021066.

XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-657979/62.

XX N-PSDB; ADC36806.

PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, or for preparing a medicament for treating
 PT cancer.
 XX
 XX Claim 11; Fig 78; 315pp; English.
 XX
 CC The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.
 XX
 SQ Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 Db 144 HLPGNKSPHRDPAPR 158
 RESULT 28
 ID ADC21797
 AC ADC21797;
 XX
 XX 18-DEC-2003 (first entry)
 DT Human PRO polypeptide #39.
 DE
 DE Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;
 KW cancer; lung; colon; breast; prostate; rectum; liver;
 KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;
 KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;
 KW arthritis; sports injury; cytostatic; antiarthritic.
 XX
 OS Homo sapiens.
 XX
 XX US2003096969-A1.
 XX
 XX 22-MAY-2003.
 XX
 XX 29-AUG-2002; 2002US-00232225.
 XX
 XX 02-JUN-2000; 2000WO-US015264.
 XX
 XX 05-JUN-2000; 2000US-0209832P.
 XX
 XX 20-JUN-2000; 2000US-0212901P.
 XX
 XX 22-JUN-2000; 2000US-0213807P.
 XX
 XX 20-JUL-2000; 2000US-0219556P.
 XX
 XX 25-JUL-2000; 2000US-0220585P.
 XX
 XX 25-JUL-2000; 2000US-0220605P.

PR 25-JUL-2000; 2000US-0220607P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220638P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 25-JUL-2000; 2000US-0220666P.
 PR 26-JUL-2000; 2000US-0220893P.
 PR 01-AUG-2000; 2000US-0222435P.
 PR 22-AUG-2000; 2000US-0227133P.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 28-NOV-2000; 2000US-0253646P.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Deanoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-765526/72.
 DR N-PSDB; ADC21796.
 XX
 PT Novel isolated PRO polypeptide useful for tissue typing, as molecular
 PT weight markers in protein electrophoresis, for treating arthritis, tumor.
 XX
 XX Claim 11; Fig 78; 308pp; English.
 XX
 CC The invention relates to human PRO polypeptides (secreted and
 CC transmembrane polypeptides) and the PRO polynucleotides encoding them.
 CC The PRO polypeptides and polynucleotides are useful as pharmaceuticals,
 CC diagnostics, biosensors or bioreactors. They are particularly useful for
 CC detecting tumours (e.g. lung tumour, colon tumour, breast tumour,
 CC prostate tumour, rectal tumour or liver tumour) in a mammal, for
 CC stimulating the release of tumour necrosis factor (TNF)-alpha from human
 CC blood, for stimulating the proliferation or differentiation of or gene
 CC chondrocyte cells, for stimulating the proliferation of or gene
 CC expression in pericyte cells or for stimulating the proliferation of
 CC normal human dermal fibroblasts. The PRO nucleic acids are useful as
 CC hybridisation probes, in chromosome and gene mapping, in generating
 CC antisense RNA and DNA, in preparing PRO polypeptides by recombinant
 CC technology, in generating transgenic animals or knock-out animals which
 CC may be used in the development and screening of therapeutically useful
 CC reagents, in gene therapy, in chromosome identification, as chromosome
 CC markers and in generating probes. The PRO polypeptides, or anti-PRO
 CC antibodies, are useful for preparing a medicament for treating a
 CC condition which is responsive to the PRO polypeptides or anti-PRO
 CC antibodies, such as pericyte-associated tumours and bone and/or cartilage
 CC disorders (e.g. arthritis, sports injuries), involving inducing the re-
 CC differentiation of chondrocytes. The PRO polypeptides are useful as
 CC molecular markers for protein electrophoresis, and in tissue typing. This
 CC sequence represents a human PRO polypeptide of the invention.
 XX
 XX Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 Db 144 HLPGNKSPHRDPAPR 158
 RESULT 29
 ID ADC49828
 ID ADC49828 standard; protein; 208 AA.

XX AC ADC49828;
 XX CC
 XX CC
 XX DT 18-DEC-2003 (first entry)
 XX DE
 XX DE Novel human secreted and transmembrane protein PRO10196.
 XX KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 XX KW antiarthritic; pericyte cell proliferation;
 XX KW chondrocyte cell differentiation; chondrocyte cell proliferation;
 XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 XX KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 XX KW gene therapy.
 XX OS Homo sapiens.
 XX OS
 XX PN US2003088064-A1.
 XX CC
 XX PD 08-MAY-2003.
 XX CC
 XX PF 14-AUG-2002; 2002US-00219075.
 XX CC
 XX PR 25-JUL-2000; 2000US-0220605P.
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX CC
 XX PA (GETH) GENENTECH INC.
 XX CC
 XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX PI WPI; 2003-801154/75.
 XX DR N-PSDB; ADC49827.
 XX CC
 XX PT New secreted and transmembrane PRO polypeptide useful for preparing a
 XX PT medicament for treating a condition that is responsive to the PRO
 XX PT polypeptide or anti-PRO antibody, e.g. cancer.
 XX CC
 XX PS Claim 11; SEQ ID NO 78; 314pp; English.
 XX CC
 XX CC The invention describes an isolated PRO (secreted and transmembrane)
 XX CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 XX CC useful for stimulating the proliferation of or gene expression in
 XX CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 XX CC for stimulating the proliferation or differentiation of chondrocyte
 XX CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 XX CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 XX CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 XX CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 XX CC PRO1478, PRO1134, PRO826, PRO1005, PRO609, PRO1071, PRO1411, PRO1309,
 XX CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 XX CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 XX CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 XX CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 XX CC PRO940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 XX CC stimulating the proliferation of normal human dermal fibroblasts cells.
 XX CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 XX CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 XX CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 XX CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 XX CC are useful for detecting the presence of tumour in a mammal which
 XX CC involves comparing the level of expression of the above PRO polypeptides
 XX CC in a test sample of cells taken from the mammal, and a control sample of
 XX CC normal cells of the same cell type, where a higher level of expression of
 XX CC the PRO polypeptides in the test sample as compared to the control sample
 XX CC is indicative of the presence of tumour in the mammal. The tumour is lung
 XX CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 XX CC liver tumour. (I) is useful as molecular weight markers, for tissue
 XX CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is

CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX SQ Sequence 208 AA;
 XX CC
 XX CC Query Match 100.0%; Score 89; DB 7; Length 208;
 XX CC Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 XX CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX CC
 XX QY 1 HLPGNKSPHRDPAPR 15
 XX DB 144 HLPGNKSPHRDPAPR 158
 XX CC
 XX CC RESULT 30
 XX CC ADC49027
 XX ID ADC49027 standard; protein; 208 AA.
 XX CC
 XX AC ADC49027;
 XX CC
 XX DT 18-DEC-2003 (first entry)
 XX CC
 XX DE Novel human secreted and transmembrane protein PRO10196.
 XX KW human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 XX KW antiarthritic; pericyte cell proliferation;
 XX KW chondrocyte cell differentiation; chondrocyte cell proliferation;
 XX KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 XX KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 XX KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 XX KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 XX KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 XX KW gene therapy.
 XX OS Homo sapiens.
 XX OS
 XX PN US2003088070-A1.
 XX CC
 XX PD 08-MAY-2003.
 XX CC
 XX PF 28-AUG-2002; 2002US-00230260.
 XX CC
 XX PR 01-JUN-2001; 2001WO-US017800.
 XX PR 29-JUN-2001; 2001WO-US021066.
 XX PR 09-APR-2002; 2002US-00119480.
 XX CC
 XX PA (GETH) GENENTECH INC.
 XX CC
 XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX PI WPI; 2003-801155/75.
 XX DR N-PSDB; ADC49026.
 XX CC
 XX PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 XX PT in gene therapy, chromosome identification, tissue typing, or as
 XX PT hybridization probes in chromosome and gene mapping.
 XX CC
 XX PS Claim 11; SEQ ID NO 78; 315pp; English.
 XX CC
 XX CC The invention describes an isolated PRO (secreted and transmembrane)
 XX CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 XX CC useful for stimulating the proliferation of or gene expression in
 XX CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 XX CC for stimulating the proliferation or differentiation of chondrocyte
 XX CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 XX CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 XX CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 XX CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,

CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1387, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1328, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO3940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 Db |||||
 144 HLPGNKSPHRDPAPR 158
 RESULT 31
 ADC49544
 ID ADC49544 standard; protein; 208 AA.
 AC ADC49544;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 KW human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003088071-A1.
 XX
 XX 08-MAY-2003.
 XX
 PF 29-AUG-2002; 2002US-00232231.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI

PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2003-801156/75.
 DR N-PSDB; ADC49543.
 XX
 PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 PT in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX
 PS Claim 11; SEQ ID NO 78; 315pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 Db |||||
 144 HLPGNKSPHRDPAPR 158
 RESULT 32
 ADC47405
 ID ADC47405 standard; protein; 208 AA.
 XX
 XX ADC47405;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003088071-A1.
 XX
 XX 08-MAY-2003.
 XX
 PF 29-AUG-2002; 2002US-00232231.
 XX
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI

KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US2003088072-A1.
 XX
 XX 08-MAY-2003.
 XX
 XX 29-AUG-2002; 2002US-00232233.
 XX
 XX 25-JUL-2000; 2000US-0220605P.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI N-PSDB; ADC47404.
 DR WPI; 2003-801157/75.
 DR N-PSDB; ADC47404.
 XX
 XX New PRO polypeptide for use as molecular weight markers for protein
 PT electrophoresis purposes and for detecting the presence of tumor in a
 PT mammal.
 XX
 XX Claim 11; Fig 78; 314pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF) -
 CC alpha from human blood. PRO982, PRO357, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1387, PRO1409, PRO1474, PRO1760, PRO1567,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1517, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 SQ Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 ID |||||
 DB 144 HLPGNKSPHRDPAPR 158
 RESULT 33
 ADC47150
 ID ADC47150 standard; protein; 208 AA.
 XX
 XX ADC47150;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10196.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; vulnery;
 KW antiarthritic; pericyte cell proliferation; chondrocyte cell proliferation;
 KW pericyte cell differentiation; tumour necrosis factor alpha release;
 KW chondrocyte cell differentiation; dermal fibroblast cell proliferation;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX US2003105288-A1.
 PN
 XX 05-JUN-2003.
 PD
 XX
 XX 13-AUG-2002; 2002US-00219070.
 PF
 XX
 XX 25-JUL-2000; 2000US-0220666P.
 PR
 XX 01-JUN-2001; 2001WO-US017800.
 PR
 XX 29-JUN-2001; 2001WO-US021066.
 PR
 XX 09-APR-2002; 2002US-00119480.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 PI N-PSDB; ADC47149.
 DR WPI; 2003-801246/75.
 DR N-PSDB; ADC47149.
 XX
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 PT as a hybridization probe, and in gene therapy.
 XX
 XX Claim 11; Fig 78; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF) -
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1387, PRO1409, PRO1474, PRO1517, PRO1760, PRO1567,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1517, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,

SQ Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 35
 ADD06260
 ID ADD06260 standard; protein; 208 AA.
 XX
 XX ADD06260;
 XX
 XX
 DT 01-JAN-2004 (first entry)
 XX
 XX Novel human secreted and transmembrane protein PRO10196.
 XX human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 XX antarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF) alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX US2003073816-A1.
 PN
 XX
 XX
 PD 17-APR-2003.
 XX
 XX 26-AUG-2002; 2002US-00227873.
 PF

XX 01-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 FI
 XX WPI; 2003-644807/61.
 DR N-PSDB; ADD06259.
 XX
 XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 PT in gene therapy, chromosome identification, tissue typing, or as
 PT hybridization probes in chromosome and gene mapping.
 XX
 XX Claim 11; SEQ ID NO 78; 314pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1186, PRO1192, PRO1244, PRO1274, PRO1309,
 CC PRO1025, PRO1181, PRO126, PRO1105, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO126, PRO1105, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4344, PRO4332,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for generating transgenic animals or knock-out animals which are useful
 CC for screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 36
 ADC77779
 ID ADC77779 standard; protein; 208 AA.
 XX
 XX ADC77779;
 AC
 XX 01-JAN-2004 (first entry)
 DT

XX DE
 XX
 XX Human; secreted and transmembrane protein PRO10196.
 KW antiarthritic; pericyte cell proliferation;
 KW chondrocyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 XX Homo sapiens.
 OS
 XX
 XX US2003088066-A1.
 FN
 XX
 XX 08-MAY-2003.
 PD
 XX
 XX 13-AUG-2002; 2002US-00219466.
 PF
 XX
 XX 01-JUN-2001; 2001WO-US017800.
 PR
 XX 29-JUN-2001; 2001WO-US021066.
 PR
 XX 09-APR-2002; 2002US-00119480.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 FI
 XX WPI; 2003-657980/62.
 DR N-PSDB; ADC77778.
 DR
 XX
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful in gene therapy, or for preparing a medicament for treating a
 PT condition that is responsive to the PRO polypeptide or anti-PRO antibody,
 PT e.g. cancer.
 PT
 XX Claim 11; Fig 78; 314pp; English.
 XX
 XX The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1186, PRO1192, PRO1244, PRO1274, PRO1309,
 CC PRO1025, PRO1181, PRO126, PRO1105, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO126, PRO1105, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4344, PRO4332,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for generating transgenic animals or knock-out animals which are useful
 CC for screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 XX Sequence 208 AA;
 SQ
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158
 |||||
 RESULT 36
 ADC77779
 ID ADC77779 standard; protein; 208 AA.
 XX
 XX ADC77779;
 AC
 XX 01-JAN-2004 (first entry)
 DT

CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 SQ Sequence 208 AA;
 Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPAPR 15
 Db 144 HLPGNKSPHRDPAPR 158
 RESULT 37
 ADD50742
 ID ADD50742 standard; protein; 208 AA.
 AC ADD50742;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Novel human secreted and transmembrane protein PRO10196.
 XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2003105291-A1.
 XX
 PD 05-JUN-2003.
 XX
 PF 26-AUG-2002; 2002US-0027877.
 XX
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-APR-2002; 2002US-00119480.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-829361/77.
 DR N-PSDB; ADD50741.
 XX
 PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 PT as a hybridization probe, and in gene therapy.
 XX
 PS Claim 11; Fig 78; 308pp; English.
 XX
 CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO357, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO4344, PRO4322,

CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptide
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (I) is useful as molecular weight markers, for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
 CC useful for chromosome and gene mapping or gene therapy. (II) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.
 XX
 SQ Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 Db 144 HLPGNKSPHRDPAPR 158

RESULT 38

ADD50988
 ID ADD50988 standard; protein; 208 AA.

AC ADD50988;

XX
 DT 15-JAN-2004 (first entry)

XX Novel human secreted and transmembrane protein PRO10196.

XX Human; secreted and transmembrane protein; PRO; cytostatic; vulnerary;
 KW antiarthritic; pericyte cell proliferation;
 KW pericyte cell differentiation; chondrocyte cell proliferation;
 KW chondrocyte cell differentiation; tumour necrosis factor alpha release;
 KW (TNF)-alpha release; dermal fibroblast cell proliferation;
 KW dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
 KW colon tumour; breast tumour; prostate tumour; rectal tumour;
 KW liver tumour; tissue typing; chromosome mapping; gene mapping;
 KW gene therapy.

XX Homo sapiens.

XX US2003105290-A1.

XX 05-JUN-2003.

XX 13-AUG-2002; 2002US-00219527.

XX 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI: 2003-829360/77.
 DR N-PSDB; ADD50987.

PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide (PRO), for use in recombinantly producing a PRO polypeptide,
 PT as a hybridization probe, and in gene therapy.

PS Claim 11; Fig 78; 309pp; English.

CC The invention describes an isolated PRO (secreted and transmembrane)
 CC polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
 CC useful for stimulating the proliferation of or gene expression in
 CC pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
 CC for stimulating the proliferation or differentiation of chondrocyte
 CC cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide
 CC are useful for stimulating the release of tumour necrosis factor (TNF)-
 CC alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214,
 CC PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
 CC PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
 CC PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1274, PRO1412,
 CC PRO1286, PRO1330, PRO1347, PRO1305, PRO1279, PRO1340, PRO1338,
 CC PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1760, PRO1567,
 CC PRO1887, PRO1928, PRO4341, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
 CC PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
 CC stimulating the proliferation of normal human dermal fibroblasts cells.
 CC PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
 CC PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
 CC inhibiting the proliferation of normal human dermal fibroblast cells. PRO
 CC polypeptides such as PRO6004, PRO4981, PRO7174, PRO5778, PRO4332, etc.,
 CC are useful for detecting the presence of tumour in a mammal which
 CC involves comparing the level of expression of the above PRO polypeptides
 CC in a test sample of cells taken from the mammal, and a control sample of
 CC normal cells of the same cell type, where a higher level of expression of
 CC the PRO polypeptides in the test sample as compared to the control sample
 CC is indicative of the presence of tumour in the mammal. The tumour is lung
 CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. (i) is useful as molecular weight markers for tissue
 CC typing, or as therapeutic agents. A polynucleotide (II) encoding (i) is
 CC useful for chromosome and gene mapping or gene therapy. (ii) is useful
 CC for generating transgenic animals or knock-out animals which are useful
 CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
 CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
 CC sport injuries). This is the amino acid sequence of a human secreted and
 CC transmembrane PRO polypeptide.

XX Sequence 208 AA;

Query Match 100.0%; Score 89; DB 7; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.2e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 |||||
 Db 144 HLPGNKSPHRDPAPR 158

RESULT 39

ADD50469

ID ADD50469 standard; protein; 208 AA.

XX ADD50469;

XX 15-JAN-2004 (first entry)

DT Human PRO polypeptide #39.

DE Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;

KW cancer; lung; colon; breast; prostate; rectum; liver;

KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;

KW pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;

KW arthritis; sports injury; cytostatic; antiarthritic.

OS Homo sapiens.

XX US2003096971-A1.

PN

XX

PD 22-MAY-2003.

PF 29-AUG-2002; 2002US-00232229.

XX 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

PA Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PV;

XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;

PI WPI; 2003-765528/72.

XX N-PSDS; ADD50468.

DR Novel isolated PRO polypeptide useful for tissue typing, as molecular

XX weight markers in protein electrophoresis, for treating arthritis, tumor.

XX Claim 11; Fig 78; 308pp; English.

XX The invention relates to human PRO polypeptides (secreted and

XX transmembrane polypeptides) and the PRO polynucleotides encoding them.

XX The PRO polypeptides and polynucleotides are useful as pharmaceuticals,

XX diagnostics, biosensors or bioreactors. They are particularly useful for

XX detecting tumours (e.g. lung tumour, colon tumour, breast tumour,

XX prostate tumour, rectal tumour or liver tumour) in a mammal, for

XX stimulating the release of tumour necrosis factor (TNF)-alpha from human

XX blood, for stimulating the proliferation or differentiation of

XX chondrocyte cells, for stimulating the proliferation of or gene

XX expression in pericyte cells or for stimulating the proliferation of

XX normal human dermal fibroblasts. The PRO nucleic acids are useful as

XX hybridisation probes, in chromosome and gene mapping, in generating

XX antisense RNA and DNA, in preparing PRO polypeptides by recombinant

XX technology, in generating transgenic animals or knock-out animals which

XX may be used in the development and screening of therapeutically useful

XX reagents, in gene therapy, in chromosome identification, as chromosome

XX markers and in generating probes. The PRO polypeptides, or anti-PRO

XX antibodies, are useful for preparing a medicament for treating a

XX condition which is responsive to the PRO polypeptides or anti-PRO

XX antibodies, such as pericyte-associated tumours and bone and/or cartilage

XX disorders (e.g. arthritis, sports injuries), involving inducing the re-

XX differentiation of chondrocytes. The PRO polypeptides are useful as

XX molecular markers for protein electrophoresis, and in tissue typing. This

XX sequence represents a human PRO polypeptide of the invention.

XX

XX Sequence 208 AA;

XX Query Match 100.0%; Score 89; DB 7; Length 208;

XX Best Local Similarity 100.0%; Pred. No. 9.2e-05;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15

|||||

Db 144 HLPGNKSPHRDPAPR 158

RESULT 40

ADD50223

ID ADD50223 standard; protein; 208 AA.

XX ADD50223;

XX 15-JAN-2004 (first entry)

DT Human PRO polypeptide #39.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide; tumour;

XX cancer; lung; colon; breast; prostate; rectum; liver;

XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell;

XX pericyte cell; dermal fibroblast; bone disorder; cartilage disorder;

XX arthritis; sports injury; cytostatic; antiarthritic.

XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:51:17 ; Search time 1.4375 Seconds
(without alignments)
543.341 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	89	100.0	209	1 FGFL HUMAN	Q9nsa1 homo sapien
2	46	51.7	729	1 COA1 PAVP9	P33484 porcine par
3	46	51.7	729	1 COA1 PAVPK	P52501 porcine par
4	46	51.7	729	1 COA1 PAVPN	P18546 porcine par
5	45	50.6	689	1 CA29 HUMAN	Q14055 homo sapien
6	44.5	50.0	545	1 YB90 YEAST	P38346 saccharomyc
7	44	49.4	253	1 GX42 MOUSE	Q91xr9 mus musculu
8	44	49.4	253	1 GX42 RAT	Q91xr8 rattus norv
9	44	49.4	546	1 ELA3 HUMAN	Q8ng57 homo sapien
10	44	49.4	552	1 CSF1 MOUSE	Q07141 mus musculu
11	44	49.4	590	1 PYRG MYCLE	P53529 mycobacteri
12	44	49.4	1478	1 THO2 HUMAN	Q8ni27 homo sapien
13	43	48.3	407	1 KASB STRO	Q02062 streptomyce
14	43	48.3	410	1 HID DROME	Q24106 drosophila
15	43	48.3	573	1 AMH2 HUMAN	Q16571 homo sapien
16	43	48.3	1049	1 ADP1 YEAST	P25371 saccharomyc
17	42	47.2	382	1 MEI3 HUMAN	Q99887 homo sapien
18	42	47.2	457	1 BAG4 MOUSE	Q8ci61 mus musculu
19	42	47.2	475	1 ETS6 DROME	P29776 drosophila
20	42	47.2	520	1 IBMP CAMV	P03559 cauliflower
21	42	47.2	520	1 IBMP CAMVW	Q05651 cauliflower
22	42	47.2	522	1 IBMP CAMVD	P03557 cauliflower
23	42	47.2	522	1 IBMP CAMVJ	P13218 cauliflower
24	42	47.2	557	1 AMH2 RAT	Q62893 rattus norv
25	42	47.2	565	1 FXJ2 MOUSE	Q9ea18 mus musculu
26	42	47.2	793	1 NBEA CHICK	Q9ddd5 gallus gall
27	42	47.2	812	1 AXN2 BRARE	P57095 brachydanio
28	42	47.2	970	1 K852 HUMAN	Q9y8x9 homo sapien
29	42	47.2	2936	1 NBEA MOUSE	Q9epn1 mus musculu
30	42	47.2	2946	1 NBEA HUMAN	Q8nfp9 homo sapien
31	41.5	46.6	392	1 GAG BLVU	P25058 bovine leuk
32	41.5	46.6	392	1 GAG BLVU	P03344 bovine leuk
33	41	46.1	312	1 US10_HSV11	P06486 herpes simp

34	41	46.1	413	1 SVI CIOIN	Q94425 ciona intes
35	41	46.1	520	1 IBMP CAMV4	P22547 cauliflower
36	41	46.1	520	1 IBMP CAMVC	P03558 cauliflower
37	41	46.1	520	1 IBMP CAMVE	Q02954 cauliflower
38	41	46.1	520	1 IBMP CAMVN	Q00957 cauliflower
39	41	46.1	556	1 FLIF BUCAP	Q8ka45 buchnera ap
40	41	46.1	574	1 FXJ2 HUMAN	Q9p0k8 homo sapien
41	41	46.1	814	1 AD15 HUMAN	Q13444 homo sapien
42	40.5	45.5	342	1 RLPA_PSEAE	Q9x6v6 pseudomonas
43	40.5	45.5	525	1 CR24_SOYBN	Q49859 glycine max
44	40	44.9	103	1 NO12_MEDTR	P03365 medicago tr
45	40	44.9	112	1 NO75_PEA	P16329 pisum sativ

ALIGNMENTS

RESULT 1
FGFL HUMAN
ID FGFL HUMAN STANDARD; PRT; 209 AA.
AC Q9NSA1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibroblast growth factor-21 precursor (FGF-21) (UNQ3115/PRO10196).
GN FGF21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461777; PubMed=10858549;
RA Nishimura T., Nakatake Y., Konishi M., Itoh N.;
RT "Identification of a novel FGF, FGF-21, preferentially expressed in the liver.";
RL Biochim. Biophys. Acta 1492:203-206(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Gu Q., Hass P.E., Heldens S., Eaton D., Foster J., Grimaldi C., Gu Q., Johnson S., Lee J., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Schoenfeld J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand Z., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genome Res. 13:2285-2270(2003).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: Belongs to the heparin-binding growth factors family.
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CC -----
CC EMBL; AB021975; BAA99415.1; -;
CC EMBL; AY359086; AAQ89444.1; -;
CC HSSP; P03968; 1BAR.
CC Genew; HGNC:3678; FGF21.
CC GO; GO:0005576; C:extracellular; TAS.
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR008996; Cytok_IL1_like.

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DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF_1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; IL1_HBGF; 1.
DR SMART: SM00442; FGF_1.
DR PROSITE: PS00247; HBGF_FGF; FALSE_NEG.
KW Growth factor; Signal.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 209 FIBROBLAST GROWTH FACTOR-21.
FT CONFLICT 23 23 MISSING (IN REF. 2).
FT CONFLICT 23 23 MISSING (IN REF. 2).
SQ SEQUENCE 209 AA; 22300 MW; 27925C52A0023823 CRC64;

Query Match 100.0%; Score 89; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 145 HLPGNKSPHRDPAPR 159

RESULT 2
COAL_PAVP9
ID COAL_PAVP9 STANDARD; PRT; 729 AA.
AC P33484;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Coat protein VP1 [Contains: Coat protein VP2].
OS Porcine parvovirus (strain 90HS) [PPV].
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=33725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89319168; PubMed=2750278;
RA Sakurai M., Nishimori T., Ushimi C., Nakajima H.;
RT "Nucleotide sequence of capsid protein gene of porcine parvovirus.";
RL Virus Res. 13:79-86(1989).
CC -!- SUBUNIT: MATURE VIRION CONTAINS THREE CAPSID PROTEINS DESIGNATED
CC VPI, VP2, AND VP3 AND A NONCAPSID PROTEIN NS-1.
CC -!- MISCELLANEOUS: VP3 MIGHT BE A POSTTRANSLATIONAL CLEAVAGE PRODUCT
CC OF VP2 IN SEVERAL AUTONOMOUS PARVOVIRUSES.
CC -!- SIMILARITY: Belongs to the parvoviruses coat protein family.
CC
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CC
CC -----
DR EMBL: U44978; AAC40230.1; -
DR EMBL: U44978; AAC40231.1; -
DR HSP: P30129; 4DPV.
DR InterPro: IPR001403; Parvo_coat.
DR InterPro: IPR008975; Viral_cap_coat.
DR Pfam: PF00740; Parvo_coat; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 729 COAT PROTEIN VP1.
FT CHAIN 151 729 COAT PROTEIN VP2.
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 282 282 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 433 433 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 471 471 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 604 604 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 651 651 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 729 AA; 80935 MW; B6345BFA0568A1F6 CRC64;

Query Match 51.7%; Score 46; DB 1; Length 729;
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGKNSPHRDPAPR 15
Db 117 PGKSPGKRPAPR 129

RESULT 4
COAL_PAVPN
ID COAL_PAVPN STANDARD; PRT; 729 AA.
AC P18546; P22964; Q89816;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coat protein VP1 [Contains: Coat protein VP2].
OS Porcine parvovirus (strain NADL-2) [PPV].
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10797;
RN [1]
RP SEQUENCE FROM N.A.

```



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DR EMBL; AL050341; CAB81611.1; -.
DR EMBL; M95610; AAA80977.1; -.
DR Genew; HGNC:2218; COL9A2.
DR MIM; 120260; -.
DR MIM; 600204; -.
DR MIM; 603932; -.
DR GO; GO:0005594; C:collagen type IX; TAS.
DR GO; GO:0001501; P:skeletal development; TAS.
DR InterPro; IPR008161; C1g helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 9.
DR Prodom; PD000007; C1g helix; 1.
DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
DR Collagen; Signal; Glycoprotein; Proteoglycan; Disease mutation;
KW Polymorphism.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 689 COLLAGEN ALPHA 2(IX) CHAIN.
FT DOMAIN 27 163 TRIPLE-HELICAL REGION 1.
FT DOMAIN 164 180 NON-HELICAL REGION 1.
FT DOMAIN 181 519 TRIPLE-HELICAL REGION 2.
FT DOMAIN 520 549 NON-HELICAL REGION 2.
FT DOMAIN 550 632 TRIPLE-HELICAL REGION 3.
FT DOMAIN 633 634 TRIPLE-HELICAL REGION 3.
FT DOMAIN 635 664 TRIPLE-HELICAL REGION 4.
FT DOMAIN 665 689 NON-HELICAL REGION 4.
FT DISULFID 174 174 INTERCHAIN (POTENTIAL).
FT DISULFID 178 178 INTERCHAIN (POTENTIAL).
FT CARBOHYD 169 169 O-LINKED (GLYCOSAMINOGLYCAN) (BY
FT VARIANT 326 326 Q -> R.
FT VARIANT 326 326 /FTIG=VAR 012659.
FT VARIANT 326 326 Q -> W (in IDD; requires 2 nucleotide
FT SEQUENCE 689 AA; 65131 MW; EB6106E02F6FA862 CRC64;
substitutions).
Query Match 50.6%; Score 45; DB 1; Length 689;
Best Local Similarity 53.8%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 PGKSPHDPAPR 15
Db 567 PGKQPHGPGPR 579

RESULT 6
YB90 YEAST
ID YB90 YEAST STANDARD; PRT; 545 AA.
AC P38346;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 61.3 kDa protein in MRPL37-RIF1 intergenic region.
GN YB270C OR YB1738.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Aigle M., Baclet M.C., Barthe C., Biteau N., Crouzet M., Doignon F.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: STRONG, TO YEAST YJL058C.
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EMBL; Z36139; CAA85233.1; -.
DR PIR; S46151; S46151.
DR GerOnline; 138813; -.
DR SGD; S0000474; YBR270C.
KW Hypothetical protein.
SQ SEQUENCE 545 AA; 61301 MW; 5655D51206EF728B CRC64;

Query Match 50.0%; Score 44.5; DB 1; Length 545;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 HLPCKSPHDPAPR 15
Db 53 HLKTSKSPH-DAAPR 66

RESULT 7
GX42 MOUSE
ID GX42 MOUSE STANDARD; PRT; 253 AA.
AC Q91XR9; Q8K4U8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipid hydroperoxide glutathione peroxidase, nuclear
DE (EC 1.1.1.12) (GPX-4).
GN GPX4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Testis;
RX MEDLINE=21242617; PubMed=11344099;
RA Pfeiffer H., Conrad M., Roethlein D., Kyriakopoulos A., Briemeier M.,
RA Borikamm G.W., Behne D.;
RT "Identification of a specific sperm nuclei selenoenzyme necessary for
RT protamine thiol cross-linking during sperm maturation.";
RL FASEB J. 15:1236-1238(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ; TISSUE=Liver;
RA Imai H., Nakagawa Y.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22453509; PubMed=12566075;
RA Yant L.J., Ran Q., Rao L., Van Remmen H., Shibata T., Belter J.G.,
RA Motta L., Richardson A., Prolla T.A.;
RT "The selenoprotein GPX4 is essential for mouse development and
RT protects from radiation and oxidative damage insults.";
RL Free Radic. Biol. Med. 34:496-502(2003).
CC -!- FUNCTION: Could play a major role in protecting mammals from the
CC toxicity of ingested lipid hydroperoxides. Essential for embryonic
CC development. Protects from radiation and oxidative damage.
CC Stabilizes the condensed chromatin in sperm nuclei and is
CC necessary for male fertility.
CC -!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
CC glutathione + 2 H(2)O.
CC -!- COFACTOR: Selenocysteine. The active-site selenocysteine is
CC encoded by the opal codon, UGA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Nuclear;
CC IsoId=Q91XR9-1; Sequence=Displayed;
CC Name=Mitochondrial;
CC IsoId=O70325-1; Sequence=External;
CC -!- TISSUE SPECIFICITY: Expressed exclusively in sperm.
CC -!- SIMILARITY: Belongs to the glutathione peroxidase family.
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 CC -----
 CC EMBL; AF274027; AAK74112.1; -;
 CC EMBL; AB030643; BAC06509.1; -;
 CC MGD; MGI:104767; Gpx4.
 CC GO; GO:0005829; C:cytosol; IDA.
 CC GO; GO:0005739; C:mitochondrion; IDA.
 CC GO; GO:0005635; C:nuclear membrane; IDA.
 CC GO; GO:0004602; P:glutathione peroxidase activity; IDA.
 CC GO; GO:0006325; P:establishment and/or maintenance of chromatin; IDA.
 CC GO; GO:0007283; P:spermatogenesis; IDA.
 CC InterPro; IPR000889; Glut_peroxidase.
 CC Pfam; PF00255; GSHPx; 1.
 CC PRINTS; PR01011; GLUTPROXDASE.
 CC PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
 CC PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
 CC Oxidoreductase; Peroxidase;
 CC Developmental protein; Selenium; Selenocysteine;
 CC Nuclear protein; Alternative splicing;
 CC ACT_SITE 129 129
 CC BY SIMILARITY.
 CC SE CYS 129 129
 CC BY SIMILARITY.
 CC SEQUENCE 253 AA; 29204 MW; C5E3E36875B830053 CRC64;
 CC
 CC Query Match 49.4%; Score 44; DB 1; Length 253;
 CC Best Local Similarity 53.8%; Pred. No. 17;
 CC Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 3 PGNKSPHRDPAPR 15
 CC ||:|:|:|
 CC DB 27 PGRQSPRKRGPR 39
 CC ||:|:|:|
 CC
 CC RESULT 8
 CC GX42 RAT STANDARD; PRT; 253 AA.
 CC ID GX42 RAT
 CC AC Q91XR8;
 CC DT 10-OCT-2003 (Rel. 42, Created)
 CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Phospholipid hydroperoxide glutathione peroxidase, nuclear
 CC (EC 1.11.1.12) (GPX-4).
 CC GN GPX4.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=101116;
 CC [1]
 CC RN SEQUENCE FROM N.A.
 CC RC STRAT=Wistar;
 CC RA Maorino M., Scapin M., Ursini F., Biasolo M., Bosello V., Flohe L.;
 CC RA "Distinct promoters determine alternative transcription of gpx-4 into
 CC RT PRGPx variants."
 CC RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC RN [2]
 CC RP SEQUENCE OF 1-250 FROM N.A., AND SUBCELLULAR LOCATION.
 CC RC TISSUE=Testis;
 CC RX MEDLINE=21242617; PubMed=11344099;
 CC RA Pfeifer H., Conrad M., Roethlein D., Kyriakopoulos A., Briemeier M.,
 CC RA Bornkamm G.W., Behne D.;
 CC RA "Identification of a specific sperm nuclei selenoenzyme necessary for
 CC RT protamine thiol cross-linking during sperm maturation."
 CC RL FASEB J. 15:1236-1238(2001).
 CC CC -1- FUNCTION: Could play a major role in protecting mammals from the
 CC toxicity of ingested lipid hydroperoxides. Essential for embryonic
 CC development. Protects from radiation and oxidative damage.
 CC CC Stabilizes the condensed chromatin in sperm nuclei and is
 CC necessary male fertility (By similarity).
 CC CC -1- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized
 CC glutathione + 2 H(2)O.

CC -1- CORACTOR: Selenocysteine. The active-site selenocysteine is
 CC encoded by the opal codon, UGA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Nuclear;
 CC IsoId=Q91XR8-1; Sequence=Displayed;
 CC Name=Mitochondrial;
 CC IsoId=P36970-1; Sequence=External;
 CC -1- SIMILARITY: Belongs to the glutathione peroxidase family.
 CC -----
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 CC -----
 CC EMBL; AJ537598; CAD61278.1; -;
 CC EMBL; AF274028; AAK74113.1; -;
 CC GO; GO:0005634; C:nucleus; ISS.
 CC GO; GO:0004602; P:glutathione peroxidase activity; ISS.
 CC GO; GO:0006325; P:establishment and/or maintenance of chromatin; ISS.
 CC GO; GO:0007283; P:spermatogenesis; ISS.
 CC InterPro; IPR000889; Glut_peroxidase.
 CC Pfam; PF00255; GSHPx; 1.
 CC PRINTS; PR01011; GLUTPROXDASE.
 CC PROSITE; PS00460; GLUTATHIONE_PEROXID_1; 1.
 CC PROSITE; PS00763; GLUTATHIONE_PEROXID_2; 1.
 CC Oxidoreductase; Peroxidase;
 CC Developmental protein; Selenium; Selenocysteine;
 CC Nuclear protein; Alternative splicing;
 CC ACT_SITE 129 129
 CC SE CYS 129 129
 CC CONFLICT 9 14 RGRCRQ -> PGRQAGIRPYGP (IN REF. 2).
 CC CONFLICT 101 101 S -> A (IN REF. 2).
 CC SEQUENCE 253 AA; 29304 MW; FSAECICF187AD7BB CRC64;
 CC
 CC Query Match 49.4%; Score 44; DB 1; Length 253;
 CC Best Local Similarity 53.8%; Pred. No. 17;
 CC Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 3 PGNKSPHRDPAPR 15
 CC ||:|:|:|
 CC DB 27 PGRQSPRKRGPR 39
 CC ||:|:|:|
 CC
 CC RESULT 9
 CC ELA3 HUMAN STANDARD; PRT; 546 AA.
 CC ID ELA3 HUMAN
 CC AC Q8NGS7;
 CC DT 10-OCT-2003 (Rel. 42, Created)
 CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE RNA polymerase II transcription factor SIII subunit A3 (Elongin A3)
 CC (EloA3).
 CC GN TCBE312.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC [1]
 CC RN SEQUENCE FROM N.A., FUNCTION, AND SUBUNIT.
 CC RX MEDLINE=22113023; PubMed=11994304;
 CC RA Yamazaki K., Guo L., Sugahara K., Zhang C., Enzan H., Nakabeppu Y.,
 CC RA Kitajima S., Aso T.;
 CC RA "Identification and biochemical characterization of a novel
 CC RT transcription elongation factor, elongin A3."
 CC RL J. Biol. Chem. 277:26444-26451(2002).
 CC CC -1- FUNCTION: SIII, also known as elongin, is a general transcription
 CC elongation factor that increases the RNA polymerase II
 CC transcription elongation past template-encoded arresting sites.

RP DISEASE.
RX MEDLINE=90259093; PubMed=2188141;
RA Yoshida H., Hayashi S.I., Kuniyada T., Ogawa M., Nishikawa S.,
RT Okamura H., Sudo T., Shultz L.D., Nishikawa S.-I.;
RA "The murine mutation osteopetrosis is in the coding region of the
RT macrophage colony stimulating factor gene.";
RL Nature 345:442-444(1990).
CC -!- FUNCTION: Granulocyte/macrophage colony-stimulating factors are
CC cytokines that act in hematopoiesis by controlling the production,
CC differentiation, and function of 2 related white cell populations
CC of the blood, the granulocytes and the monocytes-macrophages. CSF-
CC 1 induces cells of the monocyte/macrophage lineage. It plays a
CC role in immunological defenses, bone metabolism, lipoproteins
CC
CC -!- SUBUNIT: Homodimer or heterodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Extracellular. The precursors may exist as
CC integral membrane proteins (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P07141-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P07141-2; Sequence=VSP_001189;
CC Note=No experimental confirmation available;
CC -!- PTM: N-glycosylated. The predominant soluble form is a chondroitin
CC sulfate-containing proteoglycan.
CC -!- DISEASE: A defect in CSF1 is the cause of osteopetrosis.
CC Osteopetrotic mice (op/op) are severely deficient in mature
CC macrophages and osteoclasts, display failed tooth eruption, and
CC have a restricted capacity for bone remodelling.
CC -!- CAUTION: Ref.3 sequence was originally thought to originate from
CC rat, but was later shown (Ref.8 and Ref.9) to be derived from
CC mouse.
CC
CC -----
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CC
CC -----
CC EMBL; X05010; CAA28660.1; -
CC EMBL; M21952; AAA37481.1; -
CC EMBL; M21149; AAA37482.1; -
CC EMBL; M84361; AAA03032.1; -
CC EMBL; BC025593; AAH25593.1; -
CC EMBL; M15692; AAA37480.1; -
CC EMBL; M81316; AAA19866.1; -
CC PIR; A31401; A31401.
CC MGD; MGI:1339753; Csf1.
CC InterPro; IPR008001; MCSF-1.
CC Pfam; PF05337; CSF-1; 2.
CC Cytokine; Growth factor; Glycoprotein; Proteoglycan; Signal;
CC Transmembrane; Alternative splicing.
CC
CC SIGNAL 1 32
CC CHAIN 33 552 MACROPHAGE COLONY STIMULATING FACTOR-1.
CC DOMAIN 33 492 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 493 515 POTENTIAL.
CC DOMAIN 516 552 CYTOPLASMIC (POTENTIAL).
CC DISULFID 63 63 INTERCHAIN (BY SIMILARITY).
CC DISULFID 39 122 BY SIMILARITY.
CC DISULFID 80 171 BY SIMILARITY.
CC DISULFID 134 178 BY SIMILARITY.
CC DISULFID 189 189 INTERCHAIN (BY SIMILARITY).
CC DISULFID 191 191 INTERCHAIN (BY SIMILARITY).
CC CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC VARSPLTC 182 476 Missing (in isoform 2).
CC /FtId=VSP_001189.
CC
CC VARIANT 292 292 D -> G.
CC VARIANT 345 345 S -> P.

FT CONFLICT 3 3 MISSING (IN REF. 5).
FT CONFLICT 6 6 A -> R (IN REF. 5).
FT CONFLICT 7 8 AG -> PR (IN REF. 5).
FT CONFLICT 246 246 P -> A (IN REF. 1).
SQ SEQUENCE 552 AA; 60648 MW; 3886D72D70E770AF CRC64;

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAP 14
| : ||| : |||
Db 202 PASASPHQPPAP 213

RESULT 11
PYRG_MYCLE
ID PYRG_MYCLE STANDARD; PRT; 590 AA.
AC P53529;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (CTP synthetase).
GN PYRG OR MLI363 OR MLC1351.09C.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID:1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R., Robinson K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=TN;
RC MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eigmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Braham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby I., Jagels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -!- FUNCTION: Catalyzes the ATP-dependent amination of UTP to CTP with
CC either L-glutamine or ammonia as the source of nitrogen (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + UTP + NH(3) = ADP + phosphate + CTP.
CC -!- ENZYME REGULATION: Allosterically activated by GTP, when glutamine
CC is the substrate. Inhibited by CTP (By similarity).
CC -!- PATHWAY: Pyrimidine biosynthesis; conversion of UMP to CTP; third
CC (last) step.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SIMILARITY: Belongs to the CTP synthase family.
CC -!- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
CC
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CC
CC -----
CC EMBL; U00021; AAA50916.1; -
CC EMBL; Z95117; CAB08284.1; -
CC EMBL; AL583921; CAC31744.1; -
CC PIR; S72961; S72961.
CC Lepronia; MLI363; -
CC HAMAP; MF_01227; -; 1.

```
CC      -I- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing: Named isoforms=2;
```

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT *Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -!- MISCELLANEOUS: This putative ketoacyl synthase lacks the active
 CC site cysteine.
 CC -!- SIMILARITY: Belongs to the beta-ketoacyl-ACP synthases family.
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 CC -----
 CC EMBL; X63449; CAA45044.1; -;
 CC EMBL; AL939122; CAC44201.1; -;
 CC PIR; S25841; S25841.
 CC HSP; P73283; 1E5M.
 CC InterPro; IPR000794; Ketoacyl synth.
 CC Pfam; PF00109; ketoacyl-synt; 1.
 CC Pfam; PF02801; ketoacyl-synt_C; 1.
 KW Antibiotic biosynthesis; Transferase; Acyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 407 AA; 42549 MW; 59FC75A5A0D94632 CRC64;

Query Match 48.3%; Score 43; DB 1; Length 407;
 Best Local Similarity 46.7%; Pred. No. 38;
 Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
 Db 59 HLPGRLLPQDPSR 73

RESULT 14

HID DROME STANDARD; PRT; 410 AA.
 AC Q24106; Q9VVP1;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Head involution defective protein (wrinkled protein).
 GN W OR HID OR CGS123.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscophora;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP STRAIN=Canton S.
 RC STRAIN=Canton S.; TISSUE=EYE imaginal disk;
 RX MEDLINE=95347579; PubMed=7622034;
 RA Grether M.E., Abrams J.M., Agapite J., White K., Steller H.;
 RT "The head involution defective gene of Drosophila melanogaster
 RL functions in programmed cell death.";
 RL Genes Dev. 9:1694-1708(1995).
 RN [2]
 RP STRAIN=Berkley;
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cusack S., Dahlke C., Davenport L.B., Davies P., De la
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muszy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -!- FUNCTION: Required for induction of apoptosis. Hid mutants contain
 CC extra cells in the head owing to decreased levels of cell death
 CC and show a pronounced defect in the morphogenetic movements of
 CC head involution. Ectopic expression in the retina results in
 CC complete eye ablation. Seems to act genetically upstream of
 CC baculoviral anti-apoptotic p35.
 CC -!- DEVELOPMENTAL STAGE: Expression corresponds approximately to the
 CC pattern of programmed cell death in the embryo, particularly in
 CC the head.
 CC -!- SIMILARITY: LIMITED AT THE N-TERMINAL REGION, TO GRIM AND RPR.
 CC -----
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 CC -----
 CC EMBL; U31236; AAF79985.1; -;
 CC EMBL; AF003521; AAF49270.1; -;
 CC FlyBase; FBgn0003997; W.
 CC GO; GO:0008258; P:head involution; IMP.
 CC GO; GO:0006917; P:induction of apoptosis; IGI.
 CC GO; GO:0002165; P:larval/pupal development (sensu Insecta); IMP.
 CC GO; GO:0012501; P:programmed cell death; IMP.
 KW Apoptosis; Developmental protein; Polymorphism.
 FT DOMAIN 17 79 SER-RICH.
 FT DOMAIN 237 240 POLY-SER.
 FT DOMAIN 332 340 POLY-SER.
 FT VARIANT 171 171 P -> S (IN ALLELE A22).
 FT VARIANT 261 261 S -> L (IN ALLELE A206).
 FT CONFLICT 351 351 P -> S (IN REF. 1).
 SQ SEQUENCE 410 AA; 43876 MW; 63BEF913149E27E1 CRC64;

Query Match 48.3%; Score 43; DB 1; Length 410;
 Best Local Similarity 63.6%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GNKSPHRDPAPR 14

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DB      24 GNSPPHPLP 34
RESULT 15
ID      AMH2_HUMAN
AC      Q16671; Q13762; STANDARD; PRT; 573 AA.
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Anti-Mullerian hormone type II receptor precursor (EC 2.7.1.37) (AMH
DE      type II receptor) (MIS type II receptor) (MISRII) (MRII).
GN      AMHR2 OR AMHR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RX      MEDLINE=96083584; PubMed=7493017;
RA      Imbeaud S., Faure E., Lamarre I., Mattei M.-G., di Clemente N.,
RA      Tizard R., Carre-Eusebe D., Belleville C., Tragethon L., Tonkin C.,
RA      Nelson J., McAuliffe M., Bidart J.-M., Lababidi A., Josso N.,
RA      Cate R.L., Picard J.-Y.;
RT      "Insensitivity to anti-mullerian hormone due to a mutation in the
RT      human anti-mullerian hormone receptor.";
RL      Nat. Genet. 11:382-388(1995).
RN      [2]
RX      MEDLINE=96028015; PubMed=7488027;
RA      Visser J.A., McLuskey A., van Beers T., Weghuis D.O., van Kessel A.G.,
RA      Grootegeed J.A., Themmen A.P.N.;
RT      "Structure and chromosomal localization of the human anti-mullerian
RT      hormone type II receptor gene.";
RL      Biochem. Biophys. Res. Commun. 215:1029-1036(1995).
RN      [3]
RX      MEDLINE=20055680; PubMed=10589763;
RA      Masiakos P.T., MacLaughlin D.T., Maheswaran S., Teixeira J.,
RA      Fuller A.F., Jr., Shah P.C., Kehas D.J., Kenneally M.K.,
RA      Dombkowski D.M., Ha T.U., Preffer F.I., Donahoe P.K.;
RT      "Human ovarian cancer, cell lines, and primary ascites cells express
RT      the human Mullerian inhibiting substance (MIS) type II receptor,
RT      bind, and are responsive to MIS.";
RL      Clin. Cancer Res. 5:3488-3499(1999).
RN      [4]
RX      MEDLINE=97026287; PubMed=8872466;
RA      Imbeaud S., Belleville C., Messika-Zeitoun L., Rey R., di Clemente N.,
RA      Josso N., Picard J.-Y.;
RT      "A 27 base-pair deletion of the anti-Mullerian type II receptor gene
RT      is the most common cause of the persistent Mullerian duct syndrome.";
RL      Hum. Mol. Genet. 5:1269-1277(1996).
RN      [5]
RX      MEDLINE=21434063; PubMed=11549681;
RA      Messika-Zeitoun L., Guedard L., Belleville C., Dutertre M., Lina L.,
RA      Imbeaud S., Hughes I.A., Picard J.-Y., Josso N., di Clemente N.;
RT      "Autosomal recessive segregation of a truncating mutation of
RT      anti-Mullerian type II receptor in a family affected by the
RT      persistent Mullerian duct syndrome contrasts with its dominant
RT      negative activity in vitro.";
RL      J. Clin. Endocrinol. Metab. 86:4390-4397(2001).
CC      -!- FUNCTION: Receptor for anti-Mullerian hormone.
CC      -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- DISEASE: Defects in AMHR2 are the cause of persistent Mullerian
CC      duct syndrome type II (PMDS-2) [MIM:261550]; a form of male
CC      pseudohermaphroditism characterized by a failure of Mullerian
CC      duct regression in otherwise normal males.
CC      -!- SIMILARITY: Belongs to the Ser/thr family of protein kinases. TGFB

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receptor subfamily.
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EMBL; X89013; CAA61418.1; -
EMBL; U29700; AAC50328.1; -
EMBL; X91156; CAA62593.1; -
EMBL; X91157; CAA62593.1; JOINED.
EMBL; X91158; CAA62593.1; JOINED.
EMBL; X91159; CAA62593.1; JOINED.
EMBL; X91160; CAA62593.1; JOINED.
EMBL; X91161; CAA62593.1; JOINED.
EMBL; X91162; CAA62593.1; JOINED.
EMBL; X91163; CAA62593.1; JOINED.
EMBL; X91164; CAA62593.1; JOINED.
EMBL; X91165; CAA62593.1; JOINED.
EMBL; X91166; CAA62593.1; JOINED.
EMBL; AF172932; AAD48497.1; -
PIR; JC4335; JC4335
Genew; HGNC:465; AMHR2.
MIM; 600956; -
MIM; 261550; -
GO; GO:0004872; Fireceptor activity; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR000472; Activin receptor.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF01064; Activin_recpt; 1.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot_kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
Transmembrane; Glycoprotein; Signal; Pseudohermaphroditism;
Disease mutation.
SIGNAL; 1 17
CHAIN; 18 573
DOMAIN; 18 149
TRANSMEM; 150 170
DOMAIN; 171 573
DOMAIN; 203 518
NP_BIND; 209 217
BINDING; 230 230
ACT_SITE; 333 333
CARBOHYD; 66 66
VARIANT; 119 119
VARIANT; 54 54
VARIANT; 142 142
VARIANT; 282 282
VARIANT; 406 406
VARIANT; 426 426
VARIANT; 458 458
VARIANT; 491 491
VARIANT; 504 504
CONFLICT; 161 161
SEQUENCE; 573 AA; 62749 MW; 1347C10C2942FDBA CRC64;
Query Match 48.3%; Score 43; DB 1; Length 573;

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FT DOMAIN 217 256 SER/THR-RICH.
FT DOMAIN 259 266 ASP/GLU-RICH (ACIDIC).
FT DNA_BIND 269 331 HOMEBOX (TALE-TYPE).
FT CONFLICT 175 176 KM -> RP (IN REF. 2).
FT CONFLICT 209 209 M -> I (IN REF. 2).
FT CONFLICT 245 245 D -> V (IN REF. 2).
FT CONFLICT 267 267 R -> P (IN REF. 2).
FT CONFLICT 358 358 Q -> E (IN REF. 2).
FT CONFLICT 367 367 VPPG -> FRAPA (IN REF. 2).
FT CONFLICT 371 377 MSNLLEG -> DEFGTRK (IN REF. 2).
FT CONFLICT 382 AA; 41821 MW; A2C11B8061F718 CRC64;
SQ
Query Match 47.2%; Score 42; DB 1; Length 382;
Best Local Similarity 53.8%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAP 14
DB 38 VEPYGPYRPPQP 50

RESULT 18
BAG4_MOUSE
ID BAG4_MOUSE STANDARD; PRT; 457 AA.
AC Q8C161; Q91V75; Q9CWG2;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE BAG-family molecular chaperone regulator-4 (Silencer of death domains).
DE BAG4 OR SODD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., MUTAGENESIS OF LEU-387; LEU-416 AND ALA-441, AND
RP INTERACTION WITH TNFRSF12 AND HSP70.
RC STRAIN=BALB/C; TISSUE=Testis;
RX MEDLINE=21907217; PubMed=11909948;
RA Miki K., Eddy E.M.;
RT "Tumor necrosis factor receptor 1 is an ATPase regulated by silencer of death domain.";
RT Mol. Cell. Biol. 22:2536-2543 (2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RN Nature 409:685-690 (2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Brain, and Mammary gland;
RX MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

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RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
FT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Inhibits the chaperone activity of HSP70/HSC70 by
CC promoting substrate release. Prevents constitutive TNFRSF1A
CC signaling (By similarity).
CC -!- SUBUNIT: Binds to the ATPase domain of HSP70/HSC chaperones. Binds
CC to the death domain of TNFRSF12 (By similarity). Binds to the
CC death domain of TNFRSF1A in the absence of TNF and thereby
CC prevents binding of adapter molecules such as TRADD or TRAF2.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Contains 1 BAG domain.
CC
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CC
CC -----
CC EMBL; AF332863; AAL9586.1; -
CC EMBL; AK010765; BAB27167.1; -
CC EMBL; BC009102; AAH09102.1; -
CC EMBL; BC037239; AAH37239.1; ALT_INIT.
CC EMBL; BC058518; AAH58518.1; -
CC MGD; MGI:1914634; Bag4.
CC InterPro: IPR003103; BAG.
CC Pfam; PF02179; BAG; 1
CC SMART; SM00264; BAG; 1.
KW Chaperone.
FT DOMAIN 379 456 BAG.
FT DOMAIN 29 298 PRO-RICH.
FT MUTAGEN 387 387 L->P: ABOLISHES INTERACTION WITH HSP70
AND TNFRSF1A.
FT MUTAGEN 416 416 L->P: ABOLISHES INTERACTION WITH HSP70
AND TNFRSF1A.
FT MUTAGEN 441 441 A->P: ABOLISHES INTERACTION WITH HSP70
AND TNFRSF1A.
FT SEQUENCE 457 AA; 49094 MW; 5A70275BD42A6E20 CRC64;
SQ
Query Match 47.2%; Score 42; DB 1; Length 457;
Best Local Similarity 58.3%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGNGKSPHRDPAP 14
DB 279 PGNSFPQPPSP 290

RESULT 19
ETS6_DROME
ID ETS6_DROME STANDARD; PRT; 475 AA.
AC P29776; Q9VPQ9;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE DNA-binding protein D-ETS-6.
GN ETS21C OR ETS-6 OR CG2914.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophiliidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Shandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fodor C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Malishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "the genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE OF 235-352 FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX STRAIN=Canton-S; TISSUE=Larva;
RX MEDLINE=92249640; PubMed=1577186;
RA Chen T., Bunting M., Karim F.D., Thummel C.S.;
RT "Isolation and characterization of five Drosophila genes that encode an ets-related DNA binding domain";
RL Dev. Biol. 151:176-191(1992).
CC CC -1- SUBCELLULAR LOCATION: Nuclear.
CC CC -1- TISSUE SPECIFICITY: EMBRYONIC VENTRAL NERVOUS SYSTEM AND 1 PAIR OF NEURONS IN EACH THORACIC SEGMENT.
CC CC -1- DEVELOPMENTAL STAGE: Expressed throughout development.
CC CC -1- SIMILARITY: Belongs to the ETS family.
CC CC -1- CAUTION: Ref.2 sequence differs from that shown due to a frameshift in position 242.
CC CC
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CC EMBL; AB003589; AAF51484.1; -
DR EMBL; M88475; AAA28452.1; ALT_FRAME.
DR HSSP; Q01543; 1FLI.
DR FlyBase; FBgn0005660; Ets21C.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETs.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS00661; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein.
FT DNA BIND 255 335 ETS-DOMAIN.
SQ SEQUENCE 475 AA; 51802 MW; 0D382C41C03B1502 CRC64;
Query Match 47.2%; Score 42; DB 1; Length 475;
Best Local Similarity 53.8%; Pred. No. 63;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 3 PGKSPHRDPAPR 15
DB 119 PAVSSPHQAPSPR 131
RESULT 20
ID IBMP CAMVS STANDARD; PRT; 520 AA.
AC P03559;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inclusion body matrix protein (Viroplasma)
GN VI.
OS Cauliflower mosaic virus (strain Straabour) (Camv).
OC Viruses; Retroviruses; Caulimoviridae; Caulimovirus.
OX NCBI_TaxID=10648;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001865; PubMed=7407912;
RA Franck A., Guille H., Jonard G., Richards K., Hirth L.;
RT "Nucleotide sequence of cauliflower mosaic virus DNA";
RL Cell 21:285-294(1980).
CC CC -1- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON POLYCYSTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC CC -1- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC CC -1- SIMILARITY: Belongs to the caulimoviruses viroplasma family.
CC CC
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CC EMBL; V00141; CAA23461.1; -
DR PR; A04162; QOCV68.
DR InterPro; IPR002609; Caulimo_VI.
DR InterPro; IPR009027; L9_N like.
DR Pfam; PF01693; Caulimo_VI; 1.
KW Trans-acting factor; Translation regulation.
SQ SEQUENCE 520 AA; 57992 MW; DD41D89DD2D5E8E1 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 520;
Best Local Similarity 58.3%; Pred. No. 69;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY      4 GNKSPHRDPAPR 15
DB      228 GTKKPSDDPAK 239

RESULT 21
ID      IBMP CAMVW STANDARD; PRT; 520 AA.
AC      Q05651;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Inclusion body matrix protein (Viroplasm).
GN      VI.
OS      Cauliflower mosaic virus (strain W260) (CaMV).
OC      Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OX      NCBI_TaxID=31558;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=93383405; PubMed=8372449;
RA      Wintermantel W.M., Anderson E.J., Schoelz J.E.;
RT      Identification of domains within gene VI of cauliflower mosaic virus
RT      that influence systemic infection of Nicotiana bigelovii in a light-
RT      dependent manner.;;
RL      Virology 196:789-798 (1993).
CC      -!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC      POLYICISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC      -!- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC      SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC      -!- SIMILARITY: Belongs to the caulimoviruses viroplasm family.
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CC      or send an email to license@isb-sib.ch).
CC      EMBL; L09053; AAA46360.1; -.
DR      InterPro; IPR002609; Caulimo_VI.
DR      InterPro; IPR009027; L9_N_like.
DR      Pfam; PF01693; Caulimo_VI; 1.
DR      Trans-acting factor; Translation regulation.
KW      Trans-acting factor; Translation regulation.
SQ      SEQUENCE 520 AA; 57976 MW; 4BF710D55BBB9647 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 520;
Best Local Similarity 58.3%; Pred.No. 69;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 GNKSPHRDPAPR 15
DB      228 GTKKPSDDPAK 239

RESULT 22
ID      IBMP CAMVW STANDARD; PRT; 522 AA.
AC      P03557;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-AUG-1991 (Rel. 19, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Inclusion body matrix protein (Viroplasm).
GN      VI.
OS      Cauliflower mosaic virus (strain D/H) (CaMV).
OC      Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OX      NCBI_TaxID=10645;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=83106468; PubMed=7152260;
RA      Balazs E., Guilley H., Jonard G., Richards K.;
RT      "Nucleotide sequence of DNA from an altered-virulence isolate D/H of

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RT      the cauliflower mosaic virus.;;
RL      Gene 19:239-249 (1982).
CC      -!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC      POLYICISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC      -!- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC      SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC      -!- SIMILARITY: Belongs to the caulimoviruses viroplasm family.
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CC      EMBL; M10376; AAA46351.1; -.
DR      PIR; A04160; QOCV6.
DR      InterPro; IPR002609; Caulimo_VI.
DR      InterPro; IPR009027; L9_N_like.
DR      Pfam; PF01693; Caulimo_VI; 1.
DR      Trans-acting factor; Translation regulation.
KW      Trans-acting factor; Translation regulation.
SQ      SEQUENCE 522 AA; 58285 MW; F87CB62C1F30DD57 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 522;
Best Local Similarity 58.3%; Pred.No. 69;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 GNKSPHRDPAPR 15
DB      228 GTKKPSDDPAK 239

RESULT 23
ID      IBMP CAMVJ STANDARD; PRT; 522 AA.
AC      P13218;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-JAN-1990 (Rel. 13, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Inclusion body matrix protein (Viroplasm).
GN      VI.
OS      Cauliflower mosaic virus (strain S-Japan) (CaMV).
OC      Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OX      NCBI_TaxID=10646;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90016879; PubMed=2798138;
RA      Takahashi H., Shimamoto K., Suzuki M., Ehara Y.;
RT      "DNA sequence of gene VI of cauliflower mosaic virus Japanese strain
RT      S (CaMV S-Japan).";
RL      Nucleic Acids Res. 17:7981-7981 (1989).
CC      -!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC      POLYICISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
CC      -!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC      -!- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC      SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC      -!- SIMILARITY: Belongs to the caulimoviruses viroplasm family.
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CC      or send an email to license@isb-sib.ch).
CC      EMBL; X14911; CAA33037.1; -.
DR      PIR; S06092; S06092.
DR      InterPro; IPR002609; Caulimo_VI.
DR      InterPro; IPR009027; L9_N_like.
DR      Pfam; PF01693; Caulimo_VI; 1.

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KW Trans-acting factor; Translation regulation.
 SQ SEQUENCE 522 AA; 58410 MW; 8EB136BB17ED408A CRC64;

Query Match 47.2%; Score 42; DB 1; Length 522;
 Best Local Similarity 58.3%; Pred. No. 69;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 GNKSPHRDPAPR 15
 |||||
 Db 228 GYKPKSSDPAPK 239

RESULT 24
 AMH2_RAT STANDARD; PRT; 557 AA.
 AC Q62893; Q63045; Q9R0A7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Anti-Mullerian hormone type II receptor precursor (BC 2.7.1.37) (AMH
 DE type II receptor) (MIS type II receptor) (MISRII) (C14).
 GN AMH2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96107132; PubMed=8536608;
 RA Teixeira J., He W.W., Shah P.C., Morikawa N., Lee M.M., Catlin E.A.,
 RA Hudson P.L., Wing J., MacLaughlin D.T., Donahoe P.K.;
 RA "Developmental expression of a candidate mullerian inhibiting
 substance type II receptor.";
 RL Endocrinology 137:160-165(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94163972; PubMed=8119126;
 RA Baarends W.M., Van Helmond M.J.L., Post M., Van der Schoot P.J.C.M.,
 RA Hoogerbrugge J.W., de Winter J.P., Vilenbroek J.T.J., Karels B.,
 RA Wilming L.G., Meijers J.H.C., Themmen A.P.N., Grootegeed A.J.;
 RA "A novel member of the transmembrane serine/threonine kinase receptor
 family is specifically expressed in the gonads and in mesenchymal
 cells adjacent to the mullerian duct.";
 RL Development 120:189-197(1994).
 RN [3]
 RP SEQUENCE OF 1-16 FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=20040636; PubMed=10570158;
 RA Teixeira J., Kenas D.J., Antun R., Donahoe P.K.;
 RA "Transcriptional regulation of the rat mullerian inhibiting substance
 type II receptor in rodent Leydig cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:13831-13838(1999).
 CC -!- FUNCTION: Receptor for anti-Mullerian hormone.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the mesenchymal cells
 CC surrounding the Mullerian duct at embryonic days 14, 15, and 16
 CC and in tubular and follicular structures of the fetal gonads.
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. TGFB
 CC receptor subfamily.

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 EMBL; U42427; AAC52343.1; -;
 EMBL; X71916; CA50731.1; -;
 EMBL; AF092445; AAC64138.1; -;

DR PIR; S41627; S41627.
 DR InterPro; IPR000472; Activin_receptor.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF01064; Activin_rec; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 557 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR.
 FT DOMAIN 18 144 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 145 165 POTENTIAL.
 FT DOMAIN 166 557 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 201 511 PROTEIN_KINASE.
 FT NP_BIND 207 215 ATP (BY SIMILARITY).
 FT BINDING 228 228 ATP (BY SIMILARITY).
 FT ACT_SITE 331 331 BY SIMILARITY.
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 119 119 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 527 527 C -> Y (IN REF. 2).
 SQ SEQUENCE 557 AA; 59748 MW; 8EDBE9C0C32EBDD5 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 557;
 Best Local Similarity 61.5%; Pred. No. 74;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGKNSPHRDPAPR 15
 |||||
 Db 85 PGCESLHCDPVR 97

RESULT 25
 FXJ2_MOUSE STANDARD; PRT; 565 AA.
 ID FXJ2_MOUSE
 AC Q9ES18;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Forkhead box protein J2 (Fork head homologous X).
 GN FOXJ2 OR FOX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20480369; PubMed=11025217;
 RA Grandino B., Arias-de-la-Fuente C., Perez-Sanchez C., Parraga M.,
 RA Lopez-Fernandez L.A., del Mazo J., Rey-Campos J.;
 RA "Foxj2 expression is activated during spermatogenesis and very
 early in embryonic development.";
 RL Mech. Dev. 97:157-160(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Wagner L., Shenmen C.M., Schaefer G.D.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Diatchenko L., Bontade M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Transcriptional activator. Able to bind to two different
 CC type of DNA binding sites.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: Contains 1 fork-head domain.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF253052; AAG30406.1; --
 CC EMBL; BC040395; AAH40395.1; --
 CC HSSP; Q63245; 2HEFH.
 CC TRANSFAC; T04170; --
 CC MGD; MGI:1926805; Foxj2.
 CC InterPro; IPR001766; TF_Fork_head.
 CC Pfam; PF00250; Fork_head; 1.
 CC PRINTS; PR00053; FORKHEAD.
 CC ProDom; PD000425; TF_Fork_head; 1.
 CC SMART; SM00339; FH; 1.
 CC PROSITE; PS00657; FORK_HEAD_1; FALSE_NEG.
 CC PROSITE; PS00658; FORK_HEAD_2; 1.
 CC PROSITE; PS50039; FORK_HEAD_3; 1.
 CC Transcription regulation; DNA-binding; Nuclear protein; Activator.
 KW DNA_BIND 66 143 FORK-HEAD.
 FT DOMAIN 266 269 POLY-SER.
 FT DOMAIN 290 296 POLY-GLN.
 FT DOMAIN 306 314 POLY-GLN.
 FT SEQUENCE 565 AA; 61569 MW; 9178AFF3F927AD4 CRC64;
 CC
 CC Query Match 47.2%; Score 42; DB 1; Length 565;
 CC Best Local Similarity 50.0%; Pred. No. 75;
 CC Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 CC
 CC QY 1 HLPGNKSPHRDPAP 14
 CC | | | | |
 CC 470 HMPQGGSHRPAP 483
 CC
 CC DB
 CC
 CC RESULT 26
 CC ID NBEA CHICK STANDARD; PRT; 793 AA.
 CC AC Q9DD5;
 CC DT 10-OCT-2003 (Rel. 42, Created)
 CC DT 10-OCT-2003 (Rel. 42, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Neurobeachin protein (Fragment).
 CC GN NBEA.
 CC OS Gallus gallus (Chicken).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC OC Gallus.
 CC OX NCBI_TaxID=9031;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 CC RC TISSUE=Brain;
 CC RX MEDLINE=20556611; PubMed=11102458;
 CC RA Wang X., Herberg F.W., Laue M.M., Mullner C., Hu B.,
 RA Petrasch-Parwez E., Kilian M.W.;
 RT "Neurobeachin: a protein kinase A-anchoring, beige/Chediak-Higashi
 RT protein homolog implicated in neuronal membrane traffic."
 RL J. Neurosci. 20:8551-8565(2000).
 CC -!- FUNCTION: Binds to type II regulatory subunits of protein kinase A

CC and anchors/targets them to the membrane. May anchor the kinase to
 CC cytoskeletal and/or organelle-associated proteins (By
 CC similarity).
 CC -!- SUBUNIT: Interacts with RII subunit of PKA (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: Forebrain and cerebellum.
 CC -!- SIMILARITY: Belongs to the neurobeachin family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Y18277; CAC18801.1; --
 CC InterPro; IPR000409; Beige_BEACH.
 CC IPR001680; WD40.
 CC PROSITE; PS00197; BEACH; PARTIAL.
 CC PROSITE; PS00678; WD_REPEATS_1; PARTIAL.
 CC PROSITE; PS50082; WD_REPEATS_2; PARTIAL.
 CC PROSITE; PS50294; WD_REPEATS_REGION; PARTIAL.
 KW Membrane.
 FT NON_TER 1 1
 FT NON_TER 793 793
 FT SEQUENCE 793 AA; 87803 MW; 19F5AC6C49A7F2A2 CRC64;
 CC
 CC Query Match 47.2%; Score 42; DB 1; Length 793;
 CC Best Local Similarity 58.3%; Pred. No. 1.1e+02;
 CC Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 1 HLPGNKSPHRDP 12
 CC : : : : :
 CC 621 NVPGNLSPKDP 632
 CC
 CC DB
 CC
 CC RESULT 27
 CC ID AXN2 BRARE STANDARD; PRT; 812 AA.
 CC AC P57095;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE Axin 2 (Axin inhibition protein 2).
 CC GN AXIN2.
 CC OS Brachydanio rerio (Zebrafish) (Danio rerio).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 CC OC Cyprinidae; Danio.
 CC OX NCBI_TaxID=7955;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=20171051; PubMed=10704853;
 CC RA Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hirata T.,
 RA Bae Y.-K., Hibi M., Hirano T.;
 RT "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the
 RT formation of the dorsal organizer in zebrafish."
 RL Mech. Dev. 91:293-303(2000).
 CC -!- FUNCTION: Inhibitor of the Wnt signaling pathway. Down-regulates
 CC beta-catenin. Probably facilitates the phosphorylation of beta-
 CC catenin and APC by GSK3B (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- PTM: Probably phosphorylated by GSK3B and dephosphorylated by PP2A
 CC (By similarity).
 CC -!- SIMILARITY: Contains 1 RGS domain.
 CC -!- SIMILARITY: Contains 1 DIX domain.
 CC
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CC -----
DR EMBL; AB020659; BAA74875.1; -
DR EMBL; AC004542; AAC12954.1; ALT_SEQ.
DR EMBL; BC019257; AAH19257.1; -
DR EMBL; AL133637; CAB63760.1; -
DR FIR; T43455; T43455.
KW Coiled coil.
FT DOMAIN 220 300 COILED COIL (POTENTIAL).
FT DOMAIN 485 522 COILED COIL (POTENTIAL).
FT DOMAIN 679 699 COILED COIL (POTENTIAL).
FT DOMAIN 904 954 COILED COIL (POTENTIAL).
SQ SEQUENCE 970 AA; 110724 MW; 45916180788B53F6 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 970;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPNGKSPHRDPAPR 15
DB 638 LPNSKSPREVPSPK 651

RESULT 29
ID_NBEA_MOUSE STANDARD; PRT; 2936 AA.
AC Q9EPN1; Q8C931; Q9EPM9; Q9EPN0; Q9WVM9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurobeachin protein (lysosomal trafficking regulator 2).
GN NBEA OR LYST2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), FUNCTION, SUBCELLULAR
RP LOCATION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Brain;
RX MEDLINE=20556611; PubMed=11102459;
RA Wang X., Herberg F.W., Laue M.M., Mullner C., Hu B.,
RA Petrasch-Parwez E., Kilian M.M.W.;
RT "Neurobeachin: a protein kinase A-anchoring, beige/Chediak-Higashi
RT protein homolog implicated in neuronal membrane trafficking.";
RL J. Neurosci. 20:8551-8565(2000).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=22150869; PubMed=12160729;
RA Dymov V.G., Chaganti S.R., Dyomina K., Palanisamy N., Murty V.V.S.,
RA Dalla-Favera R., Chaganti R.S.K.;
RT "BC18 is a novel, evolutionarily conserved human gene family encoding
RT proteins with presumptive protein kinase A anchoring function.";
RL Genomics 80:158-165(2002).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Saito R., Kasekawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia L.E., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gassterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

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RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomica M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE OF 2220-2936 FROM N.A.
RP Tchernev V.T., McMurtrie E.B., Nguyen Q.A., Mishra V.S.,
RA Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.;
RT "Identification of LYST2, a brain-specific member of the Chediak-
RT Higashi syndrome gene family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Binds to type II regulatory subunits of protein kinase A
CC and anchors/targets them to the membrane. May anchor the kinase to
CC cytoskeletal and/or organelle-associated proteins. May have a role
CC in membrane trafficking.
CC -!- SUBUNIT: Interacts with RII subunit of PKA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane associated.
CC Associated with pleomorphic tubulovesicular endomembranes near the
CC trans sides of Golgi stacks and throughout the cell bodies and
CC cell processes. Concentrated at the postsynaptic plasma membrane
CC of a subpopulation of synapses.
CC -!- ALTERNATIVE PRODUCTS.
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9EPN1-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9EPN1-2; Sequence=VSP_050540;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q9EPN1-3; Sequence=VSP_050541;
CC Name=4;
CC IsoId=Q9EPN1-4; Sequence=VSP_050542;
CC TISSUE SPECIFICITY: Forebrain, brainstem and cerebellum.
CC -!- DEVELOPMENTAL STAGE: Highly expressed in neonatal brain, levels
CC decline in adults.
CC -!- DOMAIN: RII-alpha binding site, predicted to form an amphipathic
CC helix, could participate in protein-protein interactions with a
CC complementary surface on the R-subunit dimer.
CC -!- SIMILARITY: Belongs to the neurobeachin family.
CC -!- SIMILARITY: Contains 1 BEACH domain.
CC -!- SIMILARITY: Contains 5 WD repeats.
CC -----
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CC -----
CC EMBL; Y18276; CAC18811.1; -
CC EMBL; Y18276; CAC18812.1; -
CC EMBL; Y18276; CAC18813.1; -
CC EMBL; AK043125; AAC31466.1; -
CC EMBL; AF072372; AAC41634.1; -
CC MGD; MGI:1347075; Nbea.
CC GO; GO:0005829; C:cytosol; IDA.
CC GO; GO:0012505; C:endomembrane system; IDA.
CC GO; GO:0005802; C:Golgi trans face; IDA.
CC GO; GO:0005886; C:plasma membrane; IDA.
CC GO; GO:0045211; C:postsynaptic membrane; NAS.
CC GO; GO:0005079; F:protein kinase A anchoring activity; IDA.
CC GO; GO:0019901; F:protein kinase binding; IDA.

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DR GO: 0006892; P: post-Golgi transport; NAS.
DR InterPro; IPR008938; ARM.
DR InterPro; IPR000409; Beige_BEACH.
DR InterPro; IPR001680; WD40.
DR Pfam; PF02138; Beache; 1.
DR Pfam; PF00400; WD40; 5.
DR ProDom; PD007848; Beige_BEACH; 1.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS0197; BEACH; 1.
DR PROSITE; PS00678; WD_REPEATS_1; FALSE NEG.
DR PROSITE; PS00082; WD_REPEATS_2; FALSE NEG.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat; Membrane; Alternative splicing.
FT REPEAT 1316 1358
FT REPEAT 2708 2751
FT REPEAT 2768 2808
FT REPEAT 2850 2889
FT REPEAT 2892 2931
FT DOMAIN 2264 2553
FT VARSPPLIC 1 2197
FT VARSPPLIC 1601 1632
FT VARSPPLIC 2560 2564
FT VARSPPLIC 2220 2221
FT CONFLICT 2332 2332
FT CONFLICT 2337 2337
FT CONFLICT 2375 2375
FT CONFLICT 2431 2431
FT CONFLICT 2532 2532
FT CONFLICT 2539 2539
FT CONFLICT 2554 2554
FT CONFLICT 2561 2561
FT CONFLICT 2802 2802
FT CONFLICT 2805 2805
FT CONFLICT 2920 2936
FT CONFLICT 2936 2936
SQ SEQUENCE 2936 AA; 326738 MW; ACDFD90CA66CEA4 CRC64;
Query Match 47.2%; Score 42; DB 1; Length 2936;
Best Local Similarity 58.3%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDP 12
: ||| ||| : ||
Db 1513 NVPGNLSPKIDP 1524

RESULT 30
NBEA_HUMAN STANDARD; PRT; 2946 AA.
AC Q9NFP9; Q9HCW8; Q9NSU1; Q9NW98; Q9Y6J1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurobeachin protein (lysosomal trafficking regulator 2) (BCL8B
DE protein).
DE NBEA OR LYST2 OR BCL8B OR KIAA1544.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Brain, and Spleen;
RX MEDLINE=22150869; PubMed=12160729;
RA Dymov V.G., Chaganti S.R., Dymova K., Palanisamy N., Murty V.V.S.,
RA Dalla-Favera R., Chaganti R.S.K.;
RT "BCL8 is a novel, evolutionarily conserved human gene family encoding
RT proteins with presumptive protein kinase A anchoring function.";
RL Genomics 80:158-165(2002).
[2]

RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Testis;
RA Duesterhoft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE OF 606-1118 FROM N.A.
RP TISSUE=Embryonic head;
RC Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE OF 1919-2946 FROM N.A. (ISOFORM 1).
RP MEDLINE=20450683; PubMed=10997877;
RX Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro.";
RL DNA Res. 7:273-281(2000).
[5]
RN SEQUENCE OF 2428-2946 FROM N.A. (ISOFORM 1).
RP Tchernev V.T., McMurtre E.B., Nguyen Q.A., Mishra V.S.,
RA Barbosa M.D.P.S., McIndoe R., Kingmore S.F.;
RT "Identification of LYST2, a brain-specific member of the Chediak-
RT Higashi syndrome gene family.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[6]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 2150-2563.
RX MEDLINE=22220051; PubMed=12234919;
RA Jogl G., Shen Y., Gebauer D., Li J., Wiegmann K., Kashkar H.,
RA Kroenke M., Tong L.;
RT "Crystal structure of the BEACH domain reveals an unusual fold and
RT extensive association with a novel PH domain.";
RL EMBO J. 21:4785-4795(2002).
CC -!- FUNCTION: Binds to type II regulatory subunits of protein kinase A
CC and anchors/targets them to the membrane. May anchor the kinase to
CC cytoskeletal and/or organelle-associated proteins (By
CC similarity).
CC -!- SUBUNIT: Interacts with RII subunit of PKA (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated (By
CC similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoID=Q9NFP9-1; Sequence=Displayed;
CC Name=2;
CC IsoID=Q9NFP9-2; Sequence=VSP 050538, VSP 050539;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Predominant in many brain structures. Also
CC expressed at medium levels in spleen, thymus, prostate, testis and
CC ovary. Low level expression is seen in heart, kidney, pancreas,
CC skeletal muscle and intestine.
CC -!- DOMAIN: RII-alpha binding site, predicted to form an amphipathic
CC helix, could participate in protein-protein interactions with a
CC complementary surface on the R-subunit dimer (By
CC similarity).
CC -!- SIMILARITY: Belongs to the neurobeachin family.
CC -!- SIMILARITY: Contains 1 BEACH domain.
CC -!- SIMILARITY: Contains 5 WD repeats.
CC -!- CAUTION: Ref.3 sequence differs from that shown due to a stop
CC codon in position 762.
CC -!- CAUTION: Ref.5 sequence differs from that shown due to a
CC frameshift in position 2900.
-----
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CC EMBL; AF467288; AAMS3531.1; --
CC EMBL; ALI37748; CAB70903.1; --
CC EMBL; AK001059; BAA91485.1; ALT_SEQ.
CC EMBL; AB046764; BAB13370.1; --
CC EMBL; AF072371; AAD41633.1; ALT_FRAME.
CC PDB; 1MT1; 27-SEP-02.
CC Genew; HGNC:7648; NBEA.
CC MIM; 604889; --
CC GO; GO:0005829; C:cytosol; ISS.
CC GO; GO:0012505; C:endomembrane system; ISS.
CC GO; GO:0005802; C:Golgi trans face; ISS.
CC GO; GO:0005886; C:plasma membrane; ISS.
CC GO; GO:0043211; C:postsynaptic membrane; ISS.
CC GO; GO:0005079; F:protein kinase A anchoring activity; ISS.
CC GO; GO:0019901; F:protein kinase binding; ISS.
CC GO; GO:0006892; P:post-Golgi transport; ISS.
CC InterPro; IPR008938; ARM.
CC InterPro; IPR000409; Beige_BEACH.
CC InterPro; IPR001680; WD40.
CC Pfam; PF02138; Beach; 1.
CC Pfam; PF00400; WD40; 5.
CC ProDom; PD007848; Beige_BEACH; 1.
CC PROSITE; PS0197; BEACH; 1.
CC PROSITE; PS00678; WD_REPEATS_1; FALSE NEG.
CC PROSITE; PS00082; WD_REPEATS_2; FALSE NEG.
CC PROSITE; PS0294; WD_REPEATS_REGION; 1.
CC Repeat; WD repeat; Membrane; Alternative splicing; 3D-structure.
FT REPEAT 1326 1368
FT DOMAIN 2274 2563
FT REPEAT 2718 2761
FT REPEAT 2778 2818
FT REPEAT 2860 2899
FT REPEAT 2902 2941
FT VARSPLIC 1 2443
FT Missing (in isoform 2).
FT /FTId=VSP 050538.
FT E -> EIPKXFIKDPHTLTKDKFK (in isoform
FT 2).
FT /FTId=VSP 050539.
FT S -> N (IN REF. 5).
FT CONFLICT 2564 2564
FT CONFLICT 2706 2706
FT CONFLICT 2706 2706
FT SEQUENCE 2946 AA; 327807 MW; 6CDA70D61F1E255E CRC64;
SQ
Query Match 47.2%; Score 42; DB 1; Length 2946;
Best Local Similarity 58.3%; Pred. No. 4.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDP 12
DB 1523 NVPGNLSPIKDP 1534
RESULT 31
GAG BLVAV STANDARD; PRT; 392 AA.
AC P25058;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core protein P15 (Matrix protein); Core
DE protein P24; Core protein P12].
GN GAG.
OS Bovine leukemia virus (Australian isolate) (BLV).
OC Viruses; Retrovirdae; Deltaretrovirus.
OX NCBI_TaxID=11903;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90362060; PubMed=2167927;
RA Coulston J., Naif H., Brandon R., Kumar S., Khan S., Daniel R.C.W.,
RA Javin M.F.;
RT "Molecular cloning and sequencing of an Australian isolate of
RT proviral bovine leukaemia virus DNA: comparison with other
isolates.";
J. Gen. Virol. 71:1737-1746(1990).
RN [2]
RP STRUCTURE BY NMR OF 1-109.
RX MEDLINE=96283625; PubMed=8670827;
RA Matthews S., Mikhailov M., Burny A., Roy P.;
RT "The solution structure of the bovine leukaemia virus matrix protein
RT and similarity with lentiviral matrix proteins.";
EMBO J. 15:3267-3274(1996).
CC 1- SIMILARITY: VERY STRONG WITH THE BOVINE LEUKEMIA VIRUS GAG
CC POLYPROTEIN FROM OTHER ISOLATES.
CC 1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
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CC EMBL; D00647; BAA00543.1; --
CC PIR; JQ0554; FOLGGA.
CC InterPro; IPR003139; Gag_p19.
CC InterPro; IPR000721; Gag_p24.
CC InterPro; IPR008916; Retrov capsid C.
CC InterPro; IPR008919; Retrov capsid_N.
CC InterPro; IPR001878; Znf_CCHC.
CC Pfam; PF02228; Gag_p19; 1.
CC Pfam; PF00607; Gag_p24; 1.
CC Pfam; PF00098; zf-CCHC; 2.
CC PRINTS; PR00939; C2HCZNFINGER.
CC SMART; SM00343; Znf_C2HC; 2.
CC PROSITE; PS00158; ZF_CCHC; 1.
CC Core protein; Polyprotein; Phosphorylation; Repeat; Myristate;
CC Zinc-finger; Lipoprotein.
FT CHAIN 2 109
FT CHAIN 110 323
FT CHAIN 324 392
FT CORE PROTEIN P15.
FT CORE PROTEIN P24 (BY SIMILARITY).
FT CORE PROTEIN P12 (GENOME-BINDING PROTEIN
FT WITH REPEATED SEQUENCES).
FT CCHC-TYPE 1.
FT CCHC-TYPE 2.
FT N-myristoyl glycine (in host) (By
FT similarity).
FT REPEAT 342 362
FT REPEAT 367 387
FT SEQUENCE 392 AA; 42766 MW; A4D5F480D861B72C CRC64;
SQ
Query Match 46.6%; Score 41.5; DB 1; Length 392;
Best Local Similarity 56.2%; Pred. No. 61;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 HLPGNKSP-HRDPAPR 15
DB 325 HTPGPMGPQPPAPK 340
RESULT 32
GAG BLVAV STANDARD; PRT; 392 AA.
AC P03344;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core protein P15 (Matrix protein); Core
DE protein P24; Core protein P12].
GN GAG.
OS Bovine leukemia virus (Japanese isolate BLV-1) (BLV).
OC Viruses; Retrovirdae; Deltaretrovirus.
OX NCBI_TaxID=11907;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85140159; PubMed=29833308;
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE Virion protein US10.
GN US10.
OS Herpes simplex virus (type 1 / strain 17).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OC NCBI_TaxID=10299;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=85160822; PubMed=2984429;
RA McGeoch D.J., Dolan A., Donald S., Rixon F.J.;
RT "Sequence determination and genetic content of the short unique
RT 1 short region: two overlapping reading frames encode unrelated
RT polypeptide one of which has highly reiterated amino acid sequence.";
RL Nucleic Acids Res. 12:2473-2487(1984).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUP TOGETHER HSV-1 US10,
CC EBV-1 66, EBV-4 ORF3, AND VZV 64/69.
CC -----
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CC -----
DR EMBL; X14112; CAA32275.1; -
DR EMBL; X02138; CAA26064.2; -
DR EMBL; X00428; CAA35126.1; -
DR EMBL; L00036; AAA96678.1; -
DR PIR; A05242; Q0BE07.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR000714; EBV_Dnk.
DR Pfam; PF02053; Gene66; 1.
DR PRINTS; PRO0957; GENE66.
KW Zinc-finger.
FT ZN FING 271 293 POTENTIAL.
SQ SEQUENCE 312 AA; 34055 MW; 12D01B0E7C920EA3 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 312;
Best Local Similarity 58.3%; Pred. No. 56;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPA 13
DB 91 LPGSPGFHAPPA 102
|||: |||
|||: |||

RESULT 34
SVI_CTOIN
ID SVI_CTOIN STANDARD; PRT; 413 AA.
AC Q94425;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA
DE ligase) (IleRS) (fragment).
OS Ciona intestinalis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC Phlebobranchia; Cionidae; Ciona.
OX NCBI_TaxID=7719;
RN [1]
RN SEQUENCE FROM N.A.
RP Bird A.P., Clark V., Jones S.J.M., Leitgeb S., Lennard N.,
RA Tweedie S.;

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RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) = AMP +
CC   diphosphate + L-isoleucyl-tRNA(Ile).
CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; Z80904; CAB02584.1; -.
DR FIR; T31663; T31663.
DR HSSP; P41972; 1FFX.
DR InterPro; IPR002300; tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002301; tRNA-synt_1le.
DR InterPro; IPR009008; ValRS_IleRS_edit.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00984; TRNASYNTHILE.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; PARTIAL.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT NON_TER 1 1
FT SITE 298 302 "KMSKS" REGION.
FT BINDING 301 301 ATP (BY SIMILARITY).
FT SEQUENCE 413 AA; 46895 MW; 69B098FD71C100CE CRC64;
SQ
Query Match 46.1%; Score 41; DB 1; Length 413;
Best Local Similarity 70.0%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 GNKSPHRDPA 13
DB 315 GGNKQPDPA 324

RESULT 35
ID TBMV_CAMV4 STANDARD; PRT; 520 AA.
AC P22547;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inclusion body matrix protein (Viroplasm).
GN VI.
OS Cauliflower mosaic virus (strain D4) (CaMV).
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OX NCBI_TaxID=10642;
RN [1]
RX MEDLINE=92216136; PubMed=2134858;
RA Daubert S., Routh J.;
RT "Point mutations in cauliflower mosaic virus gene VI confer host-
RT specific symptom changes.";
RL Mol. Plant Microbe Interact. 3:341-345 (1990).
CC -!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC POLYCYSTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC -!- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC -!- SIMILARITY: Belongs to the caulimoviruses viroplasm family.
CC -----
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CC -----
EMBL; M23620; AAA03526.1; -.

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DR InterPro; IPR002609; Caulimo VI.
DR InterPro; IPR009027; L9_N-like.
DR Pfam; PF01693; Caulimo_VI_1.
KW Trans-acting factor; Translation regulation.
SQ SEQUENCE 520 AA; 58140 MW; 6884E2952B6AASD9 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 520;
Best Local Similarity 58.3%; Pred. No. 97;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 GNKSPHRDPA 15
DB 228 GTRPSSDPAPK 239

RESULT 36
ID TBMV_CAMV STANDARD; PRT; 520 AA.
AC P03558;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inclusion body matrix protein (Viroplasm).
GN VI.
OS Cauliflower mosaic virus (strain CM-1841) (CaMV).
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
OX NCBI_TaxID=10644;
RN [1]
RX MEDLINE=82014878; PubMed=6269062;
RA Gardner R.C., Howarth A.J., Hahn P., Brown-Luedi M., Shepherd R.J.,
RA Messing J.;
RT "The complete nucleotide sequence of an infectious clone of
RT cauliflower mosaic virus by M13mp7 shotgun sequencing.";
RL Nucleic Acids Res. 9:2871-2888 (1981).
CC -!- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC POLYCYSTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC -!- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC -!- SIMILARITY: Belongs to the caulimoviruses viroplasm family.
CC -----
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CC -----
DR EMBL; V00140; -; NOT_ANNOTATED_CDS.
DR FIR; A04161; QCCV6C.
DR InterPro; IPR002609; Caulimo VI.
DR InterPro; IPR009027; L9_N-like.
DR Pfam; PF01693; Caulimo_VI_1.
KW Trans-acting factor; Translation regulation.
SQ SEQUENCE 520 AA; 57907 MW; F02E788569B2F49 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 520;
Best Local Similarity 58.3%; Pred. No. 97;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 GNKSPHRDPA 15
DB 228 GTRPSSDPAPK 239

RESULT 37
ID TBMV_CAMV STANDARD; PRT; 520 AA.
AC Q02954;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Inclusion body matrix protein (Viroplasma).
 GN VI.
 OS Cauliflower mosaic virus (strain BBC) (CaMV).
 OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
 OX NCBI_TaxID=31556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93154593; PubMed=8428667;
 RA Chenault K.D., Melcher U.K.;
 RT "The complete nucleotide sequence of cauliflower mosaic virus isolate
 BCC";
 RL Gene 123:255-257(1993).
 CC -1- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
 CC POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
 CC -1- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
 CC SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
 CC -1- SIMILARITY: Belongs to the caulimoviruses viroplasma family.
 CC
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 CC
 DR EMBL; M90542; AAA62376.1; -
 DR PIR; JN0498; JN0498.
 DR InterPro; IPR002609; Caulimo VI.
 DR Pfam; PF01693; Caulimo_VI.1.
 DR Trans-acting factor; Translation regulation.
 KW SEQUENCE 520 AA; 57969 MW; 08D7D5F0215DBEC6 CRC64;
 SQ
 Query Match 46.1%; Score 41; DB 1; Length 520;
 Best Local Similarity 58.3%; Pred. No. 97;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GNKSPHRDPAPR 15
 Db 228 GTRKPSDPAKP 239
 RESULT 38
 ID IBMP CAMVN STANDARD; PRT; 520 AA.
 AC Q00957;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Inclusion body matrix protein (Viroplasma).
 GN VI.
 OS Cauliflower mosaic virus (strain NV8153) (CaMV).
 OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
 OX NCBI_TaxID=31557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chenault K.D., Steffens D.L., Melcher U.K.;
 RT "Nucleotide sequence of cauliflower mosaic virus isolate NV8153";
 RL Plant Physiol. 100:542-545(1992).
 CC -1- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
 CC POLYCISTRONIC MRNA'S DERIVED FROM CAULIFLOWER MOSAIC VIRUS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
 CC -1- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
 CC SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
 CC -1- SIMILARITY: Belongs to the caulimoviruses viroplasma family.
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 CC
 DR EMBL; M90541; AAA46359.1; -
 DR InterPro; IPR002609; Caulimo VI.
 DR Pfam; PF01693; Caulimo_VI.1.
 DR Trans-acting factor; Translation regulation.
 KW SEQUENCE 520 AA; 57799 MW; 3459A028087CB41D CRC64;
 SQ
 Query Match 46.1%; Score 41; DB 1; Length 520;
 Best Local Similarity 58.3%; Pred. No. 97;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 GNKSPHRDPAPR 15
 Db 228 GTRKPSDPAKP 239
 RESULT 39
 ID FLIF_BUCAP STANDARD; PRT; 556 AA.
 AC Q8KA45;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Flagellar M-ring protein.
 GN FLIF OR BUSG067.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Buchnera.
 OX NCBI_TaxID=98794;
 RN [1]
 RP MEDLINE=22084549; PubMed=12089438;
 RA Tamai I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
 RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;
 RT "50 million years of genomic stasis in endosymbiotic bacteria";
 RL Science 296:2376-2379(2002).
 CC -1- FUNCTION: The M ring may be actively involved in energy
 CC transduction (by similarity).
 CC -1- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
 CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
 CC MOUNTED ON A CENTRAL ROD. THE M RING IS INTEGRAL TO THE INNER
 CC MEMBRANE OF THE CELL AND MAY BE CONNECTED TO THE FLAGELLAR ROD
 CC VIA THE S RING. THE S (SUPRAMEMBRANE RING) LIES JUST DISTAL TO
 CC THE M RING. THE L AND P RINGS LIE IN THE OUTER MEMBRANE AND THE
 CC PERIPLASMIC SPACE, RESPECTIVELY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic; membrane-associated (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the flif family.
 CC
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 CC
 DR EMBL; AS014082; AAM67637.1; -
 DR InterPro; IPR000067; FlgMring FLIF.
 DR Pfam; PF01514; YscJ Flif; 1.
 DR PRINTS; PR01009; FLGMRINGFLIF.
 DR TIGRFS; TIGR00206; flif; 1.
 KW Flagellum; Membrane; Complete proteome.
 SQ SEQUENCE 556 AA; 64260 MW; 57B4D66475FE8F3 CRC64;
 Query Match 46.1%; Score 41; DB 1; Length 556;
 Best Local Similarity 63.6%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 1 HLPNGKSPHRD 11
Db 102 HFSENNSPHRD 112

RESULT 40
FXJ2 HUMAN STANDARD; PRT; 574 AA.
AC Q9P0K8; Q96PS9; Q9NSN5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Forkhead box protein J2 (Fork head homologous X).
GN FOXJ2 OR FHX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FOXJ2.L).
RX MEDLINE=2023944; PubMed=10777590;
RA Perez-Sanchez C.; Gomez-Ferreira M.A.; de la Fuente C.A.;
RA Granadino B.; Velasco G.; Esteban A.; Rey-Campos J.;
RT "FHX, a novel fork factor with a dual DNA binding specificity."
RL J. Biol. Chem. 275:12909-12916 (2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FOXJ2.S).
RX MEDLINE=20425082; PubMed=10966786;
RA Perez-Sanchez C.; de la Fuente C.A.; Gomez-Ferreira M.A.;
RA Granadino B.; Rey-Campos J.;
RT "FHX.L and FHX.S, two isoforms of the human fork-head factor FHX
(forkhead) with differential activity."
RL J. Mol. Biol. 301:795-806 (2000).
RN [3]
RP SEQUENCE OF 458-574 FROM N.A. (ISOFORM FOXJ2.L).
RC TISSUE=Welanoma;
RA Ansoerge W.; Winkner U.; Mewes H.-W.; Weil B.; Wiemann S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transcriptional activator. Able to bind to two different
CC type of DNA binding sites. Isoform FOXJ2.L behaves as a more
CC potent transactivator than FOXJ2.S.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=FOXJ2.L; Synonyms=FHX.L;
CC IsoId=Q9P0K8-1; Sequence=Displayed;
CC Name=FOXJ2.S; Synonyms=FHX.S;
CC IsoId=Q9P0K8-2; Sequence=VSP_001544;
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF155132; AAP65927.1; -.
CC EMBL; AF155133; AAK49016.1; -.
CC EMBL; AL161978; CAB82315.1; -.
CC PIR; T47161; T47161.
CC HSSP; Q63245; 2HEH.
CC TRANSFAC; T04169; -.
CC TRANSFAC; T04171; -.
CC InterPro; IPR001766; TF_Fork_head.
CC Pfam; PF00250; Fork_head; 1.
CC PRINTS; PR00053; FORKHEAD.
CC ProDom; PD000425; TF_Fork_head; 1.
CC SMART; SM00339; FHX; 1
CC PROSITE; PS00657; FORK_HEAD_1; FALSE_NEG.
```

```
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PSS0039; FORK_HEAD_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein; Activator;
KW Alternative splicing.
FT DNA BIND 66 143 FORK-HEAD.
FT DOMAIN 266 270 POLY-SER.
FT DOMAIN 291 294 POLY-GLN.
FT DOMAIN 295 298 POLY-PRO.
FT DOMAIN 299 306 POLY-GLN.
FT DOMAIN 313 321 POLY-GLN.
FT DOMAIN 390 395 POLY-PRO.
FT VARSPLIC 513 574
FT
FT
FT
SQ SEQUENCE 574 AA; 62394 MW; 258120EDAE4B11EB CRC64;
Query Match 46.1%; Score 41; DB 1; Length 574;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 HLPNGKSPHRD PAP 14
Db 479 HVPQGGTHRPAP 492
```

Search completed: March 2, 2004, 16:05:27
Job time : 2.4375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 16:00:38 ; Search time 2.125 Seconds
(without alignments)
678.999 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	58.4	1173	T31421	C-terminal domain-
2	50	56.2	165	G72619	hypothetical prote
3	48	53.9	432	C72417	sugar kinase, PGGY
4	46	51.7	723	1 VCPVPP	coat protein VP1 -
5	46	51.7	729	1 VCPVNA	coat protein VP1 -
6	46	51.7	729	1 A60006	coat protein VP1 -
7	45	50.6	517	2 AG0157	probable carbohydr
8	45	50.6	618	2 S32436	collagen alpha 2(I
9	45	50.6	1294	2 T48349	ETN2 protein - Ara
10	44.5	50.0	545	2 S46151	probable purine nu
11	44	49.4	339	2 T05726	GHI protein - soyb
12	44	49.4	552	1 A31401	macrophage colony-
13	44	49.4	552	1 S35703	colony-stimulating
14	44	49.4	590	2 S72961	CTP synthase (BC 6
15	43	48.3	105	2 C72631	hypothetical prote
16	43	48.3	280	2 T35432	probable aldehyde
17	43	48.3	407	2 S25841	beta-ketoacyl synt
18	43	48.3	573	2 JC4335	anti-mullerian hor
19	43	48.3	779	2 T21021	hypothetical prote
20	43	48.3	781	2 T41551	hypothetical prote
21	43	48.3	920	2 A45748	collagen alpha 1(V
22	43	48.3	1049	1 S19421	ATP-dependent perm
23	42	47.2	278	2 T35379	hypothetical prote
24	42	47.2	355	2 T31128	3-isopropylmalate
25	42	47.2	520	1 QOCV6S	hypothetical prote
26	42	47.2	522	1 QOCV6	hypothetical prote
27	42	47.2	522	2 S06092	inclusion body mat
28	42	47.2	557	2 S41627	probable anti-mul
29	42	47.2	568	2 JC5629	mullerian-inhibiti

30	42	47.2	818	2 T02436	proline-rich prote
31	42	47.2	1043	2 T13172	gag-like protein p
32	41.5	46.6	240	2 C86194	hypothetical prote
33	41.5	46.6	324	2 S44956	lmbi protein - Str
34	41.5	46.6	392	1 FOLJGB	gag polyprotein -
35	41.5	46.6	392	1 FOLJGA	gag polyprotein -
36	41.5	46.6	393	2 S29356	gag protein - bovi
37	41.5	46.6	1174	2 T49868	related to suppress
38	41	46.1	111	2 H82597	hypothetical prote
39	41	46.1	117	2 T47161	hypothetical prote
40	41	46.1	118	2 S54309	hypothetical 13.2K
41	41	46.1	282	2 A85076	hypothetical prote
42	41	46.1	312	1 QQBE07	US10 protein hum
43	41	46.1	413	2 T31663	isoleucine-tRNA 11
44	41	46.1	520	1 QOCV6C	hypothetical prote
45	41	46.1	520	2 JN0498	hypothetical 58K p

ALIGNMENTS

RESULT 1

T31421
C-terminal domain-binding protein rAl - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C/Accession: T31421
R/Yuryev, A.; Patturajan, M.; Litington, Y.; Joshi, R.V.; Gentile, C.; Gebara, M.; Cord
Proc. Natl. Acad. Sci. U.S.A. 93, 6975-6980, 1996
A/Title: The C-terminal domain of the largest subunit of RNA polymerase II interacts wit
A/Reference number: Z21024; MUID:96293459; PMID:8692929
A/Accession: T31421
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-1173 <YUR>
A/Cross-references: EMBL:U49056; NID:G1438531; PID:G1438532; PIDN:AAC52657.1
A/Experimental source: hippocampus

Query Match 58.4%; Score 52; DB 2; Length 1173;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAP 14
DB 224 PGDDSPHREPPP 235
||:|||||:
||:|||||:

RESULT 2

G72619
hypothetical protein APE1416 - Aeropyrum pernix (strain K1)
C/Species: Aeropyrum pernix
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C/Accession: G72619
R/Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A/Reference number: A72450; MUID:99310339; PMID:10382966
A/Accession: G72619
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-165 <KAW>
A/Cross-references: DDBJ:AF000061; NID:G5104821; PIDN:BAA80413.1; PID:dl044199; PID:G51C
A/Experimental source: strain K1
C/Genetics:
A/Accession: APE1416
C/Superfamily: Aeropyrum pernix hypothetical protein APE1416

Query Match 56.2%; Score 50; DB 2; Length 165;
Best Local Similarity 68.8%; Pred. No. 1.5;
Matches 11; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 2 LPGNK--SPHRDPAPR 15

```

Db      140 LPANSRGSPHRDPAPR 155
      ||| ||| ||| ||| |||
RESULT 3
C72417
sugar kinase, FOGY family - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: C72417
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; PMID:99287316; PMID:10360571
A:Accession: C72417
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-492 <ARN>
A:Cross-references: GB:AE001697; GB:AE000512; NID:G4980597; PIDN:AAD35210.1; PID:G498060
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0116
C:Superfamily: xylulokinase

Query Match      53.9%; Score 48; DB 2; Length 492;
Best Local Similarity 53.3%; Pred. No. 9.5;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 HLPGNKSPHRDPAPR 15
      ||| ||| ||| ||| |||
Db      340 YLNGERTPHRDPAPR 354

RESULT 4
VCPVPP
coat protein VP1 - porcine parvovirus
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1996
C:Accession: B33302
R:Ranz, A.I.; Mancus, J.J.; Diaz-Aroca, E.; Casal, J.I.
J. Gen. Virol. 70, 2541-2553, 1989
A:Title: Porcine parvovirus: DNA sequence and genome organization.
A:Reference number: A33302; PMID:90010964; PMID:2794971
A:Accession: B33302
A:Molecule type: DNA
A:Residues: 1-723 <RAN>
A:Cross-references: EMBL:D00623
C:Genetics:
A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein
F:145-723/Product: coat protein VP2 #status predicted <VP2>

Query Match      51.7%; Score 46; DB 1; Length 723;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGNKSPHRDPAPR 15
      ||| ||| ||| ||| |||
Db      111 PGSKPPGKRPAAPR 123

RESULT 5
VCPVNA
coat protein VP1 - porcine parvovirus (strain NADL-2)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C:Accession: B33743; D48472
R:Vasudevacharya, J.; Basak, S.; Srinivas, R.V.; Compans, R.W.

Virology 173, 368-377, 1989
A:Title: Nucleotide sequence analysis of the capsid genes and the right-hand terminal P
A:Reference number: A33743; PMID:90085785; PMID:2596019
A:Accession: B33743
A:Molecule type: DNA
A:Residues: 1-729 <VAS>
A:Cross-references: GB:M32787; NID:G332983; PIDN:AAA46917.1; PID:G332985
R:Bergeon, J.; Menezes, J.; Tjissen, P.
Virology 197, 86-98, 1993
A:Title: Genomic organization and mapping of transcription and translation products of
A:Reference number: A48472; PMID:94025614; PMID:8212598
A:Accession: D48472
A:Molecule type: DNA
A:Residues: 11-729 <BER>
A:Experimental source: NADL-2, ATCC VR-742
A:Note: sequence extracted from NCBI backbone (NCBIN:138789, NCBI:P:138794)
C:Genetics:
A:Introns: 10/1
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein; glycoprotein
F:151-729/Product: coat protein VP2 #status predicted <VP2>
F:132,172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #s

Query Match      51.7%; Score 46; DB 1; Length 729;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGNKSPHRDPAPR 15
      ||| ||| ||| ||| |||
Db      117 PGSKPPGKRPAAPR 129

RESULT 6
AG0006
coat protein VP1 - porcine parvovirus (strain 90HS)
N:Contains: coat protein VP2
C:Species: porcine parvovirus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C:Accession: A60006
R:Sakurai, M.; Nishimori, T.; Ushimi, C.; Nakajima, H.
Virus Res. 13, 79-86, 1989
A:Title: Nucleotide sequence of capsid protein gene of porcine parvovirus.
A:Reference number: A60006; PMID:89319168; PMID:2750278
A:Accession: A60006
A:Molecule type: DNA
A:Residues: 1-729 <SAK>
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein; glycoprotein
F:151-729/Product: coat protein VP2 #status predicted <VP2>
F:172,198,282,330,433,471,573,604,651/Binding site: carbohydrate (Asn) (covalent) #stat

Query Match      51.7%; Score 46; DB 1; Length 729;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PGNKSPHRDPAPR 15
      ||| ||| ||| ||| |||
Db      117 PGSKPPGKRPAAPR 129

RESULT 7
AG0157
probable carbohydrate kinase YPO1291 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AG0157
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.I.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: AG0157

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RESULT 9
T48349
EIN2 protein - Arabidopsis thaliana
N;Alternate names: protein F12E4.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48349
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Accession: T48349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1294 <BEV>
A;Cross-references: EMBL:AL162751
C;Genetics:
A;Map position: 5
A;Introns: 83/3; 112/3; 149/3; 220/3; 282/3; 1169/3
A;Note: F12E4.10

      Query Match      50.6%;      Score 45;      DB 2;      Length 1294;
      Best Local Similarity 61.5%;      Pred. No. 74;
      Matches 8;      Conservative 2;      Mismatches 3;      Indels 0;      Gaps 0;

Qy      1 HLPGNKSPHRDPA 13
      ||| ||| : ||:
Db      939 HLPNNKGYWDP 951

RESULT 10
S46151
probable purine nucleotide-binding protein YBR270c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1738
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S46151
R;Agle, M.; Baclet, M.C.; Barthe, C.; Biteau, N.; Crouzet, M.; Doignon, F.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45940
A;Accession: S46151
A;Molecule type: DNA
A;Residues: 1-545 <AIG>
A;Cross-references: EMBL:Z36139; NID:G536704; PID:G536705; GSPDB:GN00002; MIPS:YBR270c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YBR270c
A;Cross-references: SGD:S0000474
A;Map position: 2R
A;Note: YBR270c
C;Keywords: ATP; P-loop; purine nucleotide binding; transmembrane protein
F;259-286/Region: nucleotide-binding motif A (P-loop)
F;321-337/Domain: transmembrane #status predicted <TM>
F;265/Binding site: ATP/GTP (Lys) #status predicted

      Query Match      50.0%;      Score 44.5;      DB 2;      Length 545;
      Best Local Similarity 66.7%;      Pred. No. 36;
      Matches 10;      Conservative 1;      Mismatches 3;      Indels 1;      Gaps 1;

Qy      1 HLPGNKSPHRDPA 15
      ||| : ||| ||| |||
Db      53 HLKTSKSPH-DAAPR 66

RESULT 11
T05726
GH1 protein - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Aug-1999
C;Accession: T05726
R;Hagen, G.; Guilloyle, T.J.
submitted to the EMBL Data Library, July 1997
A;Reference number: Z15436

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A:Accession: T05726
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339 <HAG>
A:Cross-references: EMBL:AF016633; NID:g2388688; PIDN:AA870005.1; PID:g2388689
A:Experimental source: cultivar Wayne
C:Genetics:
A:Gene: GH1
C:Superfamily: auxin-induced protein aux28

Query Match 49.4%; Score 44; DB 2; Length 339;
Best Local Similarity 63.6%; Pred. No. 27;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDP 12
DB 62 LPGQSPERE 72

RESULT 12
A31401
Macrophage colony-stimulating factor precursor - mouse
N:Alternate names: colony-stimulating factor 1; M-CSF
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A31401; JN0294; A26575; A23166; A25883
R:Ladner, M.B.; Martin, G.A.; Noble, J.A.; Wittman, V.P.; Warren, M.K.; McGrogan, M.; St
Proc. Natl. Acad. Sci. U.S.A. 85, 6706-6710, 1988
A:Title: cDNA cloning and expression of murine macrophage colony-stimulating factor from
A:Reference number: A31401; MUID:88320507; PMID:2457916
A:Accession: A31401
A:Molecule type: mRNA
A:Residues: 1-552 <LAD>
A:Cross-references: GB:M21952; GB:J03862; NID:g192804; PIDN:AAA37481.1; PID:g309199
R:Harrington, M.A.; Edenberg, H.J.; Saxman, S.; Pedigo, L.M.; Daub, R.; Broxmeyer, H.E.
Gene 102, 165-170, 1991
A:Title: Cloning and characterization of the murine promoter for the colony-stimulating
A:Reference number: JN0294; MUID:91340149; PMID:1874443
A:Accession: JN0294
A:Molecule type: DNA
A:Residues: 1-13 <HAR>
A:Cross-references: GB:M81316; GB:M61708; NID:g192802; PIDN:AAA19866.1; PID:g192803
R:DeLamar, J.F.; Hession, C.; Semon, D.; Gough, N.M.; Rothenbuhler, R.; Wermod, J.J.
Nucleic Acids Res. 15, 2389-2390, 1987
A:Title: Nucleotide sequence of a cDNA encoding murine CSF-1 (macrophage-CSF).
A:Reference number: A26575; MUID:87174763; PMID:3494232
A:Accession: A26575
A:Molecule type: mRNA
A:Residues: 1-5, 'R', 7-245, 'A', 247-552 <DEL>
R:Ben-Avram, C.M.; Shively, J.E.; Shaddock, R.K.; Waheed, A.; Rajavashisth, T.; Lusis, A
Proc. Natl. Acad. Sci. U.S.A. 82, 4486-4489, 1985
A:Reference number: A23166; MUID:85242709; PMID:3925458
A:Accession: A23166
A:Molecule type: protein
A:Residues: 33-39, 'CC', 42-57 <BEN>
R:Rajavashisth, T.B.; Eng, R.; Shaddock, R.K.; Waheed, A.; Ben-Avram, C.M.; Shively, J.E
Proc. Natl. Acad. Sci. U.S.A. 84, 1157-1161, 1987
A:Title: Cloning and tissue-specific expression of mouse macrophage colony-stimulating f
A:Reference number: A25883; MUID:87147232; PMID:3493488
A:Accession: A25883
A:Molecule type: mRNA
A:Residues: 1-2, 4-5, 'RPR', 9-100 <RAJ>
A:Cross-references: GB:M15692; NID:g192800; PIDN:AAA37480.1; PID:g192801
C:Superfamily: macrophage colony-stimulating factor
C:Keywords: cytokine; glycoprotein; growth factor; macrophage
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-552/Product: macrophage colony-stimulating factor #status predicted <MAT>
F:154,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

A:Accession: T05726
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-339 <HAG>
A:Cross-references: EMBL:AF016633; NID:g2388688; PIDN:AA870005.1; PID:g2388689
A:Experimental source: cultivar Wayne
C:Genetics:
A:Gene: GH1
C:Superfamily: auxin-induced protein aux28

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAP 14
DB 202 PASASPHQPPAP 213

RESULT 13
S35703
colony-stimulating factor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S35703
R:Borycki, A.G.; Lenormand, J.L.; Guillier, M.; Leibovitch, S.A.
Biochim. Biophys. Acta 1174, 143-152, 1993
A:Title: Isolation and characterization of a cDNA clone encoding for rat CSF-1 gene. PC
A:Reference number: S35703; MUID:93363632; PMID:8357831
A:Accession: S35703
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-552 <BOR>
A:Cross-references: EMBL:M84361; NID:g203640; PIDN:AAA03032.1; PID:g203641
C:Superfamily: macrophage colony-stimulating factor

Query Match 49.4%; Score 44; DB 1; Length 552;
Best Local Similarity 58.3%; Pred. No. 44;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAP 14
DB 202 PASASPHQPPAP 213

RESULT 14
S72961
CTP synthase (EC 6.3.4.2) pyrG - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S72961
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid L247.
A:Reference number: S72589
A:Accession: S72961
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-590 <SMI>
A:Cross-references: EMBL:U00021; NID:g467141; PIDN:AAA50916.1; PID:g467152
C:Genetics:
A:Start codon: GTG
C:Superfamily: CTP synthase
C:Keywords: ligase

Query Match 49.4%; Score 44; DB 2; Length 590;
Best Local Similarity 45.0%; Pred. No. 47;
Matches 9; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY 1 HLPGNKSPHRD-----PAP 14
DB 567 HLPNSSNQHRDGVRSFPAP 586

RESULT 15
C72631
hypothetical protein APE1506 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: C72631
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: C72631
A>Status: preliminary

```


A:Molecule type: DNA
A:Residues: 1-105 <KAW>
A:Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80505.1; PID:d1044291; PID:g5104821
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1506

Query Match 48.3%; Score 43; DB 2; Length 105;
Best Local Similarity 58.3%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDP 12
||| ||| : : :
Db 56 HLPNNKASHKLP 67

RESULT 16
T35432
A:Map position: 12q13-12q13
A:Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35432
R;Murphy, L.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A:Reference number: Z21578
A:Accession: T35432
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-280 <MUR>
A:Cross-references: EMBL:AL031035; PIDN:CAA19886.1; GSPDB:GN00070; SCOEDB:SC6A9.01c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC6A9.01c

Query Match 48.3%; Score 43; DB 2; Length 280;
Best Local Similarity 61.5%; Pred. No. 31;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPA 13
||| ||| : : :
Db 2 HNPGNATPDRFPA 14

RESULT 17
S25841
A:Map position: 12q13-12q13
A:Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C:Species: Streptomyces coelicolor
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C:Accession: S25841
R;Fernandez-Moreno, M.A.; Martinez, E.; Boto, L.; Hopwood, D.A.; Malpartida, F.
J. Biol. Chem. 267, 19278-19290, 1992
A:Title: Nucleotide sequence and deduced functions of a set of cotranscribed genes of St
A:Reference number: S25840; MUID:92406871; PMID:1527048
A:Accession: S25841
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-407 <FER>
A:Cross-references: EMBL:XG3449; NID:g46805; PIDN:CAA45044.1; PID:g46807
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I; 3-oxoacyl-[acyl-carrier-prob
F;21-400/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>

Query Match 48.3%; Score 43; DB 2; Length 407;
Best Local Similarity 46.7%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
||| ||| : : :
Db 59 HIFGRLLPQDPSTR 73

RESULT 18
JC4335

anti-mullerian hormone type II receptor precursor - human
C:Species: Homo sapiens (nan)
C:Date: 06-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 04-Mar-2000
C:Accession: JC4335
R;Visser, J.A.; Mcluskey, A.; van Beers, T.; Weghuis, D.O.; van Kessel, A.G.; Grootegeoe
Biochem. Biophys. Res. Commun. 215, 1029-1036, 1995
A:Title: Structure and chromosomal localization of the human anti-muellerian hormone tyf
A:Reference number: JC4335; MUID:96028015; PMID:7488027
A:Accession: JC4335
A:Molecule type: mRNA
A:Residues: 1-573 <VIS>
A:Cross-references: GB:X91156; NID:g1107671; PIDN:CAA62593.1; PID:el98046; PID:g1107672
C:Comment: This is a receptor for anti-mullerian hormone (see PIR:WFHUM). It plays a cri
C:Genetics:
A:Gene: GDB:AMHR2
A:Cross-references: GDB:696210; OMIM:600956
A:Map position: 12q13-12q13
A:Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C:Keywords: ATP; hormone receptor; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-573/Product: anti-muellerian hormone type II receptor #status predicted <MAT>
F;17-141/Domain: extracellular hormone binding #status predicted <ELB>
F;142-167/Domain: transmembrane #status predicted <TMW>
F;201-512/Domain: protein kinase homology <KIN>

Query Match 48.3%; Score 43; DB 2; Length 573;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPAPR 15
||| ||| : : :
Db 85 PGCSLHCDPSPR 97

RESULT 19
T21021
A:Map position: 12q13-12q13
A:Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C:Accession: T21021
R;McLay, K.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19361
A:Accession: T21021
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-779 <WIL>
A:Cross-references: EMBL:Z78062; PIDN:CAB01499.1; GSPDB:GN00019; CBSP:F16D3.2
A:Experimental source: clone F16D3
C:Genetics:
A:Gene: CBSP:F16D3.2
A:Map position: 1
A:Introns: 33/2; 130/1; 189/2; 238/1; 355/2; 388/3; 473/1; 540/2; 587/3; 670/1
C:Superfamily: Caenorhabditis elegans hypothetical protein F16D3.2

Query Match 48.3%; Score 43; DB 2; Length 779;
Best Local Similarity 60.0%; Pred. No. 90;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 KSPHRDPAPR 15
||| ||| : : :
Db 206 RTPYRDPSPR 215

RESULT 20
T41551
A:Map position: 12q13-12q13
A:Introns: 16/3; 77/3; 141/3; 167/3; 207/2; 284/2; 322/3; 380/2; 429/3; 475/2
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolc
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41551
R;Wood, V.; Rajandream, M.A.; Barrrell, B.G.; Seeger, K.; Harris, D.
submitted to the EMBL Data Library, June 1998

us-10-060-765-8.ipr	A;Reference number: Z22001		A;Reference number: S25353; MUID:92327849; PMID:1626432	
	A;Accession: T41551		A;Contents: annotation	
us-10-060-765-8.ipr	A;Status: preliminary; translated from GB/EMBL/DBJ		C;Genetics:	
	A;Molecule type: DNA		A;Gene: SGD:ADP1; MIPS:YCR011C	
us-10-060-765-8.ipr	A;Residues: 1-781 <WOO>		A;Cross-references: SGD:S0000604; MIPS:YCR011C	
	A;Cross-references: EMBL:AL023794; PIDN:CAA19355.1; GSPDB:GN00068; SPDB:SPCC70.05C		A;Map position: 3R	
us-10-060-765-8.ipr	A;Experimental source: strain 972h; cosmid c70		C;Superfamily: ATP-dependent permease ADP1; ATP-binding cassette homology	
	C;Genetics:		C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein	
us-10-060-765-8.ipr	A;Gene: SPDB:SPCC70.05C		F;1-25/Domain: signal sequence #status predicted <SIG>	
	A;Map position: 3		F;26-1049/Product: ATP-dependent permease ADP1 #status predicted <MAT>	
us-10-060-765-8.ipr	Query Match		F;26-324/Domain: extracellular #status predicted <EXT>	
	Best Local Similarity 48.3%; Score 43; DB 2; Length 781;		F;325-341/Domain: transmembrane #status predicted <TM1>	
us-10-060-765-8.ipr	Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;		F;406-607/Domain: ATP-binding cassette homology <ABC>	
	QY 1 HLPGNKSPHRDP 12		F;423-430/Region: nucleotide-binding motif A (P-loop)	
us-10-060-765-8.ipr	Db 80 HVEGNNSPDQTP 91		F;550-557/Region: nucleotide-binding motif B	
	RESULT 21		F;794-810/Domain: transmembrane #status predicted <TM2>	
us-10-060-765-8.ipr	A45748		F;829-845/Domain: transmembrane #status predicted <TM3>	
	collagen alpha 1(VII) chain - mouse (fragment)		F;878-894/Domain: transmembrane #status predicted <TM4>	
us-10-060-765-8.ipr	C;Species: Mus musculus (house mouse)		F;909-925/Domain: transmembrane #status predicted <TM5>	
	C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Sep-2003		F;938-954/Domain: transmembrane #status predicted <TM6>	
us-10-060-765-8.ipr	C;Accession: A45748		F;1025-1041/Domain: transmembrane #status predicted <TM7>	
	A;Title: cDNA cloning and chromosomal mapping of the mouse type VII collagen gene (Col7a1)		F;50.114,165,221/Binding site: carboxylate (Asn) (covalent) #status predicted	
us-10-060-765-8.ipr	A;Reference number: A45748; MUID:93315168; PMID:8325648		F;429/Binding site: ATP (lys) #status predicted	
	A;Accession: A45748		Query Match	
us-10-060-765-8.ipr	A;Status: preliminary		Best Local Similarity 48.3%; Score 43; DB 1; Length 1049;	
	A;Molecule type: nucleic acid		Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;	
us-10-060-765-8.ipr	A;Residues: 1-920 <LIL>		QY 2 LPGNKSPHRDP 12	
	A;Cross-references: GB:S63654; NID:G386656; PIDN:AAB27492.1; PID:G386657		Db 307 IPGYKSPSRKP 317	
us-10-060-765-8.ipr	A;Experimental source: epidermal keratinocyte		RESULT 23	
	A;Note: sequence extracted from NCBI backbone (NCBIN:135000, NCBIF:135001)		T35379	
us-10-060-765-8.ipr	Query Match		Hypothetical protein SC66T3.22 - Streptomyces coelicolor	
	Best Local Similarity 53.8%; Score 43; DB 2; Length 920;		C;Species: Streptomyces coelicolor	
us-10-060-765-8.ipr	Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;		C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999	
	QY 3 PGNGKSPHRDP 15		C;Accession: T35379	
us-10-060-765-8.ipr	Db 236 PGSGPVGDPGR 248		R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.	
	RESULT 22		submitted to the EMBL Data Library, June 1999	
us-10-060-765-8.ipr	S19421		A;Reference number: Z21576	
	ATP-dependent permease ADP1 precursor - Yeast (Saccharomyces cerevisiae)		A;Accession: T35379	
us-10-060-765-8.ipr	N;Alternate names: protein YCR011C; protein YCR105		A;Status: preliminary; translated from GB/EMBL/DBJ	
	C;Species: Saccharomyces cerevisiae		A;Molecule type: DNA	
us-10-060-765-8.ipr	C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-Jan-2001		A;Residues: 1-278 <MUR>	
	C;Accession: S19421; S40914		A;Cross-references: EMBL:AL079348; PIDN:CAB45478.1; GSPDB:GN00070; SCOEDB:SC66T3.22	
us-10-060-765-8.ipr	R;Goffeau, A.; Purnelle, B.; Skala, J.		C;Genetics:	
	submitted to the Protein Sequence Database, March 1992		A;Gene: SCOEDB:SC66T3.22	
us-10-060-765-8.ipr	A;Reference number: S19420		Query Match	
	A;Accession: S19421		Best Local Similarity 47.2%; Score 42; DB 2; Length 278;	
us-10-060-765-8.ipr	A;Molecule type: DNA		Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
	A;Residues: 1-1049 <GOF>		QY 2 LPGNKSPHRDP 14	
us-10-060-765-8.ipr	A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42328.1; PID:g1907154; GSPDB:GN00		Db 122 LPGEPPAPAPAP 134	
	R;Purnelle, B.; Skala, J.; Goffeau, A.		RESULT 24	
us-10-060-765-8.ipr	Yeast 7, 867-872, 1991		T31128	
	A;Title: The product of the YCR105 gene located on the chromosome III from Saccharomyces		3-Isopropylmalate dehydrogenase (EC 1.1.1.85) - Sphingomonas aromaticivorans plasmid p	
us-10-060-765-8.ipr	A;Reference number: S40914; MUID:92160395; PMID:1789009		C;Species: Sphingomonas aromaticivorans	
	A;Accession: S40914		C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000	
us-10-060-765-8.ipr	A;Status: not compared with conceptual translation		R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.;	
	A;Molecule type: DNA		submitted to the EMBL Data Library, July 1998	
us-10-060-765-8.ipr	A;Residues: 1-1049 <PUR>		A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas arom	
	R;Skala, J.; Purnelle, B.; Goffeau, A.		A;Reference number: Z20992	
us-10-060-765-8.ipr	Yeast 8, 409-417, 1992		A;Accession: T31128	
	A;Title: The complete sequence of a 10.8 kb segment distal of SUF2 on the right arm of c		A;Status: preliminary; translated from GB/EMBL/DBJ	
us-10-060-765-8.ipr	K genes.		A;Molecule type: DNA	

A;Residues: 1-355 <ROM>
 A;Cross-references: EMBL:AF079317; NID:G3378261; PID:G3378269; PIDN:AAD03852.1
 C;Genetics:
 A;Genome: plasmid pNL1
 A;Note: orf047
 C;Superfamily: 3-isopropylmalate dehydrogenase
 C;Keywords: oxidoreductase

Query Match 47.2%; Score 42; DB 2; Length 355;
 Best Local Similarity 69.2%; Pred. No. 57;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LPGNKSPHRDPAP 14
 ||| ||| ||| |||
 Db 109 LPGIASPLDKAP 121

RESULT 25
 QOCV6S
 hypothetical protein 6 - cauliflower mosaic virus (strain Strasbourg)
 C;Species: cauliflower mosaic virus
 C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 23-Jul-1999
 C;Accession: A04162
 R;Frank, A.; Guille, H.; Jonard, G.; Richards, K.; Hirth, L.
 Cell 21, 285-294, 1980
 A;Title: Nucleotide sequence of cauliflower mosaic virus DNA.
 A;Reference number: A90799; MUID:81001865; PMID:7407912
 A;Accession: A04162
 A;Molecule type: DNA
 A;Residues: 1-520 <FRA>
 A;Cross-references: GB:V00141; GB:J02048; NID:G58821; PIDN:CAA23461.1; PID:G58827
 C;Superfamily: caulimovirus inclusion body matrix protein

Query Match 47.2%; Score 42; DB 1; Length 520;
 Best Local Similarity 58.3%; Pred. No. 84;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GNKSPHRDPAPR 15
 ||| ||| ||| |||
 Db 228 GTKKPSDDPAPK 239

RESULT 26
 QOCV6
 hypothetical protein 6 - cauliflower mosaic virus (strain D/H)
 C;Species: cauliflower mosaic virus
 C;Date: 31-Oct-1980 #sequence_revision 05-Apr-1983 #text_change 30-Jun-1993
 C;Accession: A04160
 R;Guille, H.
 submitted to the Nucleic Acid Sequence Database, October 1982
 A;Reference number: A94613
 A;Accession: A04160
 A;Molecule type: DNA
 A;Residues: 1-522 <GUI>
 C;Superfamily: caulimovirus inclusion body matrix protein

Query Match 47.2%; Score 42; DB 1; Length 522;
 Best Local Similarity 58.3%; Pred. No. 85;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GNKSPHRDPAPR 15
 ||| ||| ||| |||
 Db 228 GTKKPSDDPAPK 239

RESULT 27
 S06092
 inclusion body matrix protein - cauliflower mosaic virus
 C;Species: cauliflower mosaic virus
 C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
 C;Accession: S06092
 R;Takahashi, H.; Shimamoto, K.; Suzuki, M.; Ehara, Y.
 Nucleic Acids Res. 17, 7981, 1989

A;Title: DNA sequence of gene VI of cauliflower mosaic virus Japanese strain S (CaMV S-1)
 A;Reference number: S06092; MUID:90016879; PMID:2798138
 A;Accession: S06092
 A;Molecule type: DNA
 A;Residues: 1-522 <TAK>
 A;Cross-references: EMBL:X14911; NID:G58828; PIDN:CAA33037.1; PID:G58829
 C;Genetics:
 A;Gene: VI
 C;Superfamily: caulimovirus inclusion body matrix protein

Query Match 47.2%; Score 42; DB 2; Length 522;
 Best Local Similarity 58.3%; Pred. No. 85;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GNKSPHRDPAPR 15
 ||| ||| ||| |||
 Db 228 GTKKPSDDPAPK 239

RESULT 28
 S41627
 probable anti-mullerian hormone receptor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
 C;Accession: S41627
 R;Baarends, W.M.; van Helmond, M.J.L.; Post, M.; van der Schoot, P.J.C.M.; Hoogerbrugge, G.
 Development 120, 189-197, 1994
 A;Title: A novel member of the transmembrane serine/threonine kinase receptor family is
 A;Reference number: S41627; MUID:94163972; PMID:8119126
 A;Accession: S41627
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-557 <BAA>
 A;Cross-references: EMBL:X71916; NID:G453177; PIDN:CAA50731.1; PID:G453178
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
 C;Keywords: ATP
 F;199-510/Domain: protein kinase homology <KIN>

Query Match 47.2%; Score 42; DB 2; Length 557;
 Best Local Similarity 61.5%; Pred. No. 91;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PGNKSPHRDPAPR 15
 ||| ||| ||| |||
 Db 85 PGCESLHCDPVR 97

RESULT 29
 JC5629
 mullerian-inhibiting substance type II receptor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 14-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 04-Mar-2000
 C;Accession: JC5629
 R;Mishina, Y.; Tizard, R.; Deng, J.M.; Pathak, B.G.; Copeland, N.G.; Jenkins, N.A.; Cat
 Biochem. Biophys. Res. Commun. 237, 741-746, 1997
 A;Title: Sequence, genomic organization, and chromosomal location of the mouse Mullerian
 A;Reference number: JC5629; MUID:97445109; PMID:9299437
 A;Accession: JC5629
 A;Molecule type: DNA
 A;Residues: 1-568 <MIS>
 C;Comment: This receptor is involved in the sexual differentiation.

Qy 3 PGNKSPHRDPAPR 15
 ||| ||| ||| |||
 Db 85 PGCESLHCDPVR 97

Query Match 47.2%; Score 42; DB 2; Length 568;
 Best Local Similarity 61.5%; Pred. No. 92;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

A;Note: the authors translated the codon TAT for residue 7 as Thr and TAC for residue 43
R;Oroszlan, S.; Copeland, T.D.; Henderson, L.E.; Stephenson, J.R.; Gilden, R.V.
Proc. Natl. Acad. Sci. U.S.A. 76, 2996-3000, 1979
A;Title: Amino-terminal sequence of bovine leukemia virus major internal protein: Homolog
A;Reference number: A93812; MUID:79223918; PMID:223166
A;Accession: A93812
A;Molecule type: protein
A;Residues: 110-164 <ORO>
R;Copeland, T.D.; Morgan, M.A.; Oroszlan, S.
FEBS Lett. 156, 37-40, 1983
A;Title: Complete amino acid sequence of the nucleic acid-binding protein of bovine leukemia virus
A;Reference number: A91311; MUID:83210199; PMID:6303852
A;Accession: A91311
A;Molecule type: protein
A;Residues: 324-392 <COP>
C;Genetics:
A;Gene: gag
C;Superfamily: mammalian retrovirus gag polypeptide II
C;Keywords: core protein; duplication; phosphoprotein; polypeptide
F;1-109/Product: core protein p15 #status predicted <P15>
F;110-323/Product: core protein p24 #status predicted <P24>
F;324-392/Product: core protein p12 #status experimental <P12>
F;342-362,367-387/Region: duplication
Query Match 46.6%; Score 41.5; DB 1; Length 392;
Best Local Similarity 56.2%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 HLPGNKSP-HRDPAPR 15
Db 325 HTPGPKMPGPRQAPAK 340

RESULT 35
FOLGA
gag polypeptide - bovine leukemia virus (strain Australia)
N;Alternate names: core polypeptide
N;Contains: core protein p12; core protein p15; core protein p24
C;Species: bovine leukemia virus, BLV
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 28-Jul-2000
C;Accession: JQ0554
R;Coulston, J.; Naif, H.; Brandon, R.; Kumar, S.; Khan, S.; Daniel, R.C.W.; Lavin, M.F.
J. Gen. Virol. 71, 1737-1746, 1990
A;Title: Molecular cloning and sequencing of an Australian isolate of proviral bovine leukemia virus
A;Reference number: JQ0554; MUID:90362060; PMID:2167927
A;Accession: JQ0554
A;Molecule type: DNA
A;Residues: 1-392 <COU>
A;Cross-references: DDBJ:D00647; NID:g2920795; PIDN:BA00543.1; PID:g221053
C;Genetics:
A;Gene: gag
C;Superfamily: mammalian retrovirus gag polypeptide II
C;Keywords: core protein; duplication; polypeptide; tandem repeat
F;1-109/Product: core protein p15 #status predicted <MAT>
F;110-323/Product: core protein p24 #status predicted <MAC>
F;324-392/Product: core protein p12 #status predicted <MAO>
F;342-362,367-387/Region: 21-residue repeats
Query Match 46.6%; Score 41.5; DB 1; Length 392;
Best Local Similarity 56.2%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 HLPGNKSP-HRDPAPR 15
Db 325 HTPGPKMPGPRQAPAK 340

RESULT 36
S29356
gag protein - bovine leukemia virus
C;Species: bovine leukemia virus, BLV
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
C;Accession: S29356

R;Pace, N.R.; Stephens, R.M.; Burny, A.; Gilden, R.V.
Virology 142, 357-377, 1985
A;Title: The gag and pol genes of bovine leukemia virus: nucleotide sequence and analysis
A;Reference number: S29356; MUID:86045859; PMID:2997990
A;Accession: S29356
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-393 <RIC>
A;Cross-references: EMBL:M10987; NID:g210784; PIDN:AAA42794.1; PID:g210785
C;Superfamily: mammalian retrovirus gag polypeptide II
Query Match 46.6%; Score 41.5; DB 2; Length 393;
Best Local Similarity 56.2%; Pred. No. 76;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
QY 1 HLPGNKSP-HRDPAPR 15
Db 326 HTPGPKMPGPRQAPAK 341

RESULT 37
T49868
related to suppressor protein SPT23 [imported] - Neurospora crassa
N;Alternate names: protein B24P11.240
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49868
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1174 <SCH>
A;Cross-references: EMBL:AL356833; GSPDB:GM00116; NCSP:B24P11.240
A;Experimental source: BAC clone B24P11; strain OR74A
C;Genetics:
A;Gene: NCSP:B24P11.240
A;Map position: 6
A;Introns: 407/1
Query Match 46.6%; Score 41.5; DB 2; Length 1174;
Best Local Similarity 37.5%; Pred. No. 2.3e+02;
Matches 9; Conservative 3; Mismatches 1; Indels 11; Gaps 1;
QY 2 LPGNK-----SPHRDPAP 14
Db 465 LPGNQGLNFFANPTSGNPSRDPSP 488

RESULT 38
H82597
hypothetical protein XF2103 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82597
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: H82597
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-111 <SIM>
A;Cross-references: GB:AE004026; GB:AE003849; NID:g9107228; PIDN:AAF84902.1; GSPDB:GN00;
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, I.
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

Db 59 PSTSPHCHPSPR 71

Search completed: March 2, 2004, 16:08:07
Job time : 3.125 secs

Query Match 46.1%; Score 41; DB 2; Length 111;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPA 13
||| : ||| :
Db 72 HLPYQRPHPDPS 84

RESULT 39
T47161
hypothetical protein DKFZp762A1712.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
R;Accession: T47161
C;Ansong, W.; Winkler, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24375
A;Accession: T47161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <AAA>
A;Cross-references: EMBL:AL161978
A;Experimental source: adult melanoma (MeWo cell line); clone DKFZp762A1712
C;Genetics:
A;Note: DKFZp762A1712.1

Query Match 46.1%; Score 41; DB 2; Length 117;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPA 14
||| : ||| :
Db 22 HVPQGGTHRPAP 35

RESULT 40
S54309
hypothetical 13.2K protein - fowl adenovirus 1
C:Species: Aviadenovirus gall (fowl adenovirus 1, CELO)
C>Date: 08-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 28-Jul-2000
C;Accession: S54309
R;Hess, M.; Cuzange, A.; Chroboczek, J.; Ruigrok, R.; Jacrot, B.
submitted to the EMBL Data Library, February 1995
A;Description: The sequence of the two fibers of an avian adenovirus (CELO) and organis
A;Reference number: S54125
A;Accession: S54309
A;Molecule type: DNA
A;Residues: 1-118 <HES>
A;Cross-references: EMBL:X84724; NID:G780165; PIDN:CAA59209.1; PID:G780170
R;Hess, M.; Cuzange, A.; Ruigrok, R.W.H.; Chroboczek, J.; Jacrot, B.
J. Mol. Biol. 252, 379-385, 1995
A;Title: The avian adenovirus penton: two fibres and one base.
A;Reference number: S59067; MUID:96025073; PMID:7563058
A;Contents: annotation
C;Superfamily: Aviadenovirus gall hypothetical 13.2K protein

Query Match 46.1%; Score 41; DB 2; Length 118;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 PGNKSPHRDPA 15

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2004, 15:51:42 ; Search time 6.25 Seconds
(without alignments)
757.244 Million cell updates/sec

Title: US-10-060-765-8

Perfect score: 89

Sequence: 1 HLPGNKSPHRDPAPR 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTRMBL.25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_rhiz.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rviro.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	89	100.0	209	4 Q8N683	Q8N683 homo sapien
2	52	58.4	1173	11 Q63624	Q63624 rattus norv
3	50	56.2	165	17 Q9YC35	Q9YC35 aeropyrum p
4	48	53.9	385	10 Q9SSY2	Q9SSY2 cucumis sat
5	48	53.9	492	16 Q9WXX1	Q9WXX1 thermotoga
6	48	53.9	574	5 Q9BLT0	Q9BLT0 leishmania
7	48	53.9	601	16 Q7UX42	Q7UX42 rhodopirell
8	47	52.8	2936	6 Q7YRK8	Q7YRK8 canis fami
9	46	51.7	181	6 Q9TRZ5	Q9TRZ5 oryctolagus
10	45	50.6	111	16 Q87DB2	Q87DB2 xylella fas
11	45	50.6	178	10 Q7XY38	Q7XY38 griffithsia
12	45	50.6	326	16 Q7U8Z9	Q7U8Z9 synechococc
13	45	50.6	352	10 Q9LI15	Q9LI15 oryza sativ
14	45	50.6	517	16 Q8ZGK0	Q8ZGK0 versinia pe
15	45	50.6	802	4 Q9Y2J5	Q9Y2J5 homo sapien
16	45	50.6	802	4 Q86X52	Q86X52 homo sapien

17	45	50.6	1294	10 Q9S814	Q9S814 arabidopsis
18	45	50.6	1687	5 Q8T9L7	Q8T9L7 toxoplasma
19	44.5	50.0	625	10 Q8L4G8	Q8L4G8 oryza sativ
20	44	49.4	128	16 Q93JD6	Q93JD6 streptomyce
21	44	49.4	274	5 Q8T2Z8	Q8T2Z8 trypanosoma
22	44	49.4	339	10 Q22465	Q22465 glycine max
23	44	49.4	426	16 Q8AOK9	Q8AOK9 bacteroides
24	44	49.4	487	2 Q52719	Q52719 klebsiella
25	44	49.4	487	2 Q8GQNS	Q8GQNS escherichia
26	44	49.4	494	16 Q83EH5	Q83EH5 coxiella bu
27	44	49.4	520	2 Q8KZ56	Q8KZ56 uncultured
28	44	49.4	613	5 Q9U252	Q9U252 caenorhabdi
29	44	49.4	665	11 Q9EQH1	Q9EQH1 rattus norv
30	44	49.4	665	11 Q9R1X3	Q9R1X3 mus musculu
31	44	49.4	666	11 Q9Z1S8	Q9Z1S8 mus musculu
32	44	49.4	971	5 Q94527	Q94527 drosophila
33	43	48.3	105	17 Q9YBU3	Q9YBU3 aeropyrum p
34	43	48.3	142	11 Q8BW91	Q8BW91 mus musculu
35	43	48.3	182	11 Q8BLG7	Q8BLG7 mus musculu
36	43	48.3	184	11 Q8BW77	Q8BW77 mus musculu
37	43	48.3	193	10 Q8L479	Q8L479 oryza sativ
38	43	48.3	208	17 Q8TV81	Q8TV81 methanopyru
39	43	48.3	211	4 Q9NSH9	Q9NSH9 homo sapien
40	43	48.3	281	10 Q9LDR8	Q9LDR8 oryza sativ
41	43	48.3	292	16 Q8VJ12	Q8VJ12 mycobacteri
42	43	48.3	481	16 Q89I54	Q89I54 bradyrhizob
43	43	48.3	511	16 Q8CJ09	Q8CJ09 streptomyce
44	43	48.3	653	16 Q7US57	Q7US57 synechococc
45	43	48.3	670	10 Q8RVE5	Q8RVE5 oryza sativ

ALIGNMENTS

RESULT 1

Q8N683 ID Q8N683 PRELIMINARY; PRT; 209 AA.
AC Q8N683; TISSUE=Lung;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2003 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Fibroblast growth factor 21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018404; AAH18404.1; --
DR GO; GO:0008083; F:growth factor activity; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; IL1_HBGF; 1.
DR SMART; SM00442; FGF; 1.
SQ SEQUENCE 209 AA; 22284 MW; 27925C43E5167823 CRC64;

Query Match 100.0%; Score 89; DB 4; Length 209;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15

|||||
145 HLPGNKSPHRDPAPR 159

RESULT 2

Q63624 ID Q63624 PRELIMINARY; PRT; 1173 AA.

RESULT 4
O9SSY2


```

DR Pfam; PF02782; FGGY_C; 1.
DR TIGRPFAM; TIGR01312; XYIB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
DR PROSITE; PS00304; SASP_1; 1.
DR KINASE; Complete proteome.
SQ SEQUENCE 492 AA; 54405 MW; 0F6A3AB451D89E1 CRC64;

Query Match 53.9%; Score 48; DB 16; Length 492;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
DB 340 YLNGERTPHRDPPAR 354

RESULT 6
Q9BLT0 PRELIMINARY; PRT; 574 AA.
AC Q9BLT0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible monooxygenase transporter protein.
GN L6071.01.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RC STRAIN=Friedlin;
RC Zimmermann W., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RC MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL583933; CAC32260.1; -.
DR GO; GO:0004867; F:serine protease inhibitor activity; IEA.
DR InterPro; IPR006105; Try/amy1 inhib.
DR PROSITE; PS00426; CEREAL_TRYP_1.
SQ SEQUENCE 574 AA; 61489 MW; C22D8283F006965E CRC64;

Query Match 53.9%; Score 48; DB 5; Length 574;
Best Local Similarity 57.1%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 14
DB 219 HARGNNSPAREPSP 232

RESULT 7
Q7UX42 PRELIMINARY; PRT; 601 AA.
AC Q7UX42;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glutaminyl-tRNA synthetase (EC 6.1.1.18).
GN GLNS OR R81578.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=1;

RX MEDLINE=22735913; PubMed=12835416;
RX Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RX Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RX Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; EX294135; CAD72170.1; -.
SQ Aminoacyl-tRNA synthetase; Ligase; Complete proteome.
KW SEQUENCE 601 AA; 68668 MW; 0C6B526811FF4CD3 CRC64;

Query Match 53.9%; Score 48; DB 16; Length 601;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGKNSPHRDPPAPR 14
DB 181 PGKNSPHRDTP 192

RESULT 8
Q7YRK8 PRELIMINARY; PRT; 2936 AA.
AC Q7YRK8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type VII collagen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=22756273; PubMed=12874109;
RA Baldeschi C., Gache Y., Rattenholl A., Bouillie P., Danos O.,
RA Ortonne J.P., Bruckner-Tuderman L., Meneguzzi G.;
RT "Genetic correction of canine dystrophic epidermolysis bullosa
RT mediated by retroviral vectors.";
RL Hum. Mol. Genet. 12:1897-1905(2003).
DR EMBL; AV183408; AA064414.1; -.
KW Collagen.
SQ SEQUENCE 2936 AA; 293983 MW; F80CAF40E1F699B9 CRC64;

Query Match 52.8%; Score 47; DB 6; Length 2936;
Best Local Similarity 57.1%; Pred. No. 21e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 LPGNKSPHRDPAPR 15
DB 1372 LPGSRGLGDPGPR 1385

RESULT 9
Q9TRZ5 PRELIMINARY; PRT; 181 AA.
AC Q9TRZ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 0(6)-methylglutamine-DNA methyltransferase (EC 2.1.1.63).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=96181606; PubMed=8601571;
RX Sekiguchi M., Nakabeppu Y., Sakumi K., Tuzuki T.;
RT "DNA-repair methyltransferase as a molecular device for preventing
RT mutation and cancer.";
RL J. Cancer Res. Clin. Oncol. 122:199-206(1996).
DR HSSP; P06134; 1SFE.

```

DR GO: GO:0003908; F:methylated-DNA-[protein]-cysteine S-methylt. .; IEA.
 DR GO: GO:0006281; P:DNA repair; IEA.
 DR InterPro; IPR008332; MethylG_Mtase.
 DR InterPro; IPR001497; Methyltransf_1.
 DR Pfam; PF01035; Methyltransf_1; 1.
 DR Pfam; PF02870; Methyltransf_1N; 1.
 DR TIGRFAMs; TIGR00589; Ogt; 1.
 DR PROSITE; PS00374; MGMT; 1.
 DR SEQUENCE 181 AA; 19397 MW; 12DF60974AA41A16 CRC64;
 Query Match 51.7%; Score 46; DB 6; Length 181;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LFGNKSPPHRDPA 13
 DB 33 LFGKTPPADPA 44
 RESULT 10
 ID Q87DB2 PRELIMINARY; PRT; 111 AA.
 AC Q87DB2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Conserved hypothetical protein.
 GN PD0774.
 OS Xylella fastidiosa (strain Temecual / ATCC 700964).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=183190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22421331; PubMed=12533478;
 RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Moon D.H.,
 RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., da Silva F.R.,
 RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
 RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
 RA Carrier H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
 RA Coutinho L.B., Kimura E.T., Abreu I.L., Alves L.M.C., do Amaral A.M.,
 RA Martino C.L., Gigliotti E., Brito M.S., Cannavan F.S., Celestino A.V.,
 RA Baia G.S., Blanco S.R., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
 RA da Cunha A.F., Fenille R.C., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
 RA Leoni S.G., Oliveira A.R., Teukumo F., Yanai G.M., Zaros L.G.,
 RA Civerolo E.B., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
 RA Kitajima J.P.;
 RT "Comparative analyses of the complete genome sequences of Pierce's
 RT disease and citrus variegated chlorosis strains of Xylella
 RT fastidiosa";
 RL J. Bacteriol. 185:1018-1026(2003).
 DR EMBL; AE012556; AAC28642.1; --
 DR InterPro; IPR000437; Prok_LipoProt_S.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 111 AA; 13336 MW; 492CB96C4507E840 CRC64;
 Query Match 50.6%; Score 45; DB 16; Length 111;
 Best Local Similarity 53.8%; Pred. No. 14;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPA 13
 DB 72 HLPQQRPHDPS 84
 RESULT 11
 ID Q7YX38 PRELIMINARY; PRT; 178 AA.
 AC Q7YX38;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Serine palmitoyltransferase (fragment).
 OS Griffithsia japonica.
 OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiales;
 OC Griffithsia.
 OX NCBI_TaxID=83288;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu C., Lee Y., Lee H.;
 RA EMBL; AF542030; AAP80840.1; --
 DR EMBL; AF542030; AAP80840.1; --
 KW Transferase.
 FT NON-TER 178 178
 SQ SEQUENCE 178 AA; 20056 MW; 4264182D29A597FF CRC64;
 Query Match 50.6%; Score 45; DB 10; Length 178;
 Best Local Similarity 46.2%; Pred. No. 23;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 1 HLPGNKSPHRDPA 13
 DB 114 HIPGRTPHDQPS 126
 RESULT 12
 ID Q7U8Z9 PRELIMINARY; PRT; 326 AA.
 AC Q7U8Z9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative glycosyltransferase family 4 protein (EC 2.4.1.-).
 GN SYNW0460.
 OS Synecococcus sp. (strain WH8102).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
 OX NCBI_TaxID=84588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825697; PubMed=12917641;
 RA Palenik B., Brahmshah B., Larimer F.W., Land M., Hauser L., Chain P.,
 RA Lamerdin J., Regala W., Allen E.E., McCarren J., Paulsen I.,
 RA Dufresne A., Partensky F., Webb E.A., Waterbury J.;
 RT "The genome of a motile marine Synecococcus";
 RL Nature 424:1037-1042(2003).
 DR EMBL; EX563690; CAB06975.1; --
 KW Glycosyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 326 AA; 35270 MW; EDC4D8DC51EB3526 CRC64;
 Query Match 50.6%; Score 45; DB 16; Length 326;
 Best Local Similarity 57.1%; Pred. No. 44;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 LFGNKSPPHRDPA 15
 DB 34 LFNRRSSHSVPTPR 47
 RESULT 13
 ID Q9LI15 PRELIMINARY; PRT; 352 AA.
 AC Q9LI15;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (OSJNB0086P08.1 protein).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RT STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: P0708G02";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone: OSJNBa0086P08";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF001539; BAA92924.1; -;
 DR EMBL; AF002855; BAB17192.1; -;
 DR Gramene; Q9LI15; -;
 SQ SEQUENCE 352 AA; 39614 MW; B238C55E4707835B CRC64;

 Query Match 50.6%; Score 45; DB 10; Length 352;
 Best Local Similarity 52.9%; Pred. No. 47;
 Matches 9; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

 QY 1 HL--PGNKSPPHDPAPR 15
 Db 246 HLCAGEESFDRSPTEK 262

 RESULT 14
 Q8ZGKO PRELIMINARY; PRT; 517 AA.
 AC Q8ZGKO; RC
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Putative carbohydrate kinase (Putative xylose kinase).
 GN YPO1291 OR Y2893.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIM5 / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Zhubak R.B., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AJ414147; CAC90122.1; -;
 DR EMBL; AE013892; AAM86444.1; -;
 DR PIR; AG0157; AG0157.
 DR GO; GO:0016301; F:kinase activity; IEA.
 DR GO; GO:0004856; F:xylokinase activity; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR GO; GO:0005997; P:xylose metabolism; IEA.
 DR InterPro; IPR000577; FGGY_kin.
 DR InterPro; IPR006000; Xylulokinase.
 DR Pfam; PF00370; FGGY_1.
 DR Pfam; PF02782; FGGY_C; 1.

 DR TIGRfams; TIGR01312; xylB; 1.
 DR PROSITE; PS00933; FGGY_KINASES_1; 1.
 DR PROSITE; PS00445; FGGY_KINASES_2; 1.
 KW Hypothetical protein; Kinase; Complete proteome.
 SQ SEQUENCE 517 AA; 54066 MW; C836FB87C12BB111 CRC64;

 Query Match 50.6%; Score 45; DB 16; Length 517;
 Best Local Similarity 53.3%; Pred. No. 71;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

 QY 1 HLPGNKSPHDPAPR 15
 Db 357 YLNGRCFHPDPAAR 371

 RESULT 15
 Q9Y2J5 PRELIMINARY; PRT; 802 AA.
 AC Q9Y2J5; RC
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein KIAA0990 (Chondroitin synthase).
 GN KIAA0990 OR CHSY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99246663; PubMed=10231032;
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:63-70(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21486534; PubMed=11514575;
 RA Kitagawa H., Uyama T., Sugahara K.;
 RT "Molecular Cloning and Expression of a Human Chondroitin Synthase."
 RL J. Biol. Chem. 276:38721-38726(2001).
 DR EMBL; AB023207; BAA76834.1; -;
 DR EMBL; AB071402; BAB64936.1; -;
 DR InterPro; IPR008428; CHGN.
 DR Pfam; PF05679; CHGN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 802 AA; 91729 MW; 9115C204FAF298D7 CRC64;

 Query Match 50.6%; Score 45; DB 4; Length 802;
 Best Local Similarity 63.8%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

 QY 2 LPGNKSPHDP 12
 Db 519 LPGNKSPHDP 529

 RESULT 16
 Q86X52 PRELIMINARY; PRT; 802 AA.
 AC Q86X52; RC
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Carbohydrate (Chondroitin) synthase 1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RA	Strausberg R.;
RRL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC046247; AAAH46247.1; -.
SQ	SEQUENCE 802 AA; 91784 MW; 5B4C02670332FA0E CRC64;
Query Match	50.6%; Score 45; DB 4; Length 802;
Best Local Similarity	63.6%; Pred. No. 1.1e+02;
Matches	7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY	2 LPGNKSPHRDP 12 : :
DB	519 LFGSKSEHKP 529
RESULT 17	
ID	Q9S814 PRELIMINARY; PRT; 1294 AA.
AC	Q9S814;
DT	01-MAY-2000 (TREMELrel. 13, Created)
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT	01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE	EIN2.
OS	EIN2 OR F12E4.10.
GN	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsiis.
OX	NCBI_TaxID=3702;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=99316073; PubMed=10381874;
RA	Alonso J.M., Hirayama T., Roman G., Nourizadeh S., Ecker J.R.;
RT	"Ein2, a Bifunctional Transducer of Ethylene and Stress Responses in Arabidopsis.";
RT	Science 284:2148-2152 (1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd S.,
RA	Lemcke K., Mayer K.F.X.; to the EMBL/GenBank/DBJ databases.
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE FROM N.A.
RA	EU Arabidopsis sequencing project;
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Columbia;
FX	MEDLINE=97471969; PubMed=9330910;
RA	Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA	Miyajima N., Tabata S.;
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned pl clones.";
RT	DNA Res. 4:215-230(1997).
RL	EMBL; AF141203; AAD41077.1; -.
DR	EMBL; AF141202; AAD41076.1; -.
DR	EMBL; AL162751; CAB83284.1; -.
DR	EMBL; AB005240; BAB08388.1; -.
DR	Pir; T48349; T48349.
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0005215; F:transporter activity; IEA.
DR	GO; GO:0006810; P:transport; IEA.
DR	InterPro; IPR001046; Ntamp.
DR	Pfam; PF01566; Ntamp; 1.
DR	PRINTS; PR00447; NATRESASCMCP.
DR	ProDom; PD001861; Ntamp; 1.
SQ	SEQUENCE 1294 AA; 140955 MW; 1A806303B8B8E71B CRC64;
Query Match	50.6%; Score 45; DB 10; Length 1294;
Best Local Similarity	61.5%; Pred. No. 1.9e+02;
Matches	8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY	1 HLPGNKSPHRDPA 15 : :
DB	1548 HLFNGNAPSADSGLR 1562

RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL939125; CAC44605.1; -.
 KW Complete proteome.
 SQ SEQUENCE 128 AA; 12736 MW; CD0FC3CFAB94821E CRC64;

Query Match 49.4%; Score 44; DB 16; Length 128;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PGKSPHRDPAP 14
 Db 91 PRATSPHTDPAP 102

RESULT 21

ID Q8T2Z8 PRELIMINARY; PRT; 274 AA.
 AC Q8T2Z8;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE Tcclj12.7.
 DE Tcclj12.7.
 GN Tcclj12.7.
 OS Trypanosoma cruzi.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CL Brenner;
 RA Anderson B., Boncompagni E.J.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC096945; AAL90893.1; -.
 SQ SEQUENCE 274 AA; 28374 MW; 76636EA2BA24A09D CRC64;

Query Match 49.4%; Score 44; DB 5; Length 274;
 Best Local Similarity 70.0%; Pred. No. 53;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 NKSPHRDPAP 14
 Db 194 DKSPHNDPLP 203

RESULT 22

ID Q22465 PRELIMINARY; PRT; 339 AA.
 AC Q22465;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GH1 protein (Fragment).
 GN GH1.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wayne;
 RA Hagen G., Guilfoyle T.J.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016633; AAB70005.1; -.
 DR PIR; T05726; T05726.
 DR TRANSFAC; T04524; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0006445; P:regulation of translation; IEA.
 DR InterPro; IPR003311; AUX_1AA.
 DR Pfam; PF02309; AUX_1AA; 1.
 FT NON TER 1
 SQ SEQUENCE 339 AA; 36477 MW; 0B9C99BC3FD45C6F CRC64;

RESULT 19

Q8L4G8 PRELIMINARY; PRT; 625 AA.
 AC Q8L4G8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE P0676G08.4 protein (OSJNB0093M23.16 protein).
 GN P0676G08.4 OR OSJNB0093M23.16.
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoideae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC clone: P0676G08.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003854; BAC06289.1; -.
 GN Gramine; Q8L4G8; -.
 GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR004695; C4dc/mal_transpt.
 DR Pfam; PF03595; C4dc/mal_tran; 1.
 SQ SEQUENCE 625 AA; 68596 MW; 80E8CA498EC47D8 CRC64;

Query Match 50.0%; Score 44.5; DB 10; Length 625;
 Best Local Similarity 50.0%; Pred. No. 1e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

QY 1 HLPG---NKSPHRDPAP 15
 Db 23 HLAGFDVTPSPHAPSPR 40

RESULT 20

Q93JD6 PRELIMINARY; PRT; 128 AA.
 AC Q93JD6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative secreted protein.
 GN SC05991 OR STBAC16H6.26 OR SCBAC16H6.26.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdono-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., Harris K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Lake L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,
 RA Hopwood D.A.;

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RC STRAIN=1033-SP14;
RX MEDLINE=98304087; PubMed=9639934;
RA Heuel H., Shakeri-Garakani A., Turgut S., Lengeler J.W.;
RT "Genes for D-arabinitol and ribitol catabolism from Klebsiella
  pneumoniae.";
RL Microbiology 144:1631-1639(1998).
DR EMBL; AF045245; AAC26499.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004856; F:xylulokinase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005997; P:xylulose metabolism; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR006000; Xylulokinase.
DR Pfam; PF00370; FGGY_1.
DR Pfam; PF02782; FGGY_C; 1.
DR TIGRfams; TIGR01312; xylB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
DR KINASE.
KW KINASE.
SQ SEQUENCE 487 AA; 52828 MW; DF648CDB68CF34DB CRC64;

Query Match 49.4%; Score 44; DB 2; Length 487;
Best Local Similarity 46.7%; Pred. No. 96;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 336 YLSGERTPHNDPAPR 350

RESULT 25
Q8QGN5 PRELIMINARY; PRT; 487 AA.
AC Q8QGN5;
DT 01-WAR-2003 (TREMBlrel. 23, Created)
DT 01-WAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Xylulose kinase.
GN ATLK.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RA Kane P.M., LaFayette P.R., Parrott W.A.;
RT "Cloning and characterization of the arabitol operon.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378082; AAN32628.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004856; F:xylulokinase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005997; P:xylulose metabolism; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR006000; Xylulokinase.
DR Pfam; PF00370; FGGY_1.
DR Pfam; PF02782; FGGY_C; 1.
DR TIGRfams; TIGR01312; xylB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
DR KINASE.
KW KINASE.
SQ SEQUENCE 487 AA; 53077 MW; FB1857B7E66E4E86 CRC64;

Query Match 49.4%; Score 44; DB 2; Length 487;
Best Local Similarity 46.7%; Pred. No. 96;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 HLPGNKSPHRDPAPR 15
Db 336 YLSGERTPHNDPAPR 350

RESULT 26
Q8QGN5 PRELIMINARY; PRT; 487 AA.
AC Q8QGN5;
DT 01-WAR-2003 (TREMBlrel. 23, Created)
DT 01-WAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Xylulose kinase.
GN ATLK.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RA Kane P.M., LaFayette P.R., Parrott W.A.;
RT "Cloning and characterization of the arabitol operon.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378082; AAN32628.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004856; F:xylulokinase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0005997; P:xylulose metabolism; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR006000; Xylulokinase.
DR Pfam; PF00370; FGGY_1.
DR Pfam; PF02782; FGGY_C; 1.
DR TIGRfams; TIGR01312; xylB; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
DR KINASE.
KW KINASE.
SQ SEQUENCE 487 AA; 53077 MW; FB1857B7E66E4E86 CRC64;

Query Match 49.4%; Score 44; DB 10; Length 339;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LPGAQSPHRDP 12
Db 62 LPGAQSPHERP 72

RESULT 23
Q8AOK9 PRELIMINARY; PRT; 426 AA.
AC Q8AOK9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative ABC oligo/dipeptide transport, ATP-binding protein.
GN BT4012.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Hamrod J., Deng S., Carmichael L.K.,
  Chiang H.C., Hooper L.V., Gordon J.I.;
RL "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RT Science 299:2074-2076(2003).
DR EMBL; AB016943; AAO79117.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR ATP-binding; Complete proteome.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 426 AA; 48748 MW; 635D2514FF7FE8F8 CRC64;

Query Match 49.4%; Score 44; DB 16; Length 426;
Best Local Similarity 88.9%; Pred. No. 83;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 LPGAQSPHR 10
Db 323 LPGAQSPER 331

RESULT 24
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-SP14;
RX MEDLINE=97464425; PubMed=9324246;
RA Heuel H., Turgut S., Schmid K., Lengeler J.W.;
RT "Substrate recognition domains as revealed by active hybrids between
  the D-arabinitol and ribitol transporters from Klebsiella
  pneumoniae.";
RL J. Bacteriol. 179:6014-6019(1997).
RN [2]
RP SEQUENCE FROM N.A.

```

Q83EH5		Q83EH5	
ID	Q83EH5	PRELIMINARY;	PRT; 494 AA.
AC	Q83EH5;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Xylulokinase.		
GN	XYLB OR CB00346.		
OS	Coxiella burnetii.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;		
OC	Coxiellaceae; Coxiella.		
OX	NCBI_TaxID=777;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Nine Mile phase I / RSA 493;		
RX	MEDLINE=22608657; PubMed=12704232;		
RA	Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,		
RA	Nelson W.C., Ward N.L., Tettelin H., Davidse T.M., Beanan M.J.,		
RA	DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,		
RA	Khoury H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,		
RA	Thompson H.A., Samuel J.B., Fraser C.M., Heidelberg J.F.;		
RT	"Complete genome sequence of the Q-fever pathogen, Coxiella		
RT	burnetii."		
RL	Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460 (2003).		
DR	EMBL; AE016961; AAO99901.1; -.		
DR	TIGR; CB00346; -.		
DR	GO; GO:0016301; F:kinase activity; IEA.		
DR	GO; GO:0004856; F:xylulokinase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	GO; GO:0005997; P:xylulose metabolism; IEA.		
DR	InterPro; IPR000577; FGGY kin.		
DR	InterPro; IPR006000; Xylulokinase.		
DR	Pfam; PF00370; FGGY; 1.		
DR	Pfam; PF02782; FGGY; 1.		
DR	TIGRFAMS; TIGR01312; XylB; 1.		
DR	PROSITE; PS00933; FGGY_KINASES_1; 1.		
DR	PROSITE; PS00445; FGGY_KINASES_2; 1.		
KW	Kinase; Complete proteome.		
SQ	SEQUENCE 494 AA; 54281 MW; D9A2C6C9F48C254E CRC64;		
Query Match		49.4%; Score 44; DB 16; Length 494;	
Best Local Similarity		46.7%; Pred. No. 97;	
Matches		7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	
QY	1 HLPGNKSPHRDPAPR 15		
Db	337 YLSEPTPHNDPYAR 351		
RESULT 27			
ID	Q8KZ56	PRELIMINARY;	PRT; 520 AA.
AC	Q8KZ56;		
DT	01-OCT-2002 (TrEMBLrel. 22, Created)		
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Light-independent protochlorophyllide reductase, B subunit.		
GN	BCHB.		
OS	uncultured proteobacterium.		
OC	Bacteria; Proteobacteria; environmental samples.		
OX	NCBI_TaxID=153809;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21822632; PubMed=11832943;		
RA	Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,		
RA	Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;		
RT	"Unaspected diversity among marine aerobic anoxygenic phototrophs."		
RL	Nature 415:630-633 (2002).		
DR	EMBL; AE008920; AAM48617.1; -.		
DR	GO; GO:0016730; P:oxidoreductase activity, acting on iron-sul. . .; IEA.		
DR	GO; GO:0015995; P:chlorophyll biosynthesis; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	GO; GO:0019685; P:photosynthesis, dark reaction; IEA.		
Query Match		49.4%; Score 44; DB 5; Length 613;	
Best Local Similarity		58.3%; Pred. No. 1.2e+02;	
Matches		7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	1 HLPGNKSPHRDP 12		
Db	144 HFPGPPGPHRPP 155		
RESULT 29			
ID	Q9EQH1	PRELIMINARY;	PRT; 665 AA.
AC	Q9EQH1;		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	Grb2-associated binder 2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kong M., Mounier C., Wu J., Posner B.I.;		
RT	"Identification of Gab2 as the major molecule responsible for EGF-		
RT	induced PI3-kinase activation and DNA synthesis in rat hepatocytes."		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: CONTAINS 1 PH DOMAIN.		
DR	EMBL; AF230367; AAG44268.2; -.		
DR	InterPro; IPR001849; PH.		
Query Match		49.4%; Score 44; DB 2; Length 520;	
Best Local Similarity		61.5%; Pred. No. 1e+02;	
Matches		8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
QY	3 PGNKSPHRDPAPR 15		
Db	152 PGTQPSRDPAPR 164		
RESULT 28			
ID	Q9U252	PRELIMINARY;	PRT; 613 AA.
AC	Q9U252;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Y53H1A.1 protein.		
GN	Y53H1A.1.		
OS	Caenorhabditis elegans.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;		
OC	Rhabditidae; Peloderinae; Caenorhabditis.		
OX	NCBI_TaxID=6239;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	White S.;		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99069613; PubMed=9851916;		
RA	none;		
RT	"Genome sequence of the nematode C.elegans: A platform for		
RT	investigating biology."		
RL	Science 282:2012-2018 (1998).		
DR	EMBL; AL132864; CAB63392.1; -.		
DR	WormPep; Y53H1A.1; CE25431.		
SQ	SEQUENCE 613 AA; 68897 MW; B55ABCA6062C338D CRC64;		

RT Pfam; PF00169; PH; 1.
RL SMART; SM00233; PH; 1.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AF104244; AAD05166.1; -.
DR MGD; MGI1333854; Gab2.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016477; P:cell migration; IDA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IDA.
DR InterPro; IPR001849; PH.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
SQ SEQUENCE 666 AA; 73295 MW; D3B6D568CFBA3F7 CRC64;

Query Match 49.4%; Score 44; DB 11; Length 666;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGKSPHRDPA 13
||: |||||:
Db 611 PGSPSPHRKPS 621

RESULT 32

Q94527 PRELIMINARY; PRT; 971 AA.
AC Q94527; Q9VH10; Q9UGH5;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Rel/NF-kappa B homolog (Rel protein) (Transcription factor maternal isoform) (GH01881p).
DE REL OR CG11992.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX [1]
RX SEQUENCE FROM N.A. (MAJOR ISOFORM).
RX MEDLINE=96413648; PubMed=8816802;
RA Dushay M.S., Aelling B., Hultmark D.;
RT "Origins of immunity: Relish, a compound Rel-like gene in the antibacterial defense of Drosophila";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10343-10347(1996).
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=20085749; PubMed=10619029;
RX Hedengren M., Aelling B., Dushay M.S., Ando I., Ekengren S., Wihlborg M., Hultmark D.;
RT "Relish, a Central Factor in the Control of Humoral, but not Cellular Immunity in Drosophila";
RL Mol. Cell 4:827-837(1999).
RN [3]
RP SEQUENCE FROM N.A. (MAJOR ISOFORM).
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

DR Pfam; PF00169; PH; 1.
DR SMART; SM00233; PH; 1.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
SQ SEQUENCE 665 AA; 73328 MW; BEE170B69406063E CRC64;

Query Match 49.4%; Score 44; DB 11; Length 665;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGKSPHRDPA 13
||: |||||:
Db 610 PGSPSPHRKPS 620

RESULT 30

Q9R1X3 PRELIMINARY; PRT; 665 AA.
AC Q9R1X3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Gab2.
GN GAB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=99168966; PubMed=10068651;
RA Nishida K., Yoshida Y., Itoh M., Fukada T., Ohtani T., Shirogane T., Asumi T., Takahashi-Tezuka M., Iehihara K., Hibi M., Hirano T.;
RT "Gab-family adapter proteins act downstream of cytokine and growth factor receptors and T- and B-cell antigen receptors";
RL Blood 93:1809-1816(1999).
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AB018414; BAA76738.1; -.
DR MGD; MGI1333854; Gab2.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016477; P:cell migration; IDA.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IDA.
DR InterPro; IPR001849; PH.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
SQ SEQUENCE 665 AA; 73208 MW; B8955EB638174085 CRC64;

Query Match 49.4%; Score 44; DB 11; Length 665;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 PGKSPHRDPA 13
||: |||||:
Db 610 PGSPSPHRKPS 620

RESULT 31

Q9Z1S8 PRELIMINARY; PRT; 666 AA.
AC Q9Z1S8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE PH domain containing adaptor molecule p97/Gab2.
GN GAB2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
Gu H., Pratt J.C., Burakoff S.J., Neel B.G.;
RT "Cloning of p97/Gab2, the major SHP2-binding protein in hematopoietic

RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Major;
CC IsoId=Q94527-1; Sequence=Displayed;
CC Name=Maternal;
CC IsoId=Q94527-2; Sequence=VSP_050089;
CC U62005; AAB17264.1; --
DR EMBL; AF186073; AAF07931.1; --
DR EMBL; AF186073; AAF07932.1; --
DR EMBL; AE003681; AAP54333.1; ALT_INIT.
DR EMBL; AY058264; AAL13493.1; --
DR HSSP; P25799; I1KN.
DR FlyBase; FBgn0014018; Rel.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003704; F:specific RNA polymerase II transcription fa. .; NAS.
DR GO; GO:0006963; P:antibacterial polypeptide induction; IMP.
DR GO; GO:0006967; P:antifungal polypeptide induction; IMP.
DR GO; GO:0006955; P:immune response; IEP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR002909; IPT_TIG.
DR InterPro; IPR000451; NF_Rel_dor.
DR InterPro; IPR008967; P53-like.
DR Pfam; PF00023; ank; 5.
DR Pfam; PF00554; RHD; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00057; NFXTNNSCPFT.
DR SMART; SM00248; ANK; 4.
DR SMART; SM00429; IPT; 1.
DR PROSITE; PS50088; ANK_REPEAT; 2.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50254; REL_2; 1.
KW ANK repeat; Alternative splicing; Repeat.
FT VARSPLIC 1 112 Missing (in isoform Maternal).
FT /FTID=VSP_050089.
SQ SEQUENCE 971 AA; 109775 MW; EAF607357381AD32 CRC64;

Db 59 NLPGNKSPHQP 70
:|||||:|
RESULT 33
Q9YBU3 PRELIMINARY; PRT; 105 AA.
ID Q9YBU3
AC Q9YBU3
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APE1506.
GN APE1506.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococccaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KI;
RX MEDLINE=99310339; PubMed=10382966;
RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Nishijima K., Nakazawa H.,
RA Hosoyama A., Fukui S., Nagai S., Funahashi T., Tanaka T., Kudoh Y.,
RA Takamiya M., Masuda S., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Yamazaki J., Nomura N., Sako Y., Kikuchi H.,
RA Nakamura Y.,
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1";
RL DNA Res. 6:83-101(1999).
DR EMBL; AF000061; BAA80505.1; --
DR PIR; C72631; C72631.
DR KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 105 AA; 11568 MW; 5E33500281A4CC0 CRC64;
Query Match 48.3%; Score 43; DB 17; Length 105;
Best Local Similarity 58.3%; Pred. No. 28;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 HLPNKSHPHDP 12
:|||||:|
Db 56 HLPNKNASHKLP 67
:|||||:|
RESULT 34
Q8BW91 PRELIMINARY; PRT; 142 AA.
ID Q8BW91
AC Q8BW91
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Weakly similar to cyclin-dependent kinase 6 (Fragment).
GN E030030106RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL; AK053193; BAC35307.1; --
DR MGP; MGI:2442914; E030030106RIK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR ProDom; PD000001; Prot_kinase; 1.

FT NON TER 1 1
SQ SEQUENCE 142 AA; 5BD3BB72815111B CRC64;
Query Match 48.3%; Score 43; DB 11; Length 142;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;
QY 3 PGKSPHRDPA 13
DB 30 PGSSVPHRQPA 40
RESULT 35
Q8BLG7 PRELIMINARY; PRT; 182 AA.
AC Q8BLG7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Weakly similar to cyclin-dependent kinase 6 (Fragment).
GN E030030106RIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK045260; BAC32285.1;
DR MGD; MGI:2442914; E030030106RIK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
FT NON TER 1
SQ SEQUENCE 182 AA; 2C0CF1C442030048 CRC64;
Query Match 48.3%; Score 43; DB 11; Length 182;
Best Local Similarity 63.6%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 PGKSPHRDPA 13
DB 29 PGSSVPHRQPA 39
RESULT 36
Q8BW77 PRELIMINARY; PRT; 184 AA.
AC Q8BW77;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE ART-4 protein homolog.
GN NOB1P OR 1700021109RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Oviduct;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs";
RL Nature 420:563-573 (2002).
DR EMBL; AK054034; BAC35627.1;
DR MGD; MGI:1914869; Nob1p.
DR InterPro; IPR002851; DUF133.
DR InterPro; IPR006596; PINC.
DR ProDom; PD013236; DUF133; 1.
DR SMART; SM00670; PINC; 1.
SQ SEQUENCE 184 AA; 20995 MW; 705BEF164881F74E CRC64;
Query Match 48.3%; Score 43; DB 11; Length 184;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 HLPGNKSPHRDPA 14
DB 129 HLPKVNPFRRSPG 142
RESULT 37
Q8L479 PRELIMINARY; PRT; 193 AA.
AC Q8L479;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE B1129G05.17 protein (B1151A10.8 protein).
GN B1129G05.17 OR B1151A10.8.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T.; Matsumoto T.; Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:B1129G05";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T.; Matsumoto T.; Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC
clone:B1151A10";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003308; BAB91793.1;
DR EMBL; AP003413; BAB91896.1;
DR Gramene; Q8L479;
SQ SEQUENCE 193 AA; 20042 MW; A6F4D87037409BC0 CRC64;
Query Match 48.3%; Score 43; DB 10; Length 193;
Best Local Similarity 63.6%; Pred. No. 53;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 LPGNKSPHRDP 12
DB 124 LPDNRQPHRRP 134
RESULT 38
Q8TV81 PRELIMINARY; PRT; 208 AA.
AC Q8TV81
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Predicted serine protein kinase homologous to Hpr protein kinase,
DE contains a Zn-ribbon.
GN MK1512.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;

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Query Match      48.3%; Score 43; DB 4; Length 211;
Best Local Similarity 46.7%; Pred. No. 58;
Matches 7: Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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